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(54) Title: COLON AND COLON CANCER ASSOCIATED POLYNUCLEOTIDES AND POLYPEPTIDES

(57) Abstract: This invention relates to newly identified colon or colon cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "colon cancer antigens", and the use of such colon cancer antigens for targeting specific cell types and/or diagnosing, detecting, preventing and treating disorders of the colon, particularly the presence of colon cancer and colon cancer metastases. This invention relates to colon cancer antigens as well as vectors, host cells, antibodies directed to colon cancer antigens and the recombinant or synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon cancer antigens of the invention. The present invention further relates to inhibiting the production and function of the polypeptides of the present invention.

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Colon and Colon Cancer Associated Polynucleotides and Polypeptides

Field of the Invention

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This invention relates to newly identified colon or colon cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "colon cancer antigens," and the use of such colon cancer antigens for targeting specific cell types and/or diagnosing, detecting, preventing and treating disorders of the colon, particularly the presence of colon cancer and colon cancer metastases. This invention relates to colon cancer antigens as well as vectors, host cells, antibodies directed to colon cancer antigens and the recombinant or synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon cancer antigens of the invention. The present invention further relates to inhibiting the production and function of the polypeptides of the present invention.

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Background of the Invention

Cell growth is a carefully regulated process which responds to specific needs of the body. Occasionally, the intricate, and highly regulated controls dictating the rules for cellular division break down. When this occurs, the cell begins to grow and divide independently of its homeostatic regulation resulting in a condition commonly referred to as cancer. In fact, cancer is the second leading cause of death among Americans aged 25-44.

Colorectal cancers are among the most common cancers in men and women in the U.S. and are one of the leading causes of death. Other than surgical resection no other systemic or adjuvant therapy is available. Vogelstein and colleagues have described the sequence of genetic events that appear to be associated with the multistep process of colon cancer development in humans (Trends Genet 9(4):138-41 (1993)). An understanding of the molecular genetics of carcinogenesis, however, has not led to preventative or therapeutic measures. It can be expected that advances in molecular genetics will lead to better risk

assessment and early diagnosis but colorectal cancers will remain a deadly disease for a majority of patients due to the lack of an adjuvant therapy. Adjuvant or systemic treatments are likely to arise from a better understanding of the autocrine factors responsible for the continued proliferation of cancer cells.

5 Colorectal carcinoma is a malignant neoplastic disease. There is a high incidence of colorectal carcinoma in the Western world, particularly in the United States. Tumors of this type often metastasize through lymphatic and vascular channels. Many patients with colorectal carcinoma eventually die from this disease. In fact, it is estimated that 62,000 persons in the United States alone die of colorectal carcinoma annually.

10 At the present time the only systemic treatment available for colon cancer is chemotherapy. However, chemotherapy has not proven to be very effective for the treatment of colon cancers for several reasons, the most important of which is the fact that colon cancers express high levels of the MDR gene (that codes for multi-drug resistance gene products). The MDR gene products actively transport the toxic substances out of the cell
15 before the chemotherapeutic agents can damage the DNA machinery of the cell. These toxic substances harm the normal cell populations more than they harm the colon cancer cells for the above reasons.

 There is no effective systemic treatment for treating colon cancers other than surgically removing the cancers. In the case of several other cancers, including breast
20 cancers, the knowledge of growth promoting factors (such as EGF, estradiol, IGF-11) that appear to be expressed or effect the growth of the cancer cells, has been translated for treatment purposes. But in the case of colon cancers this knowledge has not been applied and therefore the treatment outcome for colon cancers remains bleak.

 Thus, the discovery of new human colon and colon cancer related polynucleotides
25 and the polypeptides encoded by them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention and treatment of disorders of the colon, particularly tumors, especially of the intestine; inflammatory disorders; enterocolitis; miscellaneous intestinal inflammatory disorders; ulcerative disorders; and/or noncancerous tumors.

Summary of the Invention

This invention relates to newly identified colon and colon cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as “colon cancer antigens.” This invention relates to colon and colon cancer related polypeptides as well as vectors, host cells, antibodies directed to colon cancer antigens and the recombinant methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon cancer antigens of the invention.

Detailed Description

Tables

Table 1 summarizes some of the colon cancer antigens encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), polynucleotide sequences (contig identifier (Contig ID:) or sequence identifier (Sequence ID:) and nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of the colon and colon cancer related polynucleotides and the polypeptides encoded thereby. The first column shows the “SEQ ID NO:X” for each of the 4277 colon and colon cancer related polynucleotide sequences of the invention. The second column provides a unique “Sequence/Contig ID” identification for each of the colon and colon cancer related polynucleotide and/or polypeptide sequences. The third column, “Gene Name,” and the fourth column, “Overlap,” provide a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database and the database accession no. for the database sequence having similarity, respectively. The sixth and seventh columns provide the location (nucleotide position nos. within the sequence/contig), “Start” and “End”, in the polynucleotide sequence “SEQ ID NO:X” that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y (column five). The eighth and ninth columns provide the “%Id” (percent identity) and “%Si” (percent similarity), respectively, observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence. The tenth column provides a

unique "Clone ID:Z" for a cDNA clone related to each contig sequence. The eleventh column provides the "Cloning vector" contained in the cDNA clone ID.

Table 2 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

5 Table 3 summarizes the expression profile of polynucleotides corresponding to the clones disclosed in Table 1. The first column provides a unique clone identifier, "Clone ID", for a cDNA clone related to each contig sequence disclosed in Table 1. Column 2, "Library Codes" shows the expression profile of tissue and/or cell line libraries which express the polynucleotides of the invention. Each Library Code in column 2 represents a tissue/cell
10 source identifier code corresponding to the Library Code and Library description provided in Table 5. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. One of skill in the art could routinely use this information to identify tissues which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue
15 expression.

Table 4, column 1, provides a nucleotide sequence identifier, "SEQ ID NO:X," that matches a nucleotide SEQ ID NO:X disclosed in Table 1, column 5. Table 4, column 2, provides the chromosomal location, "Cytologic Band or Chromosome," of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact
20 matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine
25 (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). If the putative chromosomal location of the Query overlapped with the chromosomal location of a Morbid Map entry, the OMIM reference identification number of the morbid map entry is provided in Table 4, column 3, labelled "OMIM ID." A key to the OMIM reference
30 identification numbers is provided in Table 6.

Table 5 provides a key to the Library Code disclosed in Table 3. Column 1 provides the Library Code disclosed in Table 3, column 2. Column 2 provides a description of the tissue or cell source from which the corresponding library was derived.

Table 6 provides a key to the OMIM reference identification numbers disclosed in Table 4, column 3. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). Column 2 provides diseases associated with the cytologic band disclosed in Table 4, column 2, as determined using the Morbid Map database.

Table 7 indicates public ESTs, of which at least one, two, three, four, five, ten, fifteen or more of any one or more of these public EST sequences are optionally excluded from certain embodiments of the invention.

Table 8 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in each of the preferred ORFs (SEQ ID NO:Y) encoded by the colon or colon cancer related polynucleotides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). Colon and/or colon cancer related polypeptides shown in Table 1 may possess one or more antigenic epitopes comprising residues described in Table 8. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown described in Table 8 correspond to the amino acid sequences for each colon and/or colon cancer related polypeptide sequence shown in the Sequence Listing.

Table 9 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. In addition to the individual cDNA clone deposits, the cDNA clones were deposited at the American Type Culture Collection (hereinafter "ATCC"). As mentioned below, Table 1 correlates the Clone ID names with SEQ ID NOs. Furthermore, it is possible to retrieve a given cDNA clone from the ATCC deposit by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention
5 comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4,
10 3, 2, or 1 genomic flanking gene(s).

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, the complement thereof, or the cDNA clone within the pool of cDNA clones deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight
15 incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of
20 the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M
25 NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the
30 inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations.

The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA⁺ sequences (such as any 3' terminal polyA⁺ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and

they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence. SEQ ID NO:X is identified by an integer specified in column 1 of Table 1. A translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X, SEQ ID NO:Y, is shown in column nine of Table 1. There are 4277 colon and/or colon cancer related polynucleotide sequences described in Table 1 and shown in the sequence listing. Likewise there are 4277 colon and/or colon cancer related polypeptide sequences shown in the sequence listing, one polypeptide sequence for each of the polynucleotide sequences. The polynucleotide sequences are shown in the sequence listing immediately followed by all of the polypeptide sequences.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than

about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

The polynucleotides of the invention may be arrayed onto a nitrocellulose filter and screened with labelled mRNA which has been isolated from particular normal or diseased tissues, as described in Example 3. Known polynucleotide sequences are included in the array as hybridization controls, either because of their demonstrated tissue specificity or because they represent known surface molecules which may after further study show a predominant tissue expression and be useful antibody targets.

10 **Colon and/or Colon Cancer Related Polynucleotides and Polypeptides of the Invention**

It has been discovered herein that the polynucleotides described in Table 1 are expressed at significantly enhanced levels in human colon and colon cancer tissues. Accordingly, such polynucleotides, polypeptides encoded by such polynucleotides, and antibodies specific for such polypeptides find use in the prediction, diagnosis, treatment, and prevention of disorders related to the colon, including, but not limited to colon cancer, as more fully described below.

Table 1 summarizes some of the polynucleotides encompassed by the invention (including polynucleotide sequences (SEQ ID NO:X) and the related cDNA clones (Clone ID:Z)) and further summarizes certain characteristics of these colon and/or colon cancer related polynucleotides, and the polypeptides encoded thereby.

Table 1

Seq ID No:X	Sequence/ Contig ID	Gene Name	Overlap	AA SEQ ID No:Y	HGS Nucleotide Start End	% Id	% Si	Clone ID:Z	Vector
1	390631	(AF051311) Ras-GAP SH3 binding protein [Homo sapiens] >sp O60606 O60606 RAS-GAP SH3 BINDING PROTEIN. Length = 449	gb AAC15705.1	4278	3 326	96	96	HTWEP07	pSport1
2	410299			4279	75 251			HODBA26	Uni-ZAP XR
3	456200			4280	3 443			HPMEF95	Uni-ZAP XR
4	456438	hypothetical protein (L1H 3" region) - human Length = 1280	pir B34087 B34087	4281	1 513	43	58	HCFCY21	pSport1
5	467315			4282	278 412			HMKCO08	pSport1
6	471563			4283	8 181			HBAGS04	pSport1
7	488131			4284	148 342			HALSQ75	Uni-ZAP XR
8	490848			4285	241 522			HMVBD21	pSport1
9	500696	Similar to Volbox carteri extensin (S22697) [Homo sapiens] >gb AAD33052.1 AF134303_1 (AF134303) Scar1 [Homo sapiens] >sp Q92558 Y269_HUMAN HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269. >sp AAD33052 AAD33052 Scar1. Length = 559	dbj BAA13399.1	4286	2 187	78	78	HKIMD67	Lambda ZAP II
10	504559			4287	66 152			HOOAE34	pBluescript
11	506406			4288	34 420			HHSDD62	Uni-ZAP XR
12	506619			4289	85 1119			HSLGZ32	Uni-ZAP XR
13	507852			4290	211 456			HCENL15	Uni-ZAP XR
14	509423			4291	540 755			HCQA138	Lambda ZAP II

15	509734				4292	197	316			HPMDT48	Uni-ZAP XR
16	509856				4293	172	345			HADFX66	pSport1
17	524721				4294	318	434			HONAI01	pBluescript SK-
18	524901				4295	508	819			HEBBT54	Uni-ZAP XR
19	527600				4296	11	232			H2CBG63	pBluescript SK-
20	527827				4297	159	1			HHSBA79	Uni-ZAP XR
21	529050				4298	224	388			HCQAQ89	Lambda ZAP II
22	529465				4299	241	363			HELGJ91	Uni-ZAP XR
23	530612				4300	3	239			HADBE91	Uni-ZAP XR
24	530773				4301	250	450			HSAAX52	pBluescript SK-
25	532810	long-chain acyl-CoA synthetase [Homo sapiens] >pir JX0202 JX0202 long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) - human >sp P33121 LCFB_HUMAN LONG-CHAIN-FATTY-ACID--COA LIGASE 2 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 2) (LACS 2). Length = 698	dbj BAA00931.1		4302	2	403	100	100	HACCE33	Uni-ZAP XR
26	533242	5-aminolevulinate synthase precursor [Homo sapiens] >emb CAA15886.1 (AL020991) dJ884M20.2 [Homo sapiens] >gb AAC39838.1 (AF068624) 5-aminolevulinate synthase 2 [Homo sapiens] >pir S16347 SYHUA5 5-aminolevulinate synthase (EC 2.3.1.37) precursor, erythro	emb CAA42916.1	4303	562	1626	100	100	HE8DA85	Uni-ZAP XR	

27	541126	guanylate binding protein isoform I [Homo sapiens] >pir A41268 A41268 guanine nucleotide-binding protein 1 - human >sp P32455 GBP1_HUMAN INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1). Length = 592	gb AAA35871.1	4304	140	622	92	93	HSKII86	pBluescript
28	542268			4305	259	585			HUSGI39	pSport1
29	547920	aspartyl-tRNA synthetase [Homo sapiens] >pir A34393 SYHUDT aspartate--tRNA ligase (EC 6.1.1.12) - human >sp P14868 SYD_HUMAN ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS). Length = 500	gb AAA35567.1	4306	133	240	100	100	HKIMB44	Lambda ZAP II
30	549642			4307	345	611			HBMVJ62	Uni-ZAP XR
31	550207			4308	184	390			HBXFC78	ZAP Express
32	552115			4309	41	262			HE2FR32	Uni-ZAP XR
33	552465	(AL050037) hypothetical protein [Homo sapiens] >emb CAB43247.1 (AL050037) hypothetical protein [Homo sapiens] >pir T08715 T08715 hypothetical protein DKFZp566I1024.1 - human (fragment) >sp Q9Y405 Q9Y405 HYPOTHETICAL 34.8 KD PROTEIN (FRAGMENT). Length = 3	emb CAB43247.1	4310	696	1208	80	81	HKACD58	pCMVSPORT 2.0
34	554369	precursor polypeptide (AA -29 to 315) [Homo sapiens] >pir S14902 DEHUMT methylenetetrahydrofolate dehydrogenase (NAD+) (EC 1.5.1.15) / methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9) precursor - human >sp P13995 MTDC_HUMAN BIFUNCTIONAL METHYLENETETRA	emb CAA3443.1	4311	208	339	77	82	HDAAB62	pSport1

35	557152				4312	379	600				HEPBA24	Uni-ZAP XR
36	557230				4313	222	530				HOGBL08	pCMVSPORT 2.0
37	558366	rTSbeta [Homo sapiens] >sp Q15407 Q15407 RTSBETA. Length = 416	emb CAA6176 1.1	4314	2	379	97	97	97		HCYBD62	pBluescript SK-
38	570796	protein [Homo sapiens] >sp Q14288 Q14288 HYPOTHETICAL PROTEIN (FRAGMENT). Length = 641	gb AAA88038. 1	4315	773	889	51	63			H2CBD20	pBluescript SK-
39	573181			4316	3	254					HCQAT53	Lambda ZAP II
40	573199	gamma-glutamyl transpeptidase [Homo sapiens] >emb CAA07485.1 (AJ007378) gamma- glutamyltransferase [Homo sapiens] {SUB 193-244} >emb CAA07487.1 (AJ007380) gamma- glutamyltransferase [Homo sapiens] {SUB 296-340} Length = 569	gb AAA35899. 1	4317	2	628	91	91			HETDN09	Uni-ZAP XR
41	573793			4318	283	423					HCYBE04	pBluescript SK-
42	573796	NPAT [Homo sapiens] >dbj BAA11861.1 NPAT [Homo sapiens] >sp Q16580 Q16580 NPAT (E14 AND A-T PROTEINS). Length = 1427	dbj BAA21367 .1	4319	2	892	96	96			HDPFI14	pCMVSPORT 3.0
43	574094	ORF YGR010w [Saccharomyces cerevisiae] >pir S64299 S64299 probable membrane protein YGR010w - yeast (Saccharomyces cerevisiae) >sp P53204 YGI5_YEAST HYPOTHETICAL 44.9 KD PROTEIN IN SEC9-MSB2 INTERGENIC REGION. Length = 395	emb CAA9699 3.1	4320	31	423	41	68			HJBCD90	pBluescript SK-
44	574927	methionyl-tRNA synthetase, mitochondrial [Schizosaccharomyces pombe] >pir T38454 T38454 methionyl-tRNA synthetase, mitochondrial - fission yeast (Schizosaccharomyces pombe) >sp O14000 O14000 PUTATIVE METHIONYL- TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TR	emb CAB1168 0.1	4321	2	226	48	65			HAIAB40	pCMVSPORT 3.0

45	575139				4322	151	429				H2MCA74	pBluescript SK-
46	575591	ATP:citrate lyase [Homo sapiens] >sp Q13037 Q13037 ATP:CITRATE LYASE. Length = 1101	gb AAB60340.1	4323	3	401	80	81	80	81	HWBAX42	pCMVSPORT 3.0
47	576132			4324	1	255					HLMMR55	Lambda ZAP II
48	577390			4325	59	322					HNFGN91	Uni-ZAP XR
49	577685			4326	345	557					HTWDI90	pSport1
50	578079			4327	83	256					HCQAB18	Lambda ZAP II
51	578660			4328	3	239					HELHI45	Uni-ZAP XR
52	580860	ribosomal protein L23a [Homo sapiens] >gb AAA35681.1 homology to rat ribosomal protein L23 [Homo sapiens] {SUB 10-156} Length = 156	gb AAA03341.1	4329	528	406	64	80			HNHVDV16	Uni-ZAP XR
53	581143			4330	2	361					HOAAD32	Uni-ZAP XR
54	584899			4331	10	285					HSAVM80	Uni-ZAP XR
55	600669	M130 antigen [Homo sapiens] >emb CAB45233.1 CD163 [Homo sapiens] >pir I38003 S36077 M130 antigen - human >sp Q07898 Q07898 M130 ANTIGEN PRECURSOR. Length = 1116	emb CAA8054.1.1	4332	1	408	85	86			HWLMA51	pSport1
56	611839			4333	55	231					HE8BQ01	Uni-ZAP XR
57	614078			4334	273	428					HELHD03	Uni-ZAP XR
58	614554			4335	215	340					HBMCT70	pBluescript
59	615029			4336	5	157					HL YDF04	pSport1
60	615590			4337	136	321					HDSAP04	Uni-ZAP XR

61	630230	(AF098799) RanBP7/importin 7 [Homo sapiens] >sp O95373 O95373 RANBP7/IMPORTIN 7. >emb CAB70698.1 (AL137335) hypothetical protein [Homo sapiens] {SUB 831-1038} Length = 1038	gb AAC68903. 1	4338	1	423	83	85	HWBFZ21	pCMVSPORT 3.0
62	637548			4339	492	764			HCQBH72	Lambda ZAP II
63	637605			4340	401	604			HELGH31	Uni-ZAP XR
64	638125	(AC004876) similar to neuro-endocrine specific protein VGF; similar to CAA73210 (PID:g2244659) [Homo sapiens] >sp AAD45830 AAD45830 WUGSC:H_DJ0747G18.3 protein. Length = 615	gb AAD45830. 1 AC0048	4341	199	573	68	68	HNHEU34	Uni-ZAP XR
65	638188			4342	105	254			HJMAF30	pCMVSPORT 3.0
66	638249	(AF026198) putative protein 2 [Fugu rubripes] >pir T30536 T30536 hypothetical protein 2 - Fugu rubripes (fragment) >sp O73698 O73698 HYPOTHETICAL 21.5 KD PROTEIN (FRAGMENT). Length = 187	gb AAC15584. 1	4343	3	821	49	63	HWBBK93	pCMVSPORT 3.0
67	638319	(AF118082) PRO1902 [Homo sapiens] >sp AAF22026 AAF22026 PRO1902. Length = 84	gb AAF22026. 1 AF1180	4344	1185	1400	67	73	HFXAK32	Lambda ZAP II
68	651380			4345	759	1040			HUSIT18	pSPORT
69	651876	K-ras oncogene protein [Homo sapiens] Length = 188	gb AAB41942. 1	4346	33	308	78	78	HMWBH51	Uni-ZAP XR
70	653175	(AL050120) hypothetical protein [Homo sapiens] >emb CAB43281.1 (AL050120) hypothetical protein [Homo sapiens] >pir T08766 T08766 hypothetical protein DKFZp586D211.1 - human (fragment) >sp CAB43281 CAB43281 Hypothetical 15.3 kd protein (fragment). Length	emb CAB4328 1.1	4347	1	198	100	100	HCQAW11	Lambda ZAP II
71	655544			4348	1	153			HPRAS01	Uni-ZAP XR

72	656722						4349	331	537				HWBBC13	pCMVSPORT 3.0
73	659801	(AB014509) Nck-associated protein 1 (Nap1) [Homo sapiens] >sp Q9Y2A7 Q9Y2A7 NCK-ASSOCIATED PROTEIN 1 (NAP1). Length = 1128	dbj BAA77295.1	4350	120	1058	94	94				94	HNTBM67	pCMVSPORT 3.0
74	660020			4351	321	491							HDPKC15	pCMVSPORT 3.0
75	661600			4352	132	341							HMAHP16	Uni-ZAP XR
76	664481	(AC005003) similar to zinc finger protein MAZ [Homo sapiens]; similar to AAB04121.1 (PID:g995935) >sp AAF01349 AAF01349 WUGSC:H_DJ400N23.1 protein. >emb CAB51404.1 (AL096880) hypothetical protein [Homo sapiens] {SUB 26-641} Length = 641	gb AAF01349.1 AC0050	4353	1	279	84	84					HCE1D45	Uni-ZAP XR
77	665154			4354	239	448							HBIBV81	Uni-ZAP XR
78	666790			4355	2	277							HSXBP02	Uni-ZAP XR
79	668040			4356	407	826							HCQCO19	Lambda ZAP II
80	668586			4357	169	342							HHENT19	pCMVSPORT 3.0
81	668717	(AF151895) CGI-137 protein [Homo sapiens] >gb AAF14860.1 AF110777_1 (AF110777) adrenal gland protein AD-004 [Homo sapiens] >sp Q9Y3D8 YCD7_HUMAN HYPOTHETICAL PROTEIN CGI-137. >sp AAF14860 AAF14860 Adrenal gland protein AD-004. Length = 172	gb AAD34132.1 AF1518	4358	2	535	100	100					HMTMB52	PCR II
82	668753			4359	76	171							HOGAL19	pCMVSPORT 2.0
83	671361	(AK000585) unnamed protein product [Homo sapiens] Length = 285	dbj BAA91271.1	4360	110	280	59	69					HCQAG50	Lambda ZAP II

84	674203					4361	280	402				HDPLC22	pCMV/Sport 3.0
85	674745	(AB011098) KIAA0526 protein [Homo sapiens] >emb CAA69942.1 serine palmitoyltransferase, subunit II [Homo sapiens] >gb AAD09621.1 (AF111168) serine palmitoyl transferase, subunit II [Homo sapiens] >sp O15270 LCB2_HUMAN SERINE PALMITOYLTRANSFERASE 2 (EC 2	dbj BAA25452 .1	4362	71	1243	94	94				HBMXO90	Uni-ZAP XR
86	674761			4363	194	379						HLMIS22	Lambda ZAP II
87	677212	(AF136450) goodpasture antigen-binding protein [Homo sapiens] >sp Q9Y5P4 Q9Y5P4 GOODPASTURE ANTIGEN-BINDING PROTEIN (EC 2.7.1.37). Length = 624	gb AAD30288. 1 AF1364	4364	1	675	98	98				HE8AG73	Uni-ZAP XR
88	683259			4365	63	404						HCYBF14	pBluescript SK-
89	685895			4366	1	168						HKAAS37	pCMV/Sport 2.0
90	688040	(AL122091) hypothetical protein [Homo sapiens] >emb CAB59261.1 (AL122091) hypothetical protein [Homo sapiens] >pir T34522 T34522 hypothetical protein DKFZp566D244.1 - human (fragment) >sp CAB59261 CAB59261 Hypothetical 64.0 kd protein (fragment). Length	emb CAB5926 1.1	4367	1	1167	72	81				HBXFP72	ZAP Express
91	688044	(AL110226) hypothetical protein [Homo sapiens] >emb CAB53684.1 (AL110226) hypothetical protein [Homo sapiens] >pir T14764 T14764 hypothetical protein DKFZp434H204.1 - human (fragment) >sp CAB53684 CAB53684 Hypothetical 96.7 kd protein (fragment). Length	emb CAB5368 4.1	4368	394	978	38	51				HFIYP15	pSport1

92	688077	(AF047440) ribosomal protein L33-like protein [Homo sapiens] >sp O75394 O75394 RIBOSOMAL PROTEIN L33-LIKE PROTEIN. Length = 65	gb AAC39891.1	4369	1	276	100	100	HEBAG86	Uni-ZAP XR
93	691124			4370	230	418			HLDNM81	pCMVSPORT 3.0
94	691721			4371	139	411			HARNC71	pCMVSPORT 3.0
95	693582			4372	237	428			HE2OC31	Uni-ZAP XR
96	696007	ring finger protein - fruit fly (Drosophila melanogaster) Length = 222	pir JC4296 JC4296	4373	3	767	41	62	HTXKQ20	Uni-ZAP XR
97	697955			4374	34	135			HE2OK20	Uni-ZAP XR
98	698068			4375	3	242			HMWIW31	Uni-ZAP XR
99	702853			4376	113	391			HCEEH33	Uni-ZAP XR
100	703700			4377	1	258			HAGBL85	Uni-ZAP XR
101	705461	(AC007785) BC282485_1 [Homo sapiens] >sp Q9Y6R9 Q9Y6R9 BC282485_1 (FRAGMENT). Length = 477	gb AAD38244.1 AC0077	4378	2	589	96	96	HLWAY38	pCMVSPORT 3.0
102	705692	unnamed protein product [unidentified] Length = 309	emb CAB4218.7.1	4379	2	211	64	74	H2LAN34	pBluescript SK-
103	706204			4380	914	1267			HBMTX67	Uni-ZAP XR
104	707161			4381	76	144			HE2IE28	Uni-ZAP XR
105	707464	spectrin SH3 domain binding protein 1 [Homo sapiens] >sp O76049 O76049 SPECTRIN SH3 DOMAIN BINDING PROTEIN 1. Length = 508	gb AAC39757.1	4382	185	703	88	89	HBXCG73	ZAP Express
106	709015	PRAJA1 [Mus musculus] >sp O55176 O55176 PRAJA1. Length = 424	gb AAC00205.1	4383	2	412	97	98	HATAN68	Uni-ZAP XR
107	709518			4384	1	159			HAGDD59	Uni-ZAP XR

108	711769				4385	102	323				HBFI65	Uni-ZAP XR
109	711840				4386	182	427				HSNAL84	Uni-ZAP XR
110	711878	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 ALU7_HUMAN		4387	1	189	79	85		HCND41	pSport1
111	712638				4388	254	574				HPXAA41	pBluescript
112	713301	!!!! ALU SUBFAMILY SB WARNING ENTRY !!!! Length = 587	sp P39189 ALU2_HUMAN		4389	3	149	75	77		HHSFO42	Uni-ZAP XR
113	714156				4390	600	992				HCEIE94	Uni-ZAP XR
114	714877				4391	10	168				HWLQA43	pSport1
115	715343				4392	29	241				HFXHM92	Lambda ZAP II
116	716212				4393	299	703				HHSGE44	Uni-ZAP XR
117	717222	(AK000900) unnamed protein product [Homo sapiens] Length = 136	dbj BAA91415.1		4394	1	402	37	37		HWLQI33	pSport1
118	718259				4395	527	667				HFLAW90	pSport1
119	719829				4396	71	190				HOSEP43	Uni-ZAP XR
120	721985				4397	3	101				HUSGY48	pSport1
121	722249	cerebroside sulfotransferase [Homo sapiens] >dbj BAA89503.1 (AB029901) cerebroside sulfotransferase [Homo sapiens] >gb AAD50517.1 AC005006.2 (AC005006) cerebroside sulfotransferase [Homo sapiens] >sp Q99999 Q99999 CEREBROSIDE SULFOTRANSFERASE. >sp BAA895	dbj BAA13673.1		4398	3	1319	42	61		HSLEC18	Uni-ZAP XR
122	722258	olfactomedin [Rana catesbeiana] >pir A47442 A47442 olfactomedin precursor - bullfrog >sp Q07081 OLFM_RANCA OLFACTOMEDIN PRECURSOR (OLFACTORY MUCUS PROTEIN). Length = 464	gb AAA49527.1		4399	1236	1547	37	55		HUFAC36	pSport1

123	723136	put. ring protein [Homo sapiens] >sp Q99579 Q99579 PUTATIVE RING PROTEIN. Length = 236	emb CAA6916 5.1	4400	571	143	83	87	HHFHB49	Uni-ZAP XR
124	725110			4401	174	323			HFIBH05	pSport1
125	725201	(AB020676) KIAA0869 protein [Homo sapiens] >sp O94946 O94946 KIAA0869 PROTEIN (FRAGMENT). Length = 888	dbj BAA74892 .1	4402	1	294	98	100	HKIAA57	Uni-ZAP XR
126	726122			4403	309	530			HRKAB52	pBluescript
127	727365			4404	1	915			HPCAN95	Uni-ZAP XR
128	729143			4405	609	821			HCQCV54	Lambda ZAP II
129	729231			4406	345	602			HLJEA54	pCMV Sport 1
130	731881	!!!! ALU SUBFAMILY J WARNING ENTRY !!!! Length = 591	sp P39188 AL U1_HUMAN	4407	361	462	56	65	HTWCR70	pSport1
131	732280	(AB002349) KIAA0351 [Homo sapiens] >sp O15059 O15059 KIAA0351. Length = 557	dbj BAA20808 .1	4408	155	598	81	82	HSXDD55	Uni-ZAP XR
132	732932			4409	295	483			HSTAB63	Uni-ZAP XR
133	733034	expressed-Xq28STS protein [Homo sapiens] Length = 358	gb AAF33529. 1 U82695	4410	305	553	86	89	H6BSI11	Uni-ZAP XR
134	734012			4411	64	180			HDQPP57	pCMV Sport 3.0
135	735603			4412	991	1224			HAGEX59	Uni-ZAP XR
136	739061			4413	436	621			HAVMG19	Other
137	741134	protein [Homo sapiens] >sp Q14288 Q14288 HYPOTHETICAL PROTEIN (FRAGMENT). Length = 641	gb AAA88038. 1	4414	676	314	61	69	HLEAL50	Uni-ZAP XR
138	741257	protein [Homo sapiens] >sp Q14287 Q14287 HYPOTHETICAL PROTEIN (FRAGMENT). Length = 157	gb AAA88036. 1	4415	136	195	41	52	HCPAC07	Uni-ZAP XR
139	741804			4416	196	441			HOSEQ61	Uni-ZAP XR

140	742220	initiation factor 5A [Gallus gallus] >pir 50227 A42156 translation initiation factor eIF-5A I - chicken >sp Q07460 IF51_CHICK INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D). Length = 153	gb AAA17444.1	4417	3	455	83	88	HCROB09	pSport1
141	744605			4418	255	479			HFIZP62	pSport1
142	744687			4419	231	374			HBMTK19	Uni-ZAP XR
143	745368			4420	1	114			HAGDG84	Uni-ZAP XR
144	747870			4421	343	519			HCABQ86	Uni-ZAP XR
145	750486			4422	694	897			HSAXE65	Uni-ZAP XR
146	751119	Impact [Mus musculus] >sp O55091 O55091 IMPACT PROTEIN. Length = 318	dbj BAA35139.1	4423	2	481	68	77	HE8OC67	Uni-ZAP XR
147	752557			4424	1	210			HKAHA68	pCMVSPORT 2.0
148	753226	PROTEIN (FRAGMENT). Length = 184	sp Q29229 Q29229	4425	25	810	38	51	HSFAG23	Uni-ZAP XR
149	754269			4426	737	949			HDTAT69	pCMVSPORT 2.0
150	756466	(AF099731) connexin 31.1 [Homo sapiens] >sp O95377 CXB5_HUMAN GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 31.1) (CX31.1). Length = 273	gb AAC95472.1	4427	3	293	96	96	HAICM70	Uni-ZAP XR
151	756538	homologous to mouse Rsu-1; putative [Homo sapiens] >pir I60122 I60122 rsu-1 homolog - human >sp Q15404 RSU1_HUMAN RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1). Length = 277	gb AAA60292.1	4428	93	1151	100	100	HMC670	Uni-ZAP XR
152	756649	The ha2022 gene product is novel. [Homo sapiens] >sp Q14699 Y084_HUMAN HYPOTHETICAL PROTEIN KIAA0084 (HA2022) (FRAGMENT). Length = 648	dbj BAA07644.1	4429	1	135	100	100	HE8EX74	Uni-ZAP XR

153	757213	(AK001459) unnamed protein product [Homo sapiens] Length = 245	dbj BAA91704.1	4430	3	362	84	85	HACBN11	Uni-ZAP XR
154	757508	PIBF1 protein [Homo sapiens] >sp O95664 O95664 PIBF1 PROTEIN. Length = 758	emb CAA7084.4.1	4431	3	734	87	89	HTTBS70	Uni-ZAP XR
155	757532			4432	98	385			HCRNF04	pSport1
156	757980			4433	365	622			HETIS94	Uni-ZAP XR
157	760141	(AK000743) unnamed protein product [Homo sapiens] Length = 573	dbj BAA91356.1	4434	2	763	79	79	HDPXJ71	pCMVSPORT 3.0
158	761491			4435	153	377			HRABS72	pCMVSPORT 3.0
159	761724			4436	43	183			HYAAAX74	pCMVSPORT 3.0
160	762027			4437	2	661			HSKXC19	pBluescript
161	764179			4438	112	243			HF6SG75	pBluescript
162	766961			4439	332	472			HCYBG95	pBluescript SK-
163	767593			4440	327	497			HCECT76	Uni-ZAP XR
164	768034			4441	632	919			HEIBB38	Uni-ZAP XR
165	769965	M-phase phosphoprotein 9 [Homo sapiens] >sp Q99550 MPP9_HUMAN M-PHASE PHOSPHOPROTEIN 9 (FRAGMENT). Length = 214	emb CAA6691.1.1	4442	1	465	98	99	HHEMK76	pCMVSPORT 3.0
166	771486			4443	374	664			HE9PB77	Uni-ZAP XR
167	772044	DNA polymerase epsilon catalytic subunit [Homo sapiens] >pir G02434 G02434 DNA-directed DNA polymerase (EC 2.7.7.7) epsilon catalytic chain - human Length = 2285	gb AAA90924.1	4444	129	611	100	100	HTLDW36	Uni-ZAP XR

168	772357	ect2 [Mus musculus] >pir S32372 S32372 transforming protein (ect2) - mouse >sp Q07139 ECT2_MOUSE ECT2 PROTEIN (ECT2 ONCOGENE). Length = 738	gb AAA37536.1	4445	403	738	86	93	HMWHN43	Uni-ZAP XR
169	772876	(AK000771) unnamed protein product [Homo sapiens] Length = 202	dbj BAA91373.1	4446	59	820	99	99	HUSIR49	pSport1
170	774019	(AF061739) [Homo sapiens] >sp O95792 O95792 HYPOTHETICAL 20.1 KD PROTEIN. Length = 186	gb AAD17528.1	4447	14	520	75	75	HE9HY44	Uni-ZAP XR
171	774244	(AL009196) /prediction=(method:"genefinder", version:"084"); /prediction=(method:"genscan", version:"1.0"); /match=(desc:"LD09991.5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD09991 5prime, mRNA seque>	emb CAA1571.2.1	4448	2	1123	71	86	HTTEL19	Uni-ZAP XR
172	774516	(AK000482) unnamed protein product [Homo sapiens] Length = 572	dbj BAA91194.1	4449	1	438	54	74	HMCFS02	Uni-ZAP XR
173	775355			4450	1599	1781			HDTBY31	pCMVSPORT 2.0
174	775367			4451	142	228			HUSXPI5	pSport1
175	775791			4452	588	911			HSAWS31	Uni-ZAP XR
176	777319			4453	283	477			HE8OV83	Uni-ZAP XR
177	778434	stress-activated protein kinase-3 [Homo sapiens] >emb CAB51538.1 (AL022328) dJ402G11.1 (mitogen activated protein kinase 12 (PRKM11)) [Homo sapiens] >sp P53778 MK12_HUMAN MITOGEN-ACTIVATED PROTEIN KINASE 12 (EC 2.7.1.-) (EXTRACELLULAR SIGNAL- REGULATED KI	emb CAA7151.1.1	4454	2	880	96	96	HL3AD81	Uni-ZAP XR

178	778583	(AF000198) weak similarity to HSP90 [Caenorhabditis elegans] >pir T15138 T15138 hypothetical protein T28F2.4 - Caenorhabditis elegans >sp O01658 O01658 SIMILARITY TO HSP90. Length = 817	gb AAB53055. 1	4455	3	248	29	52	HHHQ03	pCMVSPORT 3.0
179	779480			4456	331	546			HTXF140	Uni-ZAP XR
180	779588			4457	49	162			HBIMB82	pCMVSPORT 3.0
181	781085			4458	2300	2641			HTTEW79	Uni-ZAP XR
182	781286			4459	149	289			HLJB183	pCMVSPORT 1
183	781366			4460	261	605			HSAWU83	Uni-ZAP XR
184	781376			4461	23	340			HADFW62	pSPORT1
185	781832			4462	587	733			HSNAK79	Uni-ZAP XR
186	782276	(AB032969) KIAA1143 protein [Homo sapiens] >sp BAA86457 BAA86457 KIAA1143 protein (fragment). Length = 116	dbj BAA86457 .1	4463	2	472	71	71	HSUBX87	Uni-ZAP XR
187	782358			4464	1008	1289			HATEF13	Uni-ZAP XR
188	783413	D9 splice variant 1 [Mus musculus] >sp O08693 O08693 D9 SPLICE VARIANT 1. Length = 111	gb AAB53635. 1	4465	1	591	80	88	HEBFR23	Uni-ZAP XR
189	783668			4466	171	464			HARMP12	pCMVSPORT 3.0
190	783677			4467	240	380			HJMBT13	pCMVSPORT 3.0
191	785087	beta-galactosidase alpha peptide [Cloning vector pSport2] Length = 114	gb AAA67217. 1	4468	606	815	95	95	HEAAK74	Uni-ZAP XR
192	785328	unnamed protein product [unidentified] >emb CAB42218.1 unnamed protein product [unidentified] {SUB 62-446} Length = 446	emb CAB4221 2.1	4469	388	609	91	95	HAMGI86	pCMVSPORT 3.0

193	785465					4470	2	535				HDPCN86	pCMVSPORT 3.0
194	788626	(AB028639) PalBH [Homo sapiens] >sp Q9Y6W3 Q9Y6W3 PALBH (EC 3.4.22.17). Length = 813	dbj BAA78730 .1	4471	399	79	98	98	98	98	98	HMCGR90	Uni-ZAP XR
195	788838	(AL132980) putative protein [Arabidopsis thaliana] >sp CAB62631 CAB62631 Hypothetical 29.5 kd protein. Length = 263	emb CAB6263 1.1	4472	2	388	30	52	388	30	52	HHBFM33	pCMVSPORT 1
196	789286			4473	108	209						HSLF109	Uni-ZAP XR
197	789419			4474	141	410						HFIAX76	pSPORT
198	789631			4475	192	320						HLICN93	pCMVSPORT 1
199	789872			4476	3	314						HCFBE51	pSPORT
200	790190	EYA1A [Homo sapiens] >emb CAA71309.1 EYA1A [Homo sapiens] Length = 559	emb CAA7130 9.1	4477	2249	1989	90	94	1989	90	94	HFEAU63	Uni-ZAP XR
201	790547	PAP-1 [Mus musculus] >sp P97762 P97762 PAP-1. Length = 213	dbj BAA11319 .1	4478	2	313	96	98	313	96	98	HAFBC92	pBluescript SK-
202	791155			4479	168	545						HE9SD26	Uni-ZAP XR
203	791220			4480	1893	2102						HFIZG43	pSPORT
204	791749			4481	161	283						HDPUX67	pCMVSPORT 3.0
205	792034			4482	64	222						HVAAA93	pSPORT
206	792557	(AB004066) DEC1 [Homo sapiens] >pir JCS547 JCS547 basic helix-loop-helix factor DEC1 - human >sp O14503 O14503 DEC1. Length = 412	dbj BAA21720 .1	4483	231	470	92	93	470	92	93	HAMFQ15	pCMVSPORT 3.0
207	792624	PACT [Mus musculus] >sp P70287 P70287 RETINOBLASTOMA BINDING PROTEIN 6 (PACT) (FRAGMENT). Length = 1587	gb AAB49620. 1	4484	1	465	68	78	465	68	78	HADCW71	pSPORT

208	793437	actVA 4 [Streptomyces coelicolor A3(2)] >pir S18542 S18542 hypothetical protein 4 - Streptomyces coelicolor >sp Q53906 Q53906 6 ACTVA REGION GENES OF THE ACTINORHODIN BIOSYNTHETIC GENE CLUSTER. Length = 294	emb CAA4164 .0.1	4485	215	3	47	57	HCHMB04	pSportl
209	795184			4486	162	323			HLQAX49	Lambda ZAP II
210	795744	cytochrome c oxidase subunit II [Pan troglodytes] >sp P26457 COX2_PANPA CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1). Length = 227	gb AAA20069. 1	4487	3	101	96	100	HMAJP26	Uni-ZAP XR
211	796023			4488	842	1399			HBJEA52	Uni-ZAP XR
212	796181			4489	268	669			HPSNE17	pSportl
213	797079	!!!! ALU SUBFAMILY SP WARNING ENTRY !!!! Length = 593	sp P39193 AL U6_HUMAN	4490	1	174	75	79	HTECB93	Uni-ZAP XR
214	797477	!!!! ALU SUBFAMILY SB WARNING ENTRY !!!! Length = 587	sp P39189 AL U2_HUMAN	4491	1376	1450	85	90	HCYBE25	pBluescript SK-
215	797486	(AB006781) galectin-4 [Homo sapiens] >gb AAB86590.1 galectin-4 [Homo sapiens] >gb AAC51763.1 (AF014838) galectin-4 [Homo sapiens] >sp P56470 LEG4_HUMAN GALECTIN-4 (LACTOSE-BINDING LECTIN 4) (L-36 LACTOSE BINDING PROTEIN) (L36LBP). >sp AAB86590 AAB86590	dbj BAA22165 .1	4492	603	1655	93	93	HGAMA30	pSportl
216	797747			4493	3	251			HRACH60	pCMV Sport 3.0
217	800085	oncostatin M [Homo sapiens] >gb AAC05173.1 (AC004264) oncostatin M precursor [Homo sapiens] >pir A32489 A32489 oncostatin M precursor - human >sp P13725 ONCM_HUMAN ONCOSTATIN M PRECURSOR (OSM). Length = 252	gb AAA36388. 1	4494	1	273	73	75	HNFI254	pBluescript
218	801919	(AK000496) unnamed protein product [Homo sapiens] Length = 239	dbj BAA91205 .1	4495	2792	2899	55	64	HMSCL38	Uni-ZAP XR

219	805448					4496	51	200				HDQGA42	pCMV/Sport 3.0
220	806690					4497	125	349				HFIY89	pSport1
221	810870	thrombospondin-4 [Homo sapiens] >pir A55710 TSHUP4 thrombospondin 4 precursor - human >sp P35443 TSP4_HUMAN THROMBOSPONDIN 4 PRECURSOR. Length = 961	emb CAA7963 .5.1			4498	2	1333	90	90		HBOEB83	pSport1
222	811047	VCP-like ATPase [Thermoplasma acidophilum] >pir T37458 T37458 VCP-like ATPase - Thermoplasma acidophilum >sp O05209 O05209 VCP-LIKE ATPASE. Length = 745	gb AAC45089. 1			4499	184	1257	47	70		HMEBY61	Lambda ZAP II
223	812745	(AB000549) alpha,-antitrypsin-like protein [Tamias sibiricus] >sp O54760 ALSI_TAMSI ALPHA-1- ANTITRYPSIN-LIKE PROTEIN CM55-SI PRECURSOR. Length = 413	dbj BAA24419 .1			4500	2	1339	43	63		HETDK50	Uni-ZAP XR
224	812755	(AF007791) secreted cement gland protein XAG-2 homolog [Homo sapiens] >gb AAC82614.1 (AF038451) secreted cement gland protein XAG-2 homolog [Homo sapiens] >gb AAF22484.1 AF088867_1 (AF088867) putative secreted protein XAG [Homo sapiens] >pir JE0350 JE035	gb AAC77358. 1			4501	2	541	60	78		HSIEH63	Uni-ZAP XR
225	812871					4502	1	87				HLTDL01	Uni-ZAP XR
226	813482	(AK000432) unnamed protein product [Homo sapiens] Length = 379	dbj BAA91162 .1			4503	151	864	100	100		HKAJ29	pCMV/Sport 2.0
227	815696	(AF104419) decoy receptor 3 [Homo sapiens] >gb AAD29688.1 AF134240_1 (AF134240) tumor necrosis factor receptor homolog [Homo sapiens] >gb AAF33685.1 AF217793_1 (AF217793) M68C [Homo sapiens] >gb AAF33686.1 AF217794_1 (AF217794) M68E [Homo sapiens] >gb AAF	gb AAD03056. 1			4504	1	1023	86	86		HTPCH84	Uni-ZAP XR

228	821335	protein [Homo sapiens] >sp Q14287 Q14287 HYPOTHETICAL PROTEIN (FRAGMENT). Length = 157	gb AAA88036. 1	4505	1057	1323	57	76	HWDAC26	pCMV Sport 3.0
229	824071			4506	1370	1594			HMUB122	pCMV Sport 3.0
230	827298	reverse transcriptase [Homo sapiens] Length = 361	gb AAB02291. 1	4507	1279	1202	44	58	HMSDI67	Uni-ZAP XR
231	827315	GS3786 [Homo sapiens] >gb AAD54511.1 AC006364_1 (AC006364) GS3786 [Homo sapiens] >sp Q92520 G786_HUMAN PROTEIN GS3786. >sp AAD54511 AAD54511 GS3786. Length = 227	dbj BAA13251 .1	4508	764	964	63	81	HWLEZ80	pSport1
232	827562	(AJ271442) Tspan-2 protein [Rattus norvegicus] >sp CAB69827 CAB69827 Tspan-2 protein. Length = 221	emb CAB6982 7.1	4509	2	688	85	88	HAIDQ59	Uni-ZAP XR
233	827721			4510	190	411			HTJN176	pCMV Sport 2.0
234	827740			4511	716	838			HBNAP17	Uni-ZAP XR
235	828180	(AF067797) aquaporin 8 [Homo sapiens] >sp AAF19050 AAF19050 Aquaporin 8. Length = 261	gb AAF19050. 1	4512	20	883	83	83	HWLFM26	pSport1
236	828552	ORF_ID: o255#5; similar to [SwissProt Accession Number P45576] [Escherichia coli] >gb AAC74362.1 (AE000226) putative heat shock protein [Escherichia coli] >pir C64876 C64876 yciM protein precursor - Escherichia coli >sp P45576 YCIM_ECOLI HYPOTHETICAL 44.5	dbj BAA14834 .1	4513	390	7	95	98	HPWBE34	Uni-ZAP XR
237	828670			4514	222	350			HPICC36	Uni-ZAP XR
238	828919	RNA helicase [Homo sapiens] >pir S71758 S71758 DEAD box protein MrDb, Myc-regulated - human >sp Q92732 Q92732 RNA HELICASE. Length = 610	emb CAA6729 5.1	4515	2	661	99	100	HFOYL30	pSport1

239	829084					4516	1043	1288				HLXNE31	pSportl
240	829148					4517	55	279				HLHDP51	Uni-ZAP XR
241	829161	(AF019767) zinc finger protein [Homo sapiens] >sp O75312 ZPR1_HUMAN ZINC-FINGER PROTEIN ZPR1. Length = 459	gb AAC33514.1	4518	3	116	100	100				HCRMV95	pSportl
242	830123	strong similarity to class-III of pyridoxal-phosphate- dependent aminotransferases [Caenorhabditis elegans] >pir T25848 T25848 hypothetical protein T01B11.2 - Caenorhabditis elegans >sp P91408 YO1J CAEEL PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-). Leng	gb AAB37999.1	4519	2	430	49	70				HAQBZ89	Uni-ZAP XR
243	830151			4520	111	341						HYAAS90	pCMVSPORT 3.0
244	830194	(AL136543) hypothetical protein [Homo sapiens] >emb CAB66478.1 (AL136543) hypothetical protein [Homo sapiens] >sp CAB66478 CAB66478 Hypothetical 84.8 kd protein. >pir B34461 B34461 heat shock protein 90 beta - rabbit (fragment) {SUB 1-25} >sp P30947 HS9B	emb CAB66478.1	4521	3	1043	92	92				HLDCP20	pCMVSPORT 3.0
245	830231			4522	1	243						HWLJS42	pSportl
246	830316			4523	793	960						HWLEH32	pSportl
247	830343	non-muscle myosin heavy chain [Bos taurus] >sp O02717 O02717 NON-MUSCLE MYOSIN HEAVY CHAIN (FRAGMENT). Length = 625	gb AAC19403.1	4524	272	850	46	64				HWLGI62	pSportl
248	830347	(AF127035) calcium-activated chloride channel protein 2 [Homo sapiens] >sp AAD48398 AAD48398 Calcium-activated chloride channel protein 2. >dbj BAA90969.1 (AK000138) unnamed protein product [Homo sapiens] {SUB 449-917} Length = 917	gb AAD48398.1 AF1270	4525	3	656	97	97				HWLEL81	pSportl

249	830382				4526	2	229				HWHPA71	pCMVSPORT 3.0
250	830436	(AB020663) KIAA0856 protein [Homo sapiens] >sp O94938 O94938 KIAA0856 PROTEIN (FRAGMENT). Length = 1070	dbj BAA74879 .1		4527	83	523	97	98		HWABR83	pCMVSPORT 3.0
251	830465	preA-PAL-2 [synthetic construct] >emb CAA00247.1 miniactivin [synthetic construct] {SUB 20-434} >gb AAA60005.1 plasminogen activator inhibitor 2, (first expressed exon) [Homo sapiens] {SUB 20-75} Length = 434	emb CAA0150 3.1		4528	51	1319	94	94		HUVDZ54	Uni-ZAP XR
252	830498				4529	420	677				HUFAR83	pSport1
253	830540	protein kinase MUK2 [Rattus norvegicus] >gb AAB95646.1 serine/threonine protein kinase [Rattus norvegicus] >sp P35465 PAK1 RAT SERINE/THREONINE-PROTEIN KINASE PAK- ALPHA (EC 2.7.1.-) (P68-PAK) (P21- ACTIVATED KINASE) (PAK-1) (ALPHA-PAK) (PROTEIN KINASE MU	gb AAB61533. 1		4530	2	733	100	100		HTLHR67	Uni-ZAP XR
254	830568	tyrosine protein kinase [Homo sapiens] >sp Q08345 EDD1_HUMAN EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (TRK E) (PROTEIN-T	gb AAA18019. 1		4531	3	1874	84	84		HTSGO78	pBluescript
255	830582	(AL050179) hypothetical protein [Homo sapiens] >emb CAB43309.1 (AL050179) hypothetical protein [Homo sapiens] >pir T08796 T08796 tropomyosin - human (fragment) >sp Q9Y427 Q9Y427 HYPOTHETICAL 34.9 KD PROTEIN (FRAGMENT). >emb CAA24257.1 fragment from trop	emb CAB4330 9.1		4532	107	712	84	87		HSLHS76	Uni-ZAP XR
256	830586	(2"-5")oligoadenylate synthetase [Homo sapiens] Length = 364	dbj BAA00047 .1		4533	2	1192	94	94		HKACP86	pCMVSPORT 2.0

257	830685	(AB032945) KIAA1119 protein [Homo sapiens] >sp BAA86433 BAA86433 KIAA1119 protein (fragment). Length = 1260	dbj BAA86433 .1	4534	321	1106	92	92	HASAR52	Uni-ZAP XR
258	830693	(AF077301) Bcl-2-interacting protein beclin [Homo sapiens] >sp O75595 O75595 BCL-2- INTERACTING PROTEIN BECLIN. Length = 450	gb AAC68653. .1	4535	152	1504	90	90	HAHSF60	pBluescript
259	830710			4536	1	105			HCQCD01	Lambda ZAP II
260	830723	(AB015594) Pex11p [Homo sapiens] >gb AAC78658.1 (AF093668) peroxisomal biogenesis factor [Homo sapiens] >sp O75192 O75192 PEX11P. Length = 247	dbj BAA32533 .1	4537	10	612	83	83	HUSZD77	pSport1
261	830743	(AF077045) ATP synthase epsilon chain [Homo sapiens] >sp AAD27778 AAD27778 ATP synthase epsilon chain. >sp P56381 ATPE_HUMAN ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL (EC 3.6.1.34). {SUB 2-51} Length = 51	gb AAD27778. 1 AF0770	4538	53	262	100	100	HCBBA51	Uni-ZAP XR
262	830804	(AB006746) hMmTRA1b [Homo sapiens] >gb AAC99413.1 (AF098642) phospholipid scramblase; plasma membrane phospholipid scramblase [Homo sapiens] >pir JE0284 JE0284 Mm-1 cell derived transplantability-associated 1b - Human >sp O15162 O15162 PHOSPHOLIPID SCRAM	dbj BAA32568 .1	4539	68	283	100	100	HSDEI84	Uni-ZAP XR
263	830816	(AL137349) hypothetical protein [Homo sapiens] >emb CAB70704.1 (AL137349) hypothetical protein [Homo sapiens] >sp CAB70704 CAB70704 Hypothetical 60.3 kd protein (fragment). Length = 541	emb CAB7070 4.1	4540	3	1130	94	95	HFIYB72	pSport1
264	830829	(AF151847) CGI-89 protein [Homo sapiens] >sp Q9Y397 Q9Y397 CGI-89 PROTEIN. Length = 382	gb AAD34084. 1 AF1518	4541	2	370	71	85	HMTAE63	pCMVSPORT 3.0

265	830859	(AF097362) gamma-interferon inducible lysosomal thiol reductase [Homo sapiens] >sp AAF04618 AAF04618 Gamma-interferon inducible lysosomal thiol reductase. >gb AAD22672.1 AC007192_3 (AC007192) INIP_HUMAN [AA 4- 104] [Homo sapiens] {SUB 4-104} Length = 261	gb AAF04618.1 AF0973	4542	1	735	80	82	HWBEJ14	pCMVSPORT 3.0
266	830879	(AF003924) ANC_2H01 [Homo sapiens] >sp AAF21240 AAF21240 ANC_2H01. Length = 485	gb AAF21240.1 AF0039	4543	2	592	100	100	HVAAB82	pSport1
267	830901	GLY1 protein [Escherichia coli] >dbj BAA20882.1 (AB005050) threonine aldolase [Escherichia coli] >gb AAC73957.1 (AE000188) putative arylsulfatase [Escherichia coli] >pir F64825 F64825 L-allo-threonine aldolase (EC 4.1.2.-) - Escherichia coli >sp P75823	dbj BAA35584.1	4544	190	1005	94	96	HPWBX45	Uni-ZAP XR
268	831019	ORF 3 [Homo sapiens] >pir E41925 E41925 hypothetical protein 3 - human >sp Q14270 Q14270 ORF 3. Length = 143	gb AAA58464.1	4545	297	235	53	66	HODGW05	Uni-ZAP XR
269	831057	coded for by C. elegans cDNAs GenBank: CE5D1 (Z14791), CEL01F1 (M88817), CEL04B5 (M88849), and CEL04C1 (M75812); putative [Caenorhabditis elegans] >pir S44853 S44853 K12H4.3 protein - Caenorhabditis elegans >sp P34524 YM63_CAEEL HYPOTHETICAL 40.2 KD PROTEIN	gb AAA28097.1	4546	3	1106	45	68	HNTCW73	pCMVSPORT 3.0
270	831099	integrin beta 1 subunit precursor [Homo sapiens] >pir B27079 B27079 fibronectin receptor beta chain precursor - human >sp P05556 ITB1_HUMAN FIBRONECTIN RECEPTOR BETA SUBUNIT PRECURSOR (INTEGRIN BETA-1) (CD29) (INTEGRIN VLA-4 BETA SUBUNIT). >gb AAA79835.1	emb CAA3079.0.1	4547	3	1697	94	94	HA5AB03	pSport1

271	831117				4548	400	579			HMWBR70	Uni-ZAP XR
272	831163	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 ALU7_HUMAN	4549	3	161	75	83		HMSHS44	Uni-ZAP XR
273	831210	TGF-beta masking protein large subunit [Rattus norvegicus] >pir A38261 A38261 masking protein precursor - rat >sp Q00918 TGFB_RAT LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF	gb AAA42235.1	4550	1	498	86	91		HMEIJ62	Lambda ZAP II
274	831212	(AF051882) carbonic anhydrase XII precursor [Homo sapiens] >gb AAC63952.1 (AF037335) carbonic anhydrase precursor [Homo sapiens] >sp O43570 CAHC_HUMAN CARBONIC ANHYDRASE XII PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE XII) (CA-XII) (TUMOR ANTIGEN HOM-R	gb AAC39789.1	4551	206	385	100	100		HWHHW79	pCMVSPORT 3.0
275	831234			4552	202	498				HL YGG06	pSport1
276	831239			4553	420	638				HMEKY46	Lambda ZAP II
277	831268			4554	324	749				HLTER57	Uni-ZAP XR
278	831307	(AK001317) unnamed protein product [Homo sapiens] Length = 481	dbj BAA91619.1	4555	33	935	94	94		HAPOA59	Uni-ZAP XR
279	831313	reading frame v-fos (p55) [Mus musculus] >pir A01344 TVMVJ transforming protein fos - FBJ murine osteosarcoma virus >sp P01102 FOS_MSVFB P55-V-FOS TRANSFORMING PROTEIN. Length = 381	emb CAA2450.5.1	4556	1182	1670	73	85		HAGDZ30	Uni-ZAP XR
280	831386			4557	1097	1363				HKLRB18	pBluescript

281	831390	aldehyde reductase (EC 1.1.1.2) [Homo sapiens] >gb AAB92369.1 (AF036683) aldehyde reductase [Homo sapiens] >gb AAF01260.1 AF112485_1 (AF112485) aldehyde reductase [Homo sapiens] >pir A33851 A33851 alcohol dehydrogenase (NADP+) (EC 1.1.1.2) - human >sp AA	gb AAA51711.1	4558	254	1312	94	94	HKGDF04	pSport1
282	831426	(AJ245539) GalNac-T5 [Homo sapiens] >sp CAB65104 CAB65104 GalNac-T5 (fragment). Length = 668	emb CAB65104.1	4559	3	827	93	94	HKAJZ24	pCMVSPORT 2.0
283	831453	2A9 peptide [Homo sapiens] >gb AAA51905.1 calyculin [Homo sapiens] >gb AAA51906.1 put. calyculin; putative [Homo sapiens] >pir A28363 BCHUY calyculin - human >sp P06703 S106_HUMAN CALYCULIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) (PRA) (GROWTH FACTOR-IN	gb AAA35886.1	4560	1	315	83	83	HWLJE49	pSport1
284	831465	(AB014600) KIAA0700 protein [Homo sapiens] >sp O75182 O75182 KIAA0700 PROTEIN (FRAGMENT). Length = 1130	dbj BAA31675.1	4561	2	529	90	93	HJPAU37	Uni-ZAP XR
285	831558			4562	3	410			HHGCU20	Lambda ZAP II
286	831586	(AF179867) STE20-like kinase [Homo sapiens] >sp AAF14559 AAF14559 STE20-like kinase. Length = 898	gb AAF14559.1 AF1798	4563	2	850	94	94	HHEDO80	pCMVSPORT 3.0
287	831664	heterogeneous nuclear ribonucleoprotein complex K, hnRNP K [human, Peptide, 463 aa] [Homo sapiens] >dbj BAA04566.1 dC-stretch binding protein (CSBP) [Rattus norvegicus] >pir A42058 A42058 heterogeneous nuclear ribonucleoprotein complex K, hnRNP K - human	gb AAB20770.1	4564	180	1574	72	72	HFPCU40	Uni-ZAP XR

288	831687	hmPv17 [Homo sapiens] >gb AAD14014.1 1683146_1 [Homo sapiens] >pir S45343 S45343 glomerulosclerosis protein Mpv17 - human >sp P39210 MPV1_HUMAN MPV17 PROTEIN: >gb AAC24205.1 (AF038633) Mpv17 protein [Homo sapiens] {SUB 155-176} Length = 176	emb CAA5404 7.1	4565	60	305	98	100	HFKHD75	Uni-ZAP XR
289	831703			4566	52	240			HFIHX78	pSport1
290	831753			4567	1	219			HETIK68	Uni-ZAP XR
291	831757			4568	915	1208			HETBE76	Uni-ZAP XR
292	831795			4569	1490	1855			HTXOI32	Uni-ZAP XR
293	831796			4570	892	1158			HE9RY54	Uni-ZAP XR
294	831880			4571	1	444			HE6FT69	Uni-ZAP XR
295	831899			4572	1	693			HDTBQ51	pCMVSPORT 2.0
296	831910			4573	3	308			HDTAB33	pCMVSPORT 2.0
297	831931			4574	201	464			HLHGG05	Uni-ZAP XR
298	831942	(AJ388553) hypothetical protein [Canis familiaris] >sp Q9XSR5 Q9XSR5 HYPOTHETICAL 15.3 KD PROTEIN (FRAGMENT). Length = 146	emb CAB4685 2.1	4575	44	763	72	77	HDPTH11	pCMVSPORT 3.0
299	831956			4576	3	269			HDPLB15	pCMVSPORT 3.0
300	832009			4577	2	346			HDAAQ89	pSport1

301	832010	(AL021918) b34I8.1 (Kruppel related Zinc Finger protein 184) [Homo sapiens] >sp O60792 O60792 B34I8.1 (KRUPPEL RELATED ZINC FINGER PROTEIN 184). Length = 751	emb CAA1727 8.1	4578	1	348	57	69	HDFUB44	pCMVSPORT 2.0
302	832044	5-aminoimidazole-4-carboxamide ribonucleotide transformylase [Homo sapiens] >dbj BAA11559.1 5- aminoimidazole-4-carboxamide-1-beta-D-ribonucleotide transformylase/inosinase [Homo sapiens] >pir JC4642 JC4642 purH bifunctional enzyme - human >sp Q13856 Q	dbj BAA21762 1	4579	1	1794	99	99	HGCOL40	pSport1
303	832093			4580	279	422			HCRNJ73	pSport1
304	832138			4581	317	466			HODEY51	Uni-ZAP XR
305	832148			4582	246	380			HFIHN81	pSport1
306	832187			4583	26	400			HCQAI40	Lambda ZAP II
307	832343	Similarity to E.coli 2-oxoglutarate dehydrogenase (SW:ODO1_ECOLI); cDNA EST EMBL:D32590 comes from this gene; cDNA EST EMBL:D32841 comes from this gene; cDNA EST EMBL:D34051 comes from this gene; cDNA EST EMBL:D35268 comes from this gene; cDNA> >pir T2803	emb CAB0159 0.1	4584	462	1487	60	77	HWACZ95	pCMVSPORT 3.0
308	832346			4585	295	471			HBAGU45	pSport1
309	832411			4586	196	489			HRGSB33	pBluescript
310	832464			4587	145	360			HBJBC35	pCMVSPORT 3.0
311	832575	protein tyrosine kinase [Homo sapiens] >pir A55922 A55922 tyrosine kinase A6 - human >sp Q12792 Q12792 PROTEIN TYROSINE KINASE. Length = 350	gb AAC50062. 1	4588	49	1203	99	99	H2LAJ21	pBluescript SK-

312	832593	CENP-F kinetochore protein [Homo sapiens] >sp P49454 CENF_HUMAN CENP-F KINETOCHORE PROTEIN. Length = 3210	gb AAA82889.1	4589	2	811	91	92	H2LAB53	pBluescript SK-
313	832597			4590	214	318			H2CBJ07	pBluescript SK-
314	834890	TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3). Length = 204	sp Q64152 BT F3_MOUSE	4591	70	588	87	88	H2CBT12	pBluescript SK-
315	835079			4592	151	348			HOELH62	Uni-ZAP XR
316	835456	(AL035608) dJ479J7.1 (similar to CHONDROMODULIN-1) [Homo sapiens] >sp CAB55680 CAB55680 dJ479J7.1 (similar to CHONDROMODULIN-1) (fragment). Length = 263	emb CAB55680.1	4593	85	1041	79	79	HE8NG02	Uni-ZAP XR
317	835655			4594	1075	1332			HAGFG91	Uni-ZAP XR
318	836203			4595	550	990			HWLOG76	pSport1
319	836261	(AF117615) heme-binding protein [Homo sapiens] >sp Q9Y5Z5 Q9Y5Z5 HEME-BINDING PROTEIN. Length = 189	gb AAD32098.1 AF1176	4596	116	292	98	98	HBMA50	pBluescript SK-
320	836762	(AF132552) BcDNA.GM01838 [Drosophila melanogaster] >sp Q9XZ53 Q9XZ53 BCDNA.GM01838. Length = 774	gb AAD27851.1 AF1325	4597	2	1075	75	84	H2CBN10	pBluescript SK-
321	836988	(AB011176) KIAA0604 protein [Homo sapiens] >sp O60344 ECE2_HUMAN ENDOTHELIN-CONVERTING ENZYME 2 (EC 3.4.24.71) (ECE-2) (KIAA0604). Length = 765	dbj BAA25530.1	4598	89	571	87	87	HCE3I64	Uni-ZAP XR
322	838140			4599	300	476			HE2CH58	Uni-ZAP XR
323	838459	!!!! ALU SUBFAMILY J WARNING ENTRY !!!! Length = 591	sp P39188 ALU1_HUMAN	4600	1223	1354	68	76	HTHCW70	Uni-ZAP XR

324	839262	(AF000364) heterogeneous nuclear ribonucleoprotein R [Homo sapiens] >pir T02673 T02673 heterogeneous nuclear ribonucleoprotein R - human >sp O43390 O43390 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN R. Length = 633	gb AAC39540.1	4601	26	1216	99	99	HAPOF13	Uni-ZAP XR
325	839384	(AL133623) hypothetical protein [Homo sapiens] >emb CAB63749.1 (AL133623) hypothetical protein [Homo sapiens] >sp CAB63749 CAB63749 Hypothetical 130.1 kd protein (fragment). Length = 1159	emb CAB63749.1	4602	5	1069	92	93	HTGEX11	Uni-ZAP XR
326	839750	(AF100757) COP9 complex subunit 4 [Homo sapiens] >sp Q9Y677 Q9Y677 COP9 COMPLEX SUBUNIT 4. Length = 405	gb AAD43021.1	4603	1	1155	100	100	HWHGE39	pCMVSPORT 3.0
327	840028			4604	60	419			HNGIN84	Uni-ZAP XR
328	840572	putative [Homo sapiens] >pir I54339 I54339 prot-oncogene bmi-1 - human >sp P35226 BIM1_HUMAN DNA-BINDING PROTEIN BMI-1. Length = 326	gb AAA19873.1	4605	3	1172	95	95	HTGAZ34	Uni-ZAP XR
329	840675	(AL117430) hypothetical protein [Homo sapiens] >emb CAB55919.1 (AL117430) hypothetical protein [Homo sapiens] >pir T17229 T17229 hypothetical protein DKFZp434D156.1 - human >sp CAB55919 CAB55919 Hypothetical 39.8 kd protein. Length = 384	emb CAB55919.1	4606	2	592	66	66	HNTEF54	pCMVSPORT 3.0
330	840708			4607	1200	1487			HTEAF73	Uni-ZAP XR
331	840847	(AL035461) dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) [Homo sapiens] >sp CAB55278 CAB55278 dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein). Length = 301	emb CAB55278.1	4608	151	1044	93	93	HPJCI42	Uni-ZAP XR

332	840848	prohibitin [human, Peptide, 272 aa] [Homo sapiens] >pir I52690 I52690 prohibitin - human >sp P35232 PHB_HUMAN PROHIBITIN. Length = 272	gb AAB21614.1	4609	81	917	93	93	HHBHM75	pCMVSPORT 1
333	840860	NAP [Homo sapiens] >pir S40510 S40510 nucleosome assembly protein 1-like 1 - human >sp P55209 NPL1_HUMAN NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 1 (NAP-1 RELATED PROTEIN). Length = 391	gb AAC37544.1	4610	92	1309	68	68	HDTLJ39	pCMVSPORT 2.0
334	841015			4611	48	425			HE2DT31	Uni-ZAP XR
335	841017			4612	402	683			HE2AY01	Uni-ZAP XR
336	841030			4613	515	721			HWLOA34	pSport1
337	841241	Thy-1 [Homo sapiens] >pir A02106 TDHU Thy-1 membrane glycoprotein precursor - human >sp P04216 THY1_HUMAN THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN). Length = 161	gb AAA61180.1	4614	128	622	86	87	HBXFG67	ZAP Express
338	841957			4615	355	609			HWLOF51	pSport1
339	846025	(AJ010973) DEDD protein [Homo sapiens] >gb AAC33105.1 (AF083236) FLDED-1 [Homo sapiens] >gb AAC80280.1 (AF043733) death effector domain-containing testicular molecule [Homo sapiens] >gb AAD16414.1 (AF100341) death effector domain-containing protein DED	emb CAA0944.5.1	4616	1	1098	63	83	HLDOK36	pCMVSPORT 3.0
340	846362	(AC006950) IgG Fc binding protein [AA 4671-5405] [Homo sapiens] >sp O95784 O95784 IGG FC BINDING PROTEIN (FRAGMENT). Length = 735	gb AAD15624.1	4617	449	1894	93	93	HSDJF12	Uni-ZAP XR
341	846384	(AF127036) calcium-activated chloride channel protein 1 [Homo sapiens] >sp AAD25487 AAD25487 Calcium-activated chloride channel protein 1. Length = 914	gb AAD25487.1 AF1270	4618	1125	2780	96	96	HWLFF02	pSport1

342	846750	(AF132148) [Drosophila melanogaster] >sp Q9XYZ6 Q9XYZ6 HYPOTHETICAL 75.5 KD PROTEIN. Length = 653	gb AAD34736.1	4619	1	1503	47	61	HEMF121	Uni-ZAP XR
343	847289	!!! ALU SUBFAMILY SQ WARNING ENTRY !!! Length = 593		4620	322	510			HWLUW66	pSport1
344	847598	(AF145634) BcDNA.GH06193 [Drosophila melanogaster] >sp Q9Y138 Q9Y138 BCDNA.GH06193. Length = 696	sp P39194 ALU7_HUMAN	4621	710	859	85	87	HNTEG90	pCMVSPORT 3.0
345	848119	(AF145634) BcDNA.GH06193 [Drosophila melanogaster] >sp Q9Y138 Q9Y138 BCDNA.GH06193. Length = 696	gb AAD38609.1 AF1456	4622	1	243	66	88	HELGG49	Uni-ZAP XR
346	848746	ATP synthase subunit e [Homo sapiens] >sp P56385 ATP_HUMAN ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34). {SUB 2-69} Length = 69	dbj BAA23322.1	4623	250	666			HWLQO44	pSport1
347	849084	epidermal growth factor receptor kinase substrate [Homo sapiens] >pir I38728 I38728 epidermal growth factor receptor kinase substrate - human >sp Q12929 EPS8_HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8. Length = 822		4624	1	270	78	78	HFEBT64	Uni-ZAP XR
348	849114	zinc finger protein PZF [Mus musculus] >pir I48724 I48724 zinc finger protein PZF - mouse >sp Q62511 Q62511 ZINC FINGER PROTEIN PZF. Length = 455	gb AAA62280.1	4625	3	986	100	100	HUVFL24	Uni-ZAP XR
349	849143	carbonic anhydrase I (EC 4.2.1.1) [Homo sapiens] >pir I48724 I48724 zinc finger protein PZF - mouse >sp Q62511 Q62511 ZINC FINGER PROTEIN PZF. Length = 455	gb AAA81913.1	4626	62	1795	88	89	HAMGR89	pCMVSPORT 3.0
350	849155	carbonic anhydrase I (EC 4.2.1.1) [Homo sapiens] >emb CAA28663.1 carbonic anhydrase I (AA 1-261) [Homo sapiens] >pir I48724 I48724 zinc finger protein PZF - mouse >sp P00915 CAH1_HUMAN CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE	gb AAA51910.1	4627	71	859	100	100	HKLSA58	pBluescript

351	849159	carcinoembryonic antigen [Homo sapiens] >gb AA66186.1 carcinoembryonic antigen [Homo sapiens] >gb AAC62825.1 (AC005797) carcinoembryonic antigen CGM2 precursor - human [Homo sapiens] >pir A55811 A55811 carcinoembryonic antigen CGM2 precursor - human >s	emb CAA6695 5.1	4628	1	903	99	99	HWLCG11	pSport1
352	849244	(AK001553) unnamed protein product [Homo sapiens] >dbj BAA91996.1 (AK001951) unnamed protein product [Homo sapiens] Length = 227	dbj BAA91753 .1	4629	110	877	100	100	HMSJT69	Uni-ZAP XR
353	849254			4630	18	323			HRABQ68	pCMV/Sport 3.0
354	849301	ornithine decarboxylase [Homo sapiens] >gb AA59969.1 ornithine decarboxylase [Homo sapiens] >gb AA60563.1 ornithine decarboxylase [Homo sapiens] >gb AA60564.1 ornithine decarboxylase [Homo sapiens] >emb CAA39047.1 ornithine decarboxylase [Homo sapiens]	gb AA59967. 1	4631	164	1561	100	100	H2CBM53	pBluescript SK-
355	849317	(AK000500) unnamed protein product [Homo sapiens] Length = 158	dbj BAA91207 .1	4632	1	534	89	89	HPRGTG34	pBluescript
356	849332	homology to a plant EST:R1CS2753A [Homo sapiens] >sp O95571 O95571 mRNA EXPRESSED IN THYROID GLAND. Length = 227	dbj BAA34595 .1	4633	13	831	99	99	HE8DO31	Uni-ZAP XR
357	849422	(AL035071) dJ1085F17.2 (EB1 (APC binding protein)) [Homo sapiens] >gb AAC09471.1 EB1 [Homo sapiens] >pir J52726 J52726 EB1 - human >sp Q15691 Q15691 EB1. >sp CAB53072 CAB53072 DJ1085F17.2 (EB1 (APC binding protein)). Length = 268	emb CAB5307 2.1	4634	1	933	100	100	HAIDB85	Uni-ZAP XR
358	849471	thromboxane synthase [Homo sapiens] Length = 533	dbj BAA07011 .1	4635	688	1788	95	95	HMCIR67	Uni-ZAP XR

359	849492	ubiquitin conjugating-protein [Oryctolagus cuniculus] >gb AAA35982.1 HHR6B (Human homologue of yeast RAD 6); putative [Homo sapiens] >emb CAA37339.1 E2 protein [Homo sapiens] >gb AAA21087.1 ubiquitin conjugating-protein [Rattus norvegicus] >emb CAA6560	gb AAA31492.1	4636	2	595	100	100	HKAJC79	pCMVSport 2.0
360	849534	beta-galactosidase alpha peptide [Cloning vector pSport2] Length = 114	gb AAA67217.1	4637	302	508	100	100	HCRMP14	pSport1
361	849565			4638	806	1036			HPRAO21	Uni-ZAP XR
362	849583	(AF120206) XY body protein [Mus musculus] >gb AAF18303.1 AF120207_1 (AF120207) XY body protein [Mus musculus] >sp AAF18302 AAF18302 XY body protein. >sp AAF18303 AAF18303 XY body protein. Length = 840	gb AAF18302.1 AF1202	4639	1	1851	68	76	HAIBU93	Uni-ZAP XR
363	849589	(AB009282) cytochrome b5 [Homo sapiens] >sp O43169 O43169 CYTOCHROME B5 (FRAGMENT). Length = 146	dbj BAA23735.1	4640	44	508	99	100	HCFMH52	pSport1
364	849658	(AF020762) protein [Homo sapiens] >sp O43466 O43466 HYPOTHETICAL 31.3 KD PROTEIN (FRAGMENT). Length = 267	gb AAB97675.1	4641	831	968	47	53	HMVAE41	pSport1
365	849666	macrophage capping protein [Homo sapiens] >pir A43358 A43358 macrophage capping protein - human >sp P40121 CAPG HUMAN MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G). >gb AAA92670.1 Cap-G [Homo sapiens] {SUB 1-172} Length = 348	gb AAA59570.1	4642	57	1100	98	99	HMSDT39	Uni-ZAP XR
366	849679	(AJ003061) most expressed alternative spliced form [Homo sapiens] >sp O60852 O60852 PROTEIN ENCODED BY SACCHAROMYCES CEREVISIAE SPC98 HOMOLOGUE. Length = 907	emb CAA0583.2.1	4643	3	1169	95	95	HE8NK24	Uni-ZAP XR

367	849741				4644	948	1067				HWHQP08	pCMVSPORT 3.0
368	849783	lumican [Homo sapiens] Length = 338	gb AAA91639.1		4645	69	1127	95	95		HCRPJ23	pSport1
369	850211				4646	52	213				HTOAC26	Uni-ZAP XR
370	850254	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 ALU7_HUMAN		4647	1031	1144	80	87		HUVQC41	Uni-ZAP XR
371	850264	N-Acetyl-beta-D-glucosaminide [Homo sapiens] >emb CAA76985.1 glycoprotein 6-alpha-L-fucosyltransferase [Homo sapiens] >emb CAA76986.1 glycoprotein 6-alpha-L-fucosyltransferase [Homo sapiens] >emb CAA76987.1 glycoprotein 6-alpha-L-fucosyltransferase [Ho	dbj BAA19764.1		4648	601	2145	97	97		HPJEC66	Uni-ZAP XR
372	850273				4649	336	476				HCQCD86	Lambda ZAP II
373	850371				4650	69	182				HCRMX05	pSport1
374	850859	(AF124522) tetraspan NET-2 [Homo sapiens] >sp O95859 O95859 TETRASPAN NET-2. Length = 305	gb AAD17317.1		4651	1	513	99	100		HAPRB43	Uni-ZAP XR
375	851066	(AK000302) unnamed protein product [Homo sapiens] Length = 436	dbj BAA91068.1		4652	434	1033	98	98		HWHQL22	pCMVSPORT 3.0
376	851217				4653	1	273				HWLMN93	pSport1
377	852170	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 ALU7_HUMAN		4654	1550	1681	73	74		HTGFW53	Uni-ZAP XR
378	852387				4655	269	496				HANGG89	pSport1
379	852812	GDP dissociation inhibitor beta [Homo sapiens] >emb CAA73735.1 GDP dissociation inhibitor beta [Homo sapiens] >sp O43928 O43928 GDP DISSOCIATION INHIBITOR BETA. >gb AAD34588.1 (AF144713) Rab GDP dissociation inhibitor beta [Homo sapiens] {SUB 81-439} Le	emb CAA73734.1		4656	1	852	100	100		HKAAV86	pCMVSPORT 2.0

380	853175	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 ALU7_HUMAN	4657	234	608	82	84	HSACF33	pBluescript SK-
381	853230			4658	19	273			H2CBA56	pBluescript SK-
382	854063			4659	1	129			HLJBL63	pCMVSPORT 1
383	854073	(AF068754) heat shock factor binding protein 1 HSBP1 [Homo sapiens] >sp O75506 O75506 HEAT SHOCK FACTOR BINDING PROTEIN 1 HSBP1. Length = 76	gb AAC25186.1	4660	146	403	100	100	HHFOV83	Uni-ZAP XR
384	854987	no arches [Homo sapiens] >sp O95639 O95639 NO ARCHES. Length = 269	gb AAD00321.1	4661	76	408	100	100	HMTAE04	pCMVSPORT 3.0
385	855130			4662	127	333			HWLNN76	pSPORT1
386	856227	arrestin [Homo sapiens] >pir S18984 S18984 arrestin - human (fragment) >sp P32121 ARR2_HUMAN BETA-ARRESTIN 2. Length = 409	emb CAA7757.7.1	4663	1	636	59	62	HDQFE56	pCMVSPORT 3.0
387	856243	similar to citrate lyase beta chain; cDNA EST yk302b4.5 comes from this gene [Caenorhabditis elegans] >pir T18818 T18818 hypothetical protein C01G10.7 - Caenorhabditis elegans >sp Q93167 Q93167 C01G10.7 PROTEIN. Length = 324	emb CAB0270.9.1	4664	1	411	35	54	HLDBR21	pCMVSPORT 3.0
388	856354	KIAA0176 [Homo sapiens] >sp Q14681 Y176_HUMAN HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT). Length = 265	dbj BAA11493.1	4665	1	591	40	56	HHAUD91	pCMVSPORT 3.0
389	856923	(AF132951) CGI-17 protein [Homo sapiens] >sp Q9Y306 Q9Y306 CGI-17 PROTEIN. Length = 385	gb AAD27726.1 AF1329	4666	3	881	98	98	HTOHA37	Uni-ZAP XR
390	857684			4667	166	2			HDPPP71	pCMVSPORT 3.0

391	857946	(AF077034) HSPC010 [Homo sapiens] >gb AAD33954.1 AF145385_1 (AF145385) hypoxia-inducible gene 1 [Homo sapiens] >sp Q9Y241 Q9Y241 HIG1 PROTEIN (HSPC010). Length = 93	gb AAD27767.1 AF0770	4668	1	408	100	100	HBBE52	pCMVSPORT 1
392	858166			4669	641	1006			HLTDR01	Uni-ZAP XR
393	858178	KIAA0183 [Homo sapiens] >sp Q14688 Q14688 KIAA0183 PROTEIN (FRAGMENT). Length = 1062	dbj BAA11500.1	4670	1837	3153	87	87	HMECD50	Lambda ZAP II
394	858606			4671	2	307			HDPJL40	pCMVSPORT 3.0
395	858894	KIAA0021 protein [Homo sapiens] >sp BAA03499 BAA03499 KIAA0021 protein (fragment). Length = 703	dbj BAA03499.2	4672	2	1894	89	89	HDPGS38	pCMVSPORT 3.0
396	858949			4673	29	322			HCQAM69	Lambda ZAP II
397	858958			4674	2	106			HOSNC15	Uni-ZAP XR
398	859171	Similar to Human C219-reactive peptide (L34688) [Homo sapiens] >sp Q92580 Q92580 MYELOBLAST KIA0268 (FRAGMENT). >gb AAB00324.1 C219-reactive peptide [Homo sapiens] {SUB 592-727} Length = 1193	dbj BAA13448.1	4675	3	1463	84	84	HHEJQ41	pCMVSPORT 3.0
399	859352	(AF107406) GW128 [Homo sapiens] >sp Q9Y649 Q9Y649 GW128. Length = 63	gb AAD44524.1 AF1074	4676	177	398	100	100	HTXMR51	Uni-ZAP XR
400	859354	(AK001214) unnamed protein product [Homo sapiens] Length = 532	dbj BAA91559.1	4677	3	1244	99	99	HHFCX08	Uni-ZAP XR
401	859702			4678	56	310			HNTEG54	pCMVSPORT 3.0

402	860915	(AF010312) Pig7 [Homo sapiens] >gb AAB36550.1 LPS-Induced TNF-Alpha Factor [Homo sapiens] >sp Q99732 LITF_HUMAN LIPOPOLYSACCHARIDE-INDUCED TUMOR NECROSIS FACTOR-ALPHA FACTOR (LPS-INDUCED TNF-ALPHA FACTOR) (P53 INDUCED PROTEIN 7). Length = 228	gb AAC39530.1	4679	321	656	100	100	HNFZ19	Uni-ZAP XR
403	861209	collagen type XII alpha-1 [Homo sapiens] >sp Q99715 CA1C_HUMAN COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR. >pir A44036 A44036 collagen alpha 1(XII) chain - bovine (fragment) {SUB 2492-2517} Length = 3063	gb AAC51244.1	4680	91	1773	91	92	HCDEA29	Uni-ZAP XR
404	861534			4681	115	2			HCYBJ35	pBluescript SK-
405	861697	Na,K-ATPase beta subunit [Homo sapiens] >emb CAA27385.1 put. Na/K-ATPase beta (aa 1-303) [Homo sapiens] >pir A23764 PWHUNB Na+/K+-exchanging ATPase (EC 3.6.1.37) beta chain - human >sp P05026 ATNB_HUMAN SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1 CHAIN (gb AAA36352.1	4682	103	1029	96	96	HEBGA63	Uni-ZAP XR
406	861826			4683	311	841			HFACI10	Uni-ZAP XR
407	861909	(AJ242015) eMDC II protein [Homo sapiens] >sp Q9Y3S0 Q9Y3S0 EMDC II PROTEIN. Length = 775	emb CAB4208.5.1	4684	2	1318	96	96	HETCM67	Uni-ZAP XR
408	862197			4685	15	194			HCRNF78	pSport1
409	862232			4686	1	144			HRACX96	pCMVSPORT 3.0
410	862237	(AF151810) CGI-52 protein [Homo sapiens] >sp Q9Y365 Q9Y365 CGI-52 PROTEIN. Length = 359	gb AAD34047.1 AF1518	4687	654	1706	90	90	HTLAK94	Uni-ZAP XR
411	862277			4688	256	417			HCQCV31	Lambda ZAP II

412	862285				4689	533	727			HTJMG70	pCMV/Sport 2.0
413	862423				4690	93	185			HSNAT52	Uni-ZAP XR
414	862456				4691	500	880			HHFCZ67	Uni-ZAP XR
415	862486	(AB002533) Qip1 [Homo sapiens] >gb AAC25605.1 importin alpha 3 [Homo sapiens] >pir JC5505 JC5505 DNA helicase Q1 interacting protein 1 - human >sp O00629 IMA4_HUMAN IMPORTIN ALPHA-4 SUBUNIT (KARYOPHERIN ALPHA-4 SUBUNIT) (QIP1 PROTEIN). Length = 521	dbj BAA19546 .1	4692	192	1178	88	89		HHFIA95	Uni-ZAP XR
416	862709				4693	323	493			HMSOR85	Uni-ZAP XR
417	863865				4694	1	207			HBJU68	Uni-ZAP XR
418	863944	similar to Glutathione S-transferases.; cDNA EST yk536e7.3 comes from this gene [Caenorhabditis elegans] >pir T24175 T24175 hypothetical protein R11A8.5 - Caenorhabditis elegans >sp Q21925 Q21925 R11A8.5 PROTEIN. Length = 347	emb CAA9436 8.1	4695	3	1385	46	67		HDPBN09	pCMV/Sport 3.0
419	864428				4696	151	972			HFNAC49	pSport1
420	864808				4697	209	574			HHETS46	pCMV/Sport 3.0
421	864822				4698	256	447			HHATS67	pCMV/Sport 3.0
422	865044				4699	171	485			HLHTL45	pBluescript
423	865420				4700	1	696			HHEJZ45	pCMV/Sport 3.0
424	865421	(AK001431) unnamed protein product [Homo sapiens] Length = 597	dbj BAA91687 .1	4701	253	2247	97	97		HNAAF81	pSport1
425	866287				4702	359	613			HSLGX52	Uni-ZAP XR

426	866300					4703	671	967				HWLNL21	pSport1
427	866414		(AF228603) plectstrin 2 [Homo sapiens] Length = 353	gb AAF34791.1 AF2286	4704	3	647	95	96			HKADX79	pCMVSPORT 2.0
428	866987				4705	80	415					H6EAB24	Uni-ZAP XR
429	867132				4706	3	191					HRDFP67	Uni-ZAP XR
430	867388		Asparaginyl tRNA Synthetase [Homo sapiens] >emb CAA04008.1 (AJ000334) asparaginyl-tRNA synthetase [Homo sapiens] >sp O43776 SYN_HUMAN ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.22) (ASPARAGINE-- TRNA LIGASE) (ASNRS). >sp BAA34600 BAA34600 Asparag AF-17 [Homo sapiens] >pir I38533 I38533 AF17 protein - human >sp P55198 AF17_HUMAN AF-17 PROTEIN. >emb CAB63772.1 (AL133659) hypothetical protein [Homo sapiens] {SUB 670-1093} Length = 1093	dbj BAA34600.1	4707	16	1749	100	100		HDPPM58	pCMVSPORT 3.0	
431	867842			gb AAA21145.1	4708	3	461	37	40			HTAHC93	Uni-ZAP XR
432	867923		(AL050170) hypothetical protein [Homo sapiens] >emb CAB43306.1 (AL050170) hypothetical protein [Homo sapiens] >pir T08792 T08792 hypothetical protein DKFZp586E1422.1 - human (fragment) >sp Q9Y3Y1 Q9Y3Y1 HYPOTHETICAL 14.3 KD PROTEIN (FRAGMENT). Length = 1	emb CAB43306.1	4709	473	703	91	93			HPCRL51	Other
433	868035		(AF099186) EH domain-containing protein EHD1 [Mus musculus] >gb AAF24223.1 AF173156_1 (AF173156) MPAST1 [Mus musculus] >sp Q9WVK4 Q9WVK4 EH DOMAIN-CONTAINING PROTEIN EHD1. >sp AAF24223 AAF24223 MPAST1. Length = 534	gb AAD45423.1 AF0991	4710	336	851	70	74			HCRNJ44	pSport1

434	868135	BST-2 [Homo sapiens] >pir A56836 A56836 bone marrow stromal cell surface protein BST-2 - human >sp Q10589 BST2_HUMAN BONE MARROW STROMAL ANTIGEN 2 (BST-2). Length = 180	dbj BAA05679.1	4711	78	656	85	85	HFKMJ43	Uni-ZAP XR
435	868173			4712	963	1169			HMSFS13	Uni-ZAP XR
436	868224			4713	1	615			HCRQH59	pSport1
437	868655	(AK001655) unnamed protein product [Homo sapiens] Length = 372	dbj BAA91815.1	4714	2	1225	99	99	HHFJU87	Uni-ZAP XR
438	869698	nuclear protein SA-2 [Homo sapiens] >sp O00540 O00540 NUCLEAR PROTEIN SA-2. Length = 1162	emb CAA9973.2.1	4715	600	1541	93	93	HFIAU59	pSport1
439	870190	Ca2+ ATPase of fast-twitch skeletal muscle sarcolemmal reticulum, adult isoform [Homo sapiens] >sp O14983 O14983 CA2+ ATPASE OF FAST-TWITCH SKELETAL MUSCLE SARCOPLASMIC RETICULUM, ADULT ISOFORM. Length = 1001	gb AAB53113.1	4716	592	1452	88	89	HBKDR59	pSport1
440	870349	!!! ALU SUBFAMILY J WARNING ENTRY !!! Length = 591	sp P39188 ALU1_HUMAN	4717	396	536	68	79	HTHCZ54	Uni-ZAP XR
441	870419	ezrin (AA 1-586) [Homo sapiens] >pir A34400 A34400 ezrin - human >sp P15311 EZRI_HUMAN EZRIN (P81) (CYTOVILLIN) (VILLIN-2). {SUB 2-586} >gb AAA61278.1 cytovillin 2 [Homo sapiens] {SUB 12-586} Length = 586	emb CAA3589.3.1	4718	79	1386	86	86	HWABV82	pCMVSPORT 3.0
442	870522	(AF044286) histone macroH2A1.1 [Homo sapiens] >sp O75377 O75377 HISTONE MACROH2A1.1. Length = 369	gb AAC33434.1	4719	142	660	100	100	HACAC44	Uni-ZAP XR
443	870896			4720	378	629			HDTLE81	pCMVSPORT 2.0
444	871071			4721	12	158			HSWBU77	pCMVSPORT 3.0

445	871225	(AF029684) Ikb kinase-beta [Homo sapiens] >gb AAD08997.1 (AF080158) Ikb kinase-b [Homo sapiens] >sp O14920 O14920 IKB KINASE-BETA (FRAGMENT). Length = 756	gb AAC51860.1	4722	2	802	94	94	HWACJ61	pCMVSPORT 3.0
446	871428			4723	2662	2964			HKLSC04	pBluescript
447	871498	(AK001443) unnamed protein product [Homo sapiens] Length = 420	dbj BAA91694.1	4724	490	2	99	99	HCRPM84	pSport1
448	871732			4725	447	719			HLHGG41	Uni-ZAP XR
449	871756			4726	291	506			HWLNH36	pSport1
450	871821	(AL157432) hypothetical protein [Homo sapiens] Length = 221	emb CAB7565.6.1	4727	89	841	88	88	HKAAC09	pCMVSPORT 2.0
451	872327	transmembrane protein [Mus musculus] >pir A31351 A31351 probable transmembrane protein FT27 - mouse >sp P52875 PF27_MOUSE TRANSMEMBRANE PROTEIN PFT27. Length = 323	gb AAA40456.1	4728	818	952	67	77	HLHAR50	Uni-ZAP XR
452	872354	RNA splicing-related protein [Rattus norvegicus] >sp O54729 O54729 BRAIN. Length = 712	dbj BAA23885.1	4729	2	403	98	100	HSKJB43	pBluescript
453	872535	serine protease [Homo sapiens] >sp O15393 TMS2_HUMAN TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-). Length = 492	gb AAC51784.1	4730	530	1108	42	57	HNSMB24	pSport1
454	872551	predicted using GeneFinder; similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28068 comes from this gene; cDNA EST EMBL:D33966 comes from this > >pir S2831	emb CAA7961.8.1	4731	530	1807	64	80	HAIAN23	pCMVSPORT 3.0
455	872640	(AB011118) KIAA0546 protein [Homo sapiens] >pir T00325 T00325 hypothetical protein KIAA0546 - human (fragment) >sp O60293 O60293 KIAA0546 PROTEIN (FRAGMENT). Length = 632	dbj BAA25472.1	4732	2	1954	100	100	HWBAP55	pCMVSPORT 3.0

456	872655			4733	2	361			HE2IO26	Uni-ZAP XR
457	872802	(AK001631) unnamed protein product [Homo sapiens] Length = 390	dbj BAA91797.1	4734	192	923	94	95	HEGAK44	Uni-ZAP XR
458	872852			4735	1830	2150			HOGCK09	pCMVSPORT 2.0
459	873299			4736	272	505			HE9FH03	Uni-ZAP XR
460	873633	(AJ132860) receptor for activated C kinase [Bos taurus] >emb CAA83944.1 G-beta like protein [Sus scrofa] >gb AAD37978.1 (AF146043) RACK1 [Sus scrofa] >gb AA59626.1 MHC B complex protein 12.3 [Homo sapiens] >emb CAA53062.1 B complex protein mRNA 12-3	emb CAB6479.2.1	4737	1	513	100	100	HWLUI05	pSport1
461	874164	(AC005313) protein [Arabidopsis thaliana] >pir T02714 T02714 hypothetical protein T18E12.21 - Arabidopsis thaliana >sp O81062 O81062 T18E12.21 PROTEIN. Length = 344	gb AAC34490.1	4738	88	564	54	71	HCEVS38	Uni-ZAP XR
462	874307			4739	175	384			HE2BS79	Uni-ZAP XR
463	874308			4740	12	293			HHMMB54	pSport1
464	874309			4741	306	689			HKABZ52	pCMVSPORT 2.0
465	874310	hypothetical L1 protein (third intron of gene TS) - human Length = 562	pir JU0033 JU0033	4742	258	37	74	86	HCROJ11	pSport1
466	874320	(AF164119) CRIB-containing BORG3 protein [Mus musculus] >sp AAD48816 AAD48816 CRIB-containing BORG3 protein. Length = 150	gb AAD48816.1 AF1641	4743	321	767	95	97	HWLJP34	pSport1
467	874325	(AB002342) KIAA0344 [Homo sapiens] >sp O15052 O15052 KIAA0344. Length = 1246	dbj BAA20802.1	4744	3	503	59	81	HSYDL64	pCMVSPORT 3.0

468	874327	(AC005005) similar to phosphatidylinositol (4,5)bisphosphate 5-phosphatase; match to PID:g1399105 [Homo sapiens] >sp AAD15618 AAD15618 WUGSC:H_DJ412A9.2 protein (fragment). Length = 1056	gb AAD15618.1	4745	2	838	70	71	HCE1G78	Uni-ZAP XR
469	874328	AMSH [Homo sapiens] >sp O95630 O95630 AMSH. Length = 424	gb AAD05037.1	4746	173	496	63	82	HSOBR31	Uni-ZAP XR
470	874329			4747	501	752			HLLCC54	pCMVSPORT ₁
471	874330			4748	491	685			HE2LO76	Uni-ZAP XR
472	874345			4749	350	430			HTTU53	Uni-ZAP XR
473	874348			4750	3	356			HUFDS37	pSport1
474	874349	(AC004030) F21856_2 [Homo sapiens] >pir T00636 T00636 hypothetical protein F21856_2 - human >sp O43360 O43360 F21856_2. Length = 679	gb AAB97620.1	4751	2	517	87	87	HWMAJ78	pSport1
475	874350			4752	72	428			HWADK27	pCMVSPORT _{3.0}
476	874352	(AE002030) thermoresistant gluconokinase [Deinococcus radiodurans] >pir B75338 B75338 thermoresistant gluconokinase - Deinococcus radiodurans (strain R1) >sp AAF11464 AAF11464 Thermoresistant gluconokinase. Length = 172	gb AAF11464.1 AE0020	4753	1	579	52	67	HCRNT71	pSport1
477	874358	(AB033025) KIAA1199 protein [Homo sapiens] >sp BAA86513 BAA86513 KIAA1199 protein (fragment). Length = 1013	db BAA86513.1	4754	3	584	96	96	HCRQA24	pSport1

478	874362	methionine aminopeptidase [Homo sapiens] >gb AAC63402.1 eIF-2-associated p67 homolog [Homo sapiens] >pir S52112 DPHUM2 methionyl aminopeptidase (EC 3.4.11.18) 2 - human >sp P50579 AMP2_HUMAN METHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) (METAP 2) (PEPTIDASE)	gb AAA82930.1	4755	2	1501	86	86	HUVCM45	Uni-ZAP XR
479	874368			4756	3	230			HRAAG89	pCMVSPORT 3.0
480	874369	Cell division protein FtsK. [Escherichia coli] >dbj BAA35622.1 Cell division protein FtsK. [Escherichia coli] >gb AAC73976.1 (AE000191) cell division protein [Escherichia coli] >pir A64828 A64828 cell division protein ftsK - Escherichia coli >sp P46889	dbj BAA35615.1	4757	1787	1449	84	85	HSLR04	Uni-ZAP XR
481	874370	(AF195765) L2DTL protein [Homo sapiens] Length = 730	gb AAF35182.1 AF1957	4758	3	335	74	80	HNTBD52	pCMVSPORT 3.0
482	874372	suppressor of hairless protein 1 [Xenopus laevis] >sp Q91880 Q91880 SUPPRESSOR OF HAIRLESS PROTEIN 1. Length = 501	gb AAB05478.1	4759	2	472	82	88	HNTST27	pSport1
483	874396			4760	31	210			HSKJH49	pBluescript
484	874399			4761	105	1484			HOEMK72	Uni-ZAP XR
485	874400			4762	190	405			HBKDS37	pSport1
486	874401			4763	97	501			HJMAK37	pCMVSPORT 3.0
487	874403			4764	619	936			HUSGS50	pSport1
488	874407	(AJ004856) connexin31 [Homo sapiens] >gb AAC95471.1 (AF099730) connexin 31 [Homo sapiens] >gb AAD11816.1 (AF052692) connexin 31; gap junctional protein cx31 [Homo sapiens] >pir JE0274 JE0274 connexin 31 - human >sp O75712 CXB3_HUMAN GAP JUNCTION BETA-3	emb CAA06165.1	4765	3	863	77	77	HTOJL45	Uni-ZAP XR

489	874410				4766	175	444			HLTGR10	Uni-ZAP XR
490	874411				4767	168	530			HWLQF84	pSport1
491	874413				4768	248	427			HCQBD69	Lambda ZAP II
492	874414				4769	312	545			HATBE07	Uni-ZAP XR
493	874416	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	4770	3	110	88	97	HCQDD86	Lambda ZAP II	
494	874417				4771	89	349			HUCNE27	pSport1
495	874422				4772	168	347			HCRNL83	pSport1
496	874423				4773	17	202			HCRNJ94	pSport1
497	874424				4774	216	476			HCROK63	pSport1
498	874426				4775	788	997			HCQDC45	Lambda ZAP II
499	874427	(AF118637) feline leukemia virus subgroup C receptor FLVCR [Homo sapiens] >sp Q9Y5Y0 Q9Y5Y0 C-RECEPTOR. >dbj BAA91679.1 (AK001419) unnamed protein product [Homo sapiens] {SUB 277-555} Length = 555	gb AAD45243.1 AF1186	4776	2	385	96	96	HCYBG26	pBluescript SK-	
500	874428				4777	204	497			HCRNV56	pSport1
501	874432				4778	532	828			HCYBL48	pBluescript SK-
502	874433				4779	16	258			HTODN93	Uni-ZAP XR

503	874435	(AL110261) hypothetical protein [Homo sapiens] >emb CAB53702.1 (AL110261) hypothetical protein [Homo sapiens] >pir T14782 T14782 hypothetical protein DKFZp586B0621.1 - human (fragment) >sp CAB53702 CAB53702 Hypothetical 22.8 kd protein (fragment). Length	emb CAB53702.1	4780	316	600	98	98	HWLQK42	pSport1
504	874436			4781	45	197			HODDJ01	Uni-ZAP XR
505	874437	anthracycline-associated resistance ARX [Homo sapiens] >gb AAD24434.1 AF110957_1 (AF110957) SUMO-1 activating enzyme subunit 2 [Homo sapiens] >sp O95605 O95605 ANTHRACYCLINE-ASSOCIATED RESISTANCE ARX. Length = 640	gb AAC99992.1	4782	3	1367	91	91	HNTDB90	pCMVSPORT 3.0
506	874438			4783	872	1105			HFPBQ02	Uni-ZAP XR
507	874447			4784	236	541			HTXSK90	Uni-ZAP XR
508	874449			4785	998	1258			HTECD58	Uni-ZAP XR
509	874452	beta-galactosidase alpha peptide [Cloning vector pSport2] Length = 114	gb AAA67217.1	4786	432	623	82	82	HWLQH59	pSport1
510	874455			4787	9	176			HHEPP22	pCMVSPORT 3.0
511	874458	(AF075724) [Legionella pneumophila] >sp O85769 O85769 HYPOTHETICAL 24.8 KD PROTEIN. Length = 218	gb AAC32842.1	4788	2	823	43	59	HLDDD01	pCMVSPORT 3.0
512	874459	(AF155575) peroxisomal D2,D4-dienoyl-CoA reductase [Mus musculus] >sp Q9WV68 Q9WV68 PEROXISOMAL D2,D4-DIENOYL-COA REDUCTASE. Length = 292	gb AAD38196.1 AF1555	4789	1	531	85	90	HWLRA47	pSport1
513	874460			4790	47	244			HCRMX57	pSport1
514	874461			4791	285	488			HFPEC02	Uni-ZAP XR

515	874467				4792	32	283			HMEI02	Lambda ZAP II
516	874468				4793	480	743			HKCSZ54	pBluescript
517	874469	!!!! ALU SUBFAMILY SX WARNING ENTRY !!!! Length = 591	sp P39195 ALU8_HUMAN		4794	185	262	59	61	H2CBM49	pBluescript SK-
518	874470	The KIAA0147 gene product is related to adenylyl cyclase. [Homo sapiens] >sp Q14160 Q14160 KIAA0147 PROTEIN (FRAGMENT). Length = 1551	dbj BAA09768.1		4795	2	1213	69	69	HUVGR86	Uni-ZAP XR
519	874472				4796	10	246			HCYBN52	pBluescript SK-
520	874473				4797	186	476			HDPFO58	pCMVSPORT 3.0
521	874474				4798	146	415			H2CBC28	pBluescript SK-
522	874475				4799	724	879			HCRQF18	pSport1
523	874479				4800	36	305			HE2CI70	Uni-ZAP XR
524	874480				4801	360	593			HSPAX64	pSport1
525	874481	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 ALU7_HUMAN		4802	39	176	72	77	HCRPE10	pSport1
526	874482				4803	355	612			HTOJA79	Uni-ZAP XR
527	874484				4804	938	1150			HGBGI31	Uni-ZAP XR
528	874485				4805	3	320			HCRMF12	pSport1
529	874486	(AF000996) ubiquitous TPR motif, Y isoform [Homo sapiens] Length = 1079	gb AAC51843.1		4806	2	187	75	77	HCQDD11	Lambda ZAP II
530	874492				4807	101	325			HCRPA46	pSport1

531	874495	(AL030998) dJ46618.1 (Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase) LIKE) [Homo sapiens] >sp O75659 O75659 DJ46618.1 (COAGULATION FACTOR V (ACTIVATED PROT	emb CAA1974 2.1	4808	2	562	93	94	HCRPV94	pSport1
532	874498			4809	235	615			HCRPX62	pSport1
533	874499	(AF216312) type II membrane serine protease [Homo sapiens] Length = 423	gb AAF31436. 1 AF2163	4810	2	649	98	98	HFKJJ16	Uni-ZAP XR
534	874503			4811	1	417			HL1SB93	pBluescript
535	874504			4812	41	403			HDTLA27	pCMVSPORT 2.0
536	874505	(AF045644) F57H12.7 gene product [Caenorhabditis elegans] >pir T32979 T32979 hypothetical protein F57H12.7 - Caenorhabditis elegans >sp O45100 O45100 F57H12.7 PROTEIN. Length = 262	gb AAC02603. 1	4813	3	1094	40	57	HCHCJ20	pSport1
537	874506	(AF153191) nm23-H7 [Homo sapiens] >gb AAD34622.1 AF153191_1 (AF153191) nm23-H7 [Homo sapiens] >sp Q9Y5B8 Q9Y5B8 NM23-H7. Length = 376	gb AAD34622. 1 AF1531	4814	1232	798	100	100	HLDOG81	pCMVSPORT 3.0
538	874508	54k protein (AA 1-504) [Canis familiaris] >emb CAA60132.1 SRP 54 [Homo sapiens] >gb AAC50994.1 signal recognition particle [Homo sapiens] >pir S05197 S05197 signal recognition particle 54K protein - dog >pir S54143 S54143 SRP 54 protein - human (fragment	emb CAA3438 5.1	4815	2	1213	99	99	HPMLY88	Uni-ZAP XR
539	874518			4816	2	199			HIDAC50	pSport1
540	874519			4817	2	271			HLCA01	pSport1
541	874522	(AF099066) serine/threonine-protein kinase NEK3 [Mus musculus] >sp Q9Z0X9 Q9Z0X9 SERINE/THREONINE-PROTEIN KINASE NEK3. Length = 509	gb AAD16286. 1	4818	2	463	75	82	HCRNF16	pSport1

542	874524	product specific to adipose tissue [Homo sapiens] >sp Q15847 Q15847 HYPOTHETICAL 7.9 KD PROTEIN. Length = 76	dbj BAA08226 .1	4819	89	277	75	81	HOEKX93	Uni-ZAP XR
543	874527	HUMAN NDR [unidentified] >emb CAA84485.1 Ndr protein kinase [Homo sapiens] >emb CAB39180.1 d 108K11.2 (Ndr protein kinase) [Homo sapiens] >pir 38133 38133 protein kinase (EC 2.7.1.-) Ndr - human >sp Q15208 Q15208 NDR PROTEIN KINASE. Length = 465	emb CAA0338 7.1	4820	1	783	93	93	HTTFP72	Uni-ZAP XR
544	874528	(AF062476) retinoic acid-responsive protein; STRA6 [Mus musculus] >sp O70491 O70491 RETINOIC ACID-RESPONSIVE PROTEIN. Length = 670	gb AAC16016. 1	4821	1	534	64	77	HCRND05	pSport1
545	874529	similar to Na+/H+ antiporter [Bacillus subtilis] >dbj BAA12644.1 YqkI [Bacillus subtilis] >pir B69967 B69967 Na+/H+ antiporter homolog yqkI - Bacillus subtilis >sp P54571 YQKI_BACSU HYPOTHETICAL NA+/H+ ANTIPTER IN ANSB-SPOIIM INTERGENIC REGION. Length	emb CAB1428 8.1	4822	1	534	32	53	HCRNP66	pSport1
546	874531			4823	150	269			HAPCK19	Uni-ZAP XR
547	874533			4824	830	1036			HWLIN80	pSport1
548	874534	(AF022109) HsCdc18p [Homo sapiens] >gb AAB38317.1 Cdc6-related protein [Homo sapiens] >sp Q99741 Q99741 CDC6-RELATED PROTEIN. Length = 560	gb AAC52071. 1	4825	3	920	96	96	HWMA02	pSport1
549	874537	(AF034800) liprin-alpha3 [Homo sapiens] >sp AAC26101 AAC26101 Liprin-alpha3 (fragment). Length = 443	gb AAC26101. 1	4826	192	572	83	84	HCRQI74	pSport1
550	874540	(AB014603) KIAA0703 protein [Homo sapiens] >sp O75185 O75185 KIAA0703 PROTEIN. Length = 963	dbj BAA31678 .1	4827	2	235	77	77	HCRMT48	pSport1
551	874543			4828	796	978			HDTJO85	pCMVSPORT 2.0

552	874544								1877				HIBEM35	Other
553	874545			CHOX M product [Gallus gallus] >pir J50145 J50145 homeotic protein Hox M - chicken >sp P23459 HXD8_CHICK_HOMEOBOX PROTEIN HOX-D8 (CHOX-M). Length = 188	emb CAA4044 5.1	4830	1	489	75	80			HE9QB35	Uni-ZAP XR
554	874546			centromere autoantigen B (CENP-B) [Homo sapiens] >pir S18735 S18735 centromere protein B - human >sp P07199 CENB_HUMAN MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B). >gb AAB70165.1 (AF002714) centromere protein B; CENP-B [Homo sapiens] {	emb CAA3887 9.1	4831	3	551	72	72			HCHMS55	pSport1
555	874550			peroxisome proliferator activated receptor gamma 2 [Homo sapiens] >gb AAC51248.1 ligand activated transcription factor PPARGgamma2 [Homo sapiens] >pir JC4859 JC4859 peroxisome proliferator-activated receptor gamma-2 - human >sp Q15832 Q15832 PEROXISOME PR	gb AAB04028. 1	4832	1	939	95	95			HCRPG51	pSport1
556	874551			(AF078850) steroid dehydrogenase homolog [Homo sapiens] >sp Q9Y6G8 Q9Y6G8 STEROID DEHYDROGENASE HOMOLOG. Length = 312	gb AAD44482. 1	4833	24	584	99	99			HKMLN95	pBluescript
557	874552					4834	623	919					HMIAD35	Uni-ZAP XR
558	874553			KHS1 [Homo sapiens] >sp Q9Y4K4 Q9Y4K4 KHS1. Length = 846	gb AAB48435. 1	4835	238	1140	91	92			HSYAM68	pCMVSPORT 3.0
559	874556			E2F-related transcription factor [Homo sapiens] >pir A48585 A48585 transcription factor DP-1 - human >sp Q14186 TDPI_HUMAN TRANSCRIPTION FACTOR DP-1 (E2F DIMERIZATION PARTNER 1) (DRTF1-POLYPEPTIDE-1) (DRTF1). Length = 410	gb AAA58440. 1	4836	138	1202	87	87			HDPAM86	pCMVSPORT 3.0
560	874559			(AK001902) unnamed protein product [Homo sapiens] Length = 484	dbj BAA91969 .1	4837	2	790	99	99			HNTMD17	pSport1

561	874560	gap junction protein (aa 1-283) [Homo sapiens] >pir B29005 B29005 gap junction protein Cx32 - human >sp P08034 CXB1_HUMAN GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 32) (CX32) (GAP JUNCTION 28 KD LIVER PROTEIN). Length = 283	emb CAA2785 6.1	4838	47	901	96	96	HEEAX65	Uni-ZAP XR
562	874561	!!!! ALU SUBFAMILY SX WARNING ENTRY !!!! Length = 591	sp P39195 AL U8_HUMAN	4839	2	136	72	77	HHFJL44	Uni-ZAP XR
563	874562	(AB018255) KIAA0712 protein [Homo sapiens] >sp O94820 O94820 KIAA0712 PROTEIN. Length = 1587	dbj BAA34432 .1	4840	3	842	75	76	HWHGD94	pCMVSPORT 3.0
564	874563			4841	242	481			HWLAC81	pSport1
565	874564	Nuclear localization signal at AA 569-573, 576-580, 579-583; acidic transcr. activ. domain 620-640;; homeobox motif 653-676 [Homo sapiens] >pir A47456 A47456 down-regulated in adenoma (DRA) - human >sp P40879 DRA_HUMAN DRA PROTEIN (DOWN-REGULATED IN ADENO	gb AAA58443. 1	4842	109	363	86	91	HWLEQ08	pSport1
566	874565			4843	583	828			HSQDM57	Uni-ZAP XR
567	874567	STM-7 [Homo sapiens] >sp Q92749 Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN). >gb AAC50916.1 type I phosphatidylinositol-4-phosphate 5-kinase beta [Homo sapiens] (SUB 112-502) >gb AAC50914.1 type I phosphati	emb CAA6322 4.1	4844	2	1291	93	93	HTEJC93	Uni-ZAP XR
568	874569			4845	123	311			HWLMQ11	pSport1

569	874570	(AL117555) hypothetical protein [Homo sapiens] >emb CAB55990.1 (AL117555) hypothetical protein [Homo sapiens] >pir T17300 T17300 hypothetical protein DKFZp5641171.1 - human (fragment) >sp CAB55990 CAB55990 Hypothetical 14.8 kd protein (fragment). Length	emb CAB55990.1	4846	102	485	75	79	HNSAD12	pSport1
570	874571	NBK [Homo sapiens] >emb CAA18260.2 (AL022237) bK1191B2.2 (BCL2-interacting killer (apoptosis-inducing) (NBK, BP4, BIP1)) [Homo sapiens] >gb AAC50413.1 Bik [Homo sapiens] >gb AAC79124.1 apoptosis inducer Nbk [Homo sapiens] >gb AAF01156.1 (AF174424) BCL	emb CAA62013.1	4847	3	527	100	100	HBJEN48	Uni-ZAP XR
571	874573	Eps8 [Mus musculus] >pir S39983 S39983 eps8 protein - mouse >sp Q08509 EPS8_MOUSE EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8. Length = 821	gb AAA16358.1	4848	3	539	35	56	HWMBM13	pSport1
572	874577			4849	136	468			H6BSM15	Uni-ZAP XR
573	874578			4850	87	428			HCQBD30	Lambda ZAP II
574	874580	(AF168132) RU1 [Homo sapiens] >sp AAF19794 AAF19794 RU1. Length = 866	gb AAF19794.1 AF1681	4851	202	1158	82	82	HTEEZ83	Uni-ZAP XR
575	874581			4852	858	1154			HBXCF35	ZAP Express
576	874584			4853	101	277			HWMBF85	pSport1
577	874588	(AL137514) hypothetical protein [Homo sapiens] >emb CAB70780.1 (AL137514) hypothetical protein [Homo sapiens] >sp CAB70780 CAB70780 Hypothetical 11.2 kd protein. Length = 97	emb CAB70780.1	4854	154	426	100	100	HCROA06	pSport1
578	874590			4855	686	937			HAPAY77	Uni-ZAP XR
579	874592			4856	304	618			HUSYW93	pSport1

580	874594	(AF123462) neurexin III [Homo sapiens] >sp Q9Y486 Q9Y486 NEUREXIN III (FRAGMENT). Length = 334	gb AAD13621.1	4857	2	496	79	82	HCROE11	pSport1
581	874595			4858	500	643			HWLVF65	pSport1
582	874601			4859	3	260			HWLWU62	pSport1
583	874603	(AF070637) [Homo sapiens] >sp O75547 O75547 HYPOTHETICAL 28.8 KD PROTEIN (FRAGMENT). Length = 256	gb AAC25392.1	4860	708	1139	38	64	HWLFG75	pSport1
584	874605	carcinoembryonic antigen [Homo sapiens] >gb AAB59513.1 carcinoembryonic antigen precursor [Homo sapiens] >pir A36319 A36319 carcinoembryonic antigen precursor - human >sp P06731 CCEM_HUMAN CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (gb AAA51967.1	4861	2	1786	92	92	HBCCB62	Uni-ZAP XR
585	874607	(AL117637) hypothetical protein [Homo sapiens] >emb CAB56026.1 (AL117637) hypothetical protein [Homo sapiens] >pir T17336 T17336 hypothetical protein DKFZp434I225.1 - human (fragment) >sp CAB56026 CAB56026 Hypothetical 45.3 kd protein (fragment). Length	emb CAB56026.1	4862	3	404	90	91	HWLVN89	pSport1
586	874608	A4 protein [Homo sapiens] >gb AAB92356.1 A4 differentiation-dependent protein [Homo sapiens] >gb AAF05827.1 AF196779_4 (AF196779) A4 differentiation-dependent protein [Homo sapiens] >pir S32567 S32567 A4 protein - human >sp Q04941 A4P_HUMAN INTESTINAL ME	gb AAA35499.1	4863	2	628	100	100	HTXQF81	Uni-ZAP XR
587	874609			4864	488	874			HCQDD61	Lambda ZAP II

588	874610	UDP-GalNAc:polypeptide N-acetyl-galactosaminyltransferase [Homo sapiens] >sp O00208 O00208 UDP-GALNAc:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE. Length = 578	emb CAA6987.5.1	4865	240	1187	50	66	HMCZ52	Uni-ZAP XR
589	874611			4866	96	755			HDPMG95	pCMVSPORT 3.0
590	874612			4867	103	366			HETAD58	Uni-ZAP XR
591	874614			4868	657	848			HUFAT62	pSport1
592	874615			4869	76	273			HODCH47	Uni-ZAP XR
593	874618	(AK000496) unnamed protein product [Homo sapiens] Length = 239	dbj BAA91205.1	4870	242	484	66	70	HWLV180	pSport1
594	874619	(AK000213) unnamed protein product [Homo sapiens] Length = 441	dbj BAA91013.1	4871	29	451	95	95	HNGBW96	Uni-ZAP XR
595	874620	(AC007231) putative cation transport protein [Arabidopsis thaliana] >sp AAD32753 AAD32753 Putative cation transport protein. Length = 300	gb AAD32753.1 AC0072	4872	3	725	44	70	HOSOL09	Uni-ZAP XR
596	874621	carcinoma-associated antigen GA733-2 [Homo sapiens] >gb AAB00775.1 carcinoma-associated antigen GA733-2 [Homo sapiens] >pir B48149 B48149 epithelial glycoprotein antigen GA733-2 precursor - human Length = 314	gb AAA35861.1	4873	6	1130	86	86	HWLMK56	pSport1
597	874622			4874	151	468			HWMBE67	pSport1
598	874623	occludin [Homo sapiens] >gb AAC50451.1 occludin [Homo sapiens] >pir G02533 G02533 occludin - human >sp Q16625 OCLN_HUMAN OCCLUDIN. Length = 522	gb AAB00195.1	4875	160	432	98	98	H2CAA08	pBluescript SK-
599	874624			4876	749	1012			HCRNH24	pSport1
600	874625			4877	708	971			HUFDO17	pSport1

601	874626				4878	613	870			HE8QX06	Uni-ZAP XR
602	874628				4879	46	363			HWMC68	pSport1
603	874630				4880	1213	1434			HWAG158	pCMVSPORT 3.0
604	874631	p67 myc protein [Homo sapiens] >gb AAA20042.1 c-myc protein [Homo sapiens] {SUB 16-454} >emb CAA46984.1 this region determines c-myc mRNA stability [Homo sapiens] {SUB 395-454} Length = 454	dbj BAA01374.2	4881	58	100	660	100	100	HAAAAA25	pSport1
605	874632			4882	186		365			HHEIW79	pCMVSPORT 3.0
606	874635	(AF068229) lysyl hydroxylase 3 [Homo sapiens] >gb AAC39753.1 (AF046889) lysyl hydroxylase isoform 3 [Homo sapiens] >gb AAD45831.1 AC004876_4 (AC004876) lysyl hydroxylase 3 [Homo sapiens] >sp O60568 PLO3_HUMAN PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENA	gb AAC34808.1	4883	120	97	2330	97	97	HNGGK17	Uni-ZAP XR
607	874636			4884	236		454			HCRQG35	pSport1
608	874638	(AB007917) KIAA0448 protein [Homo sapiens] >dbj BAA89250.1 (AB024568) heparan sulfate 2-sulfotransferase [Homo sapiens] >sp O75036 O75036 KIAA0448 PROTEIN. >sp BAA89250 BAA89250 Heparan sulfate 2-sulfotransferase. Length = 356	dbj BAA32293.1	4885	175	96	402	96	97	HSODQ11	Uni-ZAP XR
609	874639			4886	1		282			HWLMR54	pSport1
610	874640	(AF176555) A-kinase anchoring protein 220 [Homo sapiens] >sp AAF07045 AAF07045 A-kinase anchoring protein 220. >dbj BAA31604.1 (AB014529) KIAA0629 protein [Homo sapiens] {SUB 1290-1901} Length = 1901	gb AAF07045.1 AF1765	4887	392	95	496	95	96	HWLNI19	pSport1

611	874642	interleukin-15 receptor alpha chain precursor [Homo sapiens] >sp Q13261 Q13261 INTERLEUKIN-15 RECEPTOR ALPHA CHAIN PRECURSOR. >gb AAB88175.1 (AF035279) similar to interleukin-15 receptor alpha chain precursor [Homo sapiens] {SUB 37-267} Length = 267	gb AAC50312.1	4888	23	328	73	73	HFPHT42	Uni-ZAP XR
612	874644			4889	673	879			HLWCT94	pCMVSPORT 3.0
613	874645			4890	308	532			HWMBL25	pSportl
614	874646			4891	237	464			HWLOU23	pSportl
615	874650			4892	162	479			HWLOZ82	pSportl
616	874651			4893	128	697			HWMBF50	pSportl
617	874652			4894	199	390			HLVZA23	pSportl
618	874653			4895	444	133			HWLNL53	pSportl
619	874654			4896	154	366			HWLOZ25	pSportl
620	874655			4897	320	625			HWMBV27	pSportl
621	874656			4898	312	470			HCRQH42	pSportl
622	874657			4899	64	201			HWLOR14	pSportl
623	874658			4900	27	260			HWMBB03	pSportl
624	874659			4901	508	651			HWLOW57	pSportl
625	874660			4902	96	227			HWLOO77	pSportl
626	874662			4903	193	318			HWLOZ54	pSportl
627	874665			4904	2	310			HWLMO19	pSportl
628	874667			4905	234	467			HWLMA68	pSportl
629	874670	(AB015614) SET-binding protein (SEB) [Mus musculus] >sp Q9Z180 Q9Z180 SET-BINDING PROTEIN (SEB) (FRAGMENT). Length = 197	dbj BAA36338.1	4906	47	703	79	88	HWLNH87	pSportl
630	874671			4907	208	513			HOOHE79	pSportl
631	874672			4908	35	208			HWLOJ08	pSportl
632	874673	(AF151107) 3'-5' exonuclease TREX2 [Homo sapiens] >sp AAD48776 AAD48776 3'-5' exonuclease TREX2. Length = 236	gb AAD48776.1	4909	1	600	90	90	HBCBF08	Uni-ZAP XR

633	874675				4910	458	655			HWHGZ23	pCMV/Sport 3.0
634	874678				4911	171	293			HWLOP85	pSport1
635	874679	(AL021918) b34I8.1 (Kruppel related Zinc Finger protein 184) [Homo sapiens] >sp O60792 O60792 B34I8.1 (KRUPPEL RELATED ZINC FINGER PROTEIN 184). Length = 751	emb CAA1727 8.1	4912	1	765	98	98		HUSGX66	pSport1
636	874680			4913	2	355				HCRQM95	pSport1
637	874682	Glucosamine-6-phosphate isomerase (EC 5.3.1.10) (glucosamine-6-phosphate deaminase). [Escherichia coli] >dbj BAA3326.1 Glucosamine-6-phosphate isomerase (EC 5.3.1.10) (glucosamine-6-phosphate deaminase). [Escherichia coli] >gb AA24191.1 glucosamine-	dbj BAA3321 1	4914	549	1106	90	90		HPWAI57	Uni-ZAP XR
638	874683			4915	2	424				HWLOQ35	pSport1
639	874684	!!!! ALU SUBFAMILY SB WARNING ENTRY !!!! Length = 587	sp P39189 AL U2_HUMAN	4916	1	150	68	73		HE2EA79	Uni-ZAP XR
640	874688	putative ATPase [Haematobia irritans] >sp P46441 N2B_HAEIR PUTATIVE ATPASE N2B (HFN2B). Length = 464	gb AAA91360. 1	4917	3	638	45	66		HWLOI43	pSport1
641	874689			4918	93	389				HCRQM44	pSport1
642	874695			4919	253	924				HCRMZ25	pSport1
643	874696			4920	1	246				HCRQB95	pSport1
644	874697			4921	119	241				HWLXN82	pSport1
645	874699			4922	38	211				HWLXW08	pSport1
646	874700	(AF030881) pol polyprotein [Fugu rubripes] >sp AAC33526 AAC33526 Pol polyprotein (fragment). Length = 1187	gb AAC33526. 2	4923	71	349	32	53		HWLVR69	pSport1
647	874701	(AK000385) unnamed protein product [Homo sapiens] Length = 152	dbj BAA91131 1	4924	1	129	78	81		H2CBD62	pBluescript SK-
648	874702			4925	68	397				HMSAQ57	Uni-ZAP XR
649	874703			4926	403	678				HCRD17	pSport1

650	874704	(AB005549) atypical PKC specific binding protein [Rattus norvegicus] >pir T13948 T13948 atypical protein kinase C isotype-specific interacting protein ASIP - rat >sp Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. Length = 1337	dbj BAA34216.1	4927	3	821	78	83	H2CBN90	pBluescript SK-
651	874707	(AJ271784) chromokinesin [Homo sapiens] Length = 1232	emb CAB7542.7.1	4928	60	539	100	100	H2CBP17	pBluescript SK-
652	874708	(AK001355) unnamed protein product [Homo sapiens] Length = 291	dbj BAA91645.1	4929	81	989	94	94	HTTDU01	Uni-ZAP XR
653	874709			4930	228	473			H2CBH38	pBluescript SK-
654	874710			4931	1	363			H2CBX48	pBluescript SK-
655	874711			4932	956	1141			H2CBT32	pBluescript SK-
656	874713			4933	260	1105			HAGBH67	Uni-ZAP XR
657	874714	beta-galactosidase [Expression vector pBSII-LUCINT] Length = 69	gb AAB53629.1	4934	339	500	95	100	HE2LX05	Uni-ZAP XR
658	874715	(AK000157) unnamed protein product [Homo sapiens] Length = 301	dbj BAA90980.1	4935	1	876	91	91	HAHCU44	Uni-ZAP XR
659	874717	ORF2: function [Homo sapiens] >sp O76040 O76040 ORF2: FUNCTION . Length = 131	gb AAB61715.1	4936	303	145	73	80	HFRAM50	Uni-ZAP XR
660	874718	POM1 [Plasmodium chabaudi chabaudi] >sp Q25658 Q25658 POM1 (FRAGMENT). Length = 597	gb AAA84746.1	4937	11	811	48	66	HAIJD60	pCMVSPORT 3.0
661	874719	(AL049989) hypothetical protein [Homo sapiens] >emb CAB43229.1 (AL049989) hypothetical protein [Homo sapiens] >pir T08691 T08691 hypothetical protein DKFZp564F052.1 - human (fragment) >sp Q9Y3Z7 Q9Y3Z7 HYPOTHETICAL 48.5 KD PROTEIN (FRAGMENT). Length = 42	emb CAB4322.9.1	4938	1	1341	98	98	HTPHK47	Uni-ZAP XR

662	874720	RLF [Homo sapiens] >sp Q13129 Q13129 ZN-15 RELATED ZINC FINGER PROTEIN (RLF). Length = 1914	gb AAC50396. 1	4939	1	969	36	49	HAMGM27	pCMVSPORT 3.0
663	874723			4940	25	129			HWLXA56	pSport1
664	874724	CCHA PROTEIN PRECURSOR. [Escherichia coli] >gb AAC75510.1 (AE000332) detox protein [Escherichia coli] >pir H65020 H65020 ccha protein - Escherichia coli (strain K-12) >sp BAA16335 BAA16335 CCHA PROTEIN PRECURSOR.. >sp P77606 EUTM_ECOLI ETHANOLAMINE UTILI	dbj BAA16335 .1	4941	176	3	98	98	HGCMC86	Uni-ZAP XR
665	874725			4942	146	289			HOSPA23	Uni-ZAP XR
666	874726			4943	473	712			HBAHC42	pSport1
667	874727			4944	668	793			HUSGQ45	pSport1
668	874728			4945	396	626			HBMXP34	Uni-ZAP XR
669	874732			4946	1300	1635			HHEME74	pCMVSPORT 3.0
670	874737			4947	81	281			HCNDN66	Lambda ZAP II
671	874741	alanine aminotransférase [Homo sapiens] Length = 493	dbj BAA01186 .1	4948	12	842	66	82	H2CBI61	pBluescript SK-
672	874744			4949	111	329			HCQAE09	Lambda ZAP II
673	874745	!!! ALU SUBFAMILY SQ WARNING ENTRY !!! Length = 593	sp P39194 AL U7_HUMAN	4950	259	357	75	82	HCNDP23	Lambda ZAP II
674	874746			4951	1	225			HCQBE66	Lambda ZAP II
675	874747			4952	89	178			HCQAK59	Lambda ZAP II

676	874748	fork head-related protein [Homo sapiens] >sp P55318 HN3G_HUMAN HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G) (FORK HEAD-RELATED PROTEIN FKH H3). Length = 347	gb AAA58477.1	4953	3	248	96	96	HCQAR64	Lambda ZAP II
677	874749	unnamed protein product [unidentified] Length = 180	emb CAB6919.5.1	4954	3	362	55	67	HWMAC48	pSport1
678	874750			4955	202	333			HCQBE76	Lambda ZAP II
679	874751			4956	58	261			HWLCA32	pSport1
680	874752			4957	22	354			HWLHH20	pSport1
681	874753			4958	307	492			HCQBI72	Lambda ZAP II
682	874754			4959	347	478			HCQBH60	Lambda ZAP II
683	874755			4960	2	166			HHMMB17	pSport1
684	874756			4961	233	442			HCQCB28	Lambda ZAP II
685	874757			4962	1	282			HCQCC66	Lambda ZAP II
686	874758			4963	73	225			HOELS72	Uni-ZAP XR
687	874759			4964	3	125			HCQCB62	Lambda ZAP II
688	874760			4965	1	153			HCQCC13	Lambda ZAP II
689	874763			4966	182	661			HCQCF83	Lambda ZAP II
690	874764			4967	1	171			HCQAF27	Lambda ZAP II
691	874765			4968	929	1132			HCQC156	Lambda ZAP II
692	874766			4969	1	147			HCQCD88	Lambda ZAP II

693	874767	CTP synthetase homolog [Mus musculus] >sp P70303 P70303 CTP SYNTHETASE HOMOLOG (CTPSH). Length = 586	gb AAB17729. 1	4970	2	598	70	78	HE8OJ09	Uni-ZAP XR
694	874768			4971	1	219			HCQCR67	Lambda ZAP II
695	874769	expressed ubiquitously with strong expression in brain [Homo sapiens] >gb AAD15417.1 (AC004912) KIAA0193 [Homo sapiens] >sp Q12765 Y193_HUMAN HYPOTHETICAL PROTEIN KIAA0193. >sp AAD15417 AAD15417 KIAA0193. Length = 346	dbj BAA12106 .1	4972	477	1379	47	68	HPHAA27	Uni-ZAP XR
696	874772			4973	209	406			HCROV23	pSport1
697	874773			4974	287	490			HCRMZ75	pSport1
698	874774			4975	171	557			HCRMZ85	pSport1
699	874775			4976	1	162			HCRM08	pSport1
700	874776			4977	312	545			HBIPL82	pCMVSPORT 3.0
701	874778	(AK000025) unnamed protein product [Homo sapiens] Length = 334	dbj BAA90891 .1	4978	539	961	92	92	HBXBV89	ZAP Express
702	874779	hypothetical protein (L1H 3" region) - human Length = 1280	pir B34087 B3 4087	4979	14	250	51	66	HCRPM45	pSport1
703	874780			4980	1	168			HCQCT75	Lambda ZAP II
704	874781			4981	1	237			HCRPO92	pSport1
705	874783			4982	3	314			HCRNM87	pSport1
706	874784			4983	448	642			HBIFU36	Uni-ZAP XR
707	874785			4984	43	330			HCRPZ29	pSport1
708	874786			4985	2	232			HCRON58	pSport1

709	874787	5"-nucleotidase [Homo sapiens] >pir S11032 S11032 5"-nucleotidase (EC 3.1.3.5) precursor - human >sp P21589 5NTD_HUMAN 5"-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO- NUCLEOTIDASE) (5"-NT) (CD73 ANTIGEN). >gb AAA96950.1 5"-nucleotidase [Homo sapiens] {	emb CAA3927 1.1	4986	87	947	89	89	HCRNG90	pSport1
710	874788			4987	146	388			HCQDT67	Lambda ZAP II
711	874790	(AB024705) fls485 [Homo sapiens] >sp Q9Y2M2 Q9Y2M2 FLS485. Length = 353	dbj BAA76932 1.1	4988	249	605	98	98	HCYAC32	pBluescript SK-
712	874791	(AJ005324) glutamate permease [synthetic construct] >emb CAA06474.1 (AJ005327) glutamate permease [synthetic construct] >emb CAA06477.1 (AJ005330) glutamate permease [synthetic construct] >gb AA24514.1 gltS [Escherichia coli] {SUB 437- 459} Length = 45	emb CAA0647 1.1	4989	11	127	81	87	HCYBK32	pBluescript SK-
713	874793			4990	1	291			HWMCE07	pSport1
714	874795			4991	123	362			HCROL83	pSport1
715	874796	(AF007551) Bet1p homolog [Homo sapiens] >gb AAD47132.1 AC006378_1 (AC006378) Bet1p homolog [Homo sapiens] >sp O15155 O15155 BET1P HOMOLOG. >sp AAD47132 AAD47132 Bet1p homolog. Length = 118	gb AAB62941. 1	4992	112	522	87	87	HCYBM89	pBluescript SK-
716	874797			4993	53	388			HCRNX33	pSport1
717	874800			4994	505	699			HCYBM31	pBluescript SK-
718	874801			4995	311	415			HDAA73	pSport1
719	874802			4996	353	469			HDACJ67	pSport1
720	874803			4997	1	471			H2CBL90	pBluescript SK-
721	874804			4998	524	655			HPCOE53	pSport1

722	874805				4999	188	319				HDPGS84	pCMVSPORT 3.0
723	874807				5000	123	236				HCRMQ21	pSport1
724	874809				5001	256	357				HDTBM35	pCMVSPORT 2.0
725	874810				5002	3	359				HCYBL83	pBluescript SK-
726	874812				5003	2	220				HDTJE91	pCMVSPORT 2.0
727	874813				5004	306	605				HE6BJ48	Uni-ZAP XR
728	874815	cDNA EST EMBL:M88866 comes from this gene [Caenorhabditis elegans] >pir T20358 T20358 hypothetical protein D2030.8 - Caenorhabditis elegans >sp P90793 P90793 D2030.8 PROTEIN. Length = 648	emb CAA9812 0.1		5005	1	843	33	51		HE8NK63	Uni-ZAP XR
729	874816				5006	618	752				HDTHF30	pCMVSPORT 2.0
730	874818				5007	672	956				HDPRY54	pCMVSPORT 3.0
731	874819				5008	516	761				HE2LN12	Uni-ZAP XR
732	874820				5009	78	326				HWLUR88	pSport1
733	874821				5010	881	1108				HE8SB04	Uni-ZAP XR
734	874822				5011	108	392				HE9QM31	Uni-ZAP XR
735	874827	(AL117629) hypothetical protein [Homo sapiens] >emb CAB56021.1 (AL117629) hypothetical protein [Homo sapiens] >pir T17331 T17331 hypothetical protein DKFZp434C245.1 - human (fragment) >sp CAB56021 CAB56021 Hypothetical 21.0 kd protein (fragment). Length	emb CAB5602 1.1		5012	1	270	73	74		HTELU32	Uni-ZAP XR

736	874828	predicted using GeneFinder; Similarity to E.coli guanosine-3", 5"-bis(diphosphate)- pyrophosphohydrolase (SW:P17580) [Caenorhabditis elegans] >pir T28096 T28096 hypothetical protein ZK909.3 - Caenorhabditis elegans >sp O18307 O18307 ZK909.3 PROTEIN. Leng	emb CAB0503 0.1	5013	3	536	47	57	HEMGV90	Uni-ZAP XR
737	874829			5014	17	202			HDTMC78	pCMVSPORT 2.0
738	874830			5015	505	774			HFOXN77	pSport1
739	874832	methy thioadenosine phosphorylase [Homo sapiens] >pir I38969 I38969 5"-methy thioadenosine phosphorylase (EC 2.4.2.28) - human >sp Q13126 MTAP_HUMAN 5"- METHYLTHIOADENOSINE PHOSPHORYLASE (EC 2.4.2.28) (MTA PHOSPHORYLASE) (MTAPASE). Length = 283	gb AAA81646. 1	5016	3	155	90	90	HWLMW61	pSport1
740	874835	Gem [Homo sapiens] >pir A54575 A54575 35K GTP-binding protein Gem - human >sp P55040 GEM_HUMAN GTP-BINDING PROTEIN GEM (GTP-BINDING MITOGEN- INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR). Length = 296	gb AAA64911. 1	5017	2	1000	94	94	HHFLR55	Uni-ZAP XR
741	874836			5018	249	551			HWLQO14	pSport1
742	874837			5019	95	250			HHGDC54	Lambda ZAP II
743	874843			5020	567	719			HMSCD54	Uni-ZAP XR
744	874844			5021	339	575			HISCH48	pSport1
745	874845			5022	188	424			HHGDL18	Lambda ZAP II
746	874847			5023	2	424			HOSMQ26	Uni-ZAP XR
747	874849			5024	41	130			HISDK89	pSport1

748	874851	M130 antigen [Homo sapiens] >emb CAB45233.1 CD163 [Homo sapiens] >pir 38003 S36077 M130 antigen - human >sp Q07898 Q07898 M130 ANTIGEN PRECURSOR. Length = 1116	emb CAA8054 1.1	5025	62	784	95	96	HLSAA22	pSport1
749	874852			5026	23	178			HFOX45	pSport1
750	874854			5027	2	589			HWLOV52	pSport1
751	874855			5028	261	488			HKCAA14	Uni-ZAP XR
752	874856	f198 [Escherichia coli] >gb AAC77483.1 (AE000453) orf, hypothetical protein [Escherichia coli] >pir E65179 E65179 hypothetical 22.4 kD protein in trpT-pssR intergenic region - Escherichia coli (strain K-12) >sp P22788 YIFA_ECOLI HYPOTHETICAL 22.4 KD PROT	gb AAA67566. 1	5029	390	1	90	91	HMAA02	Uni-ZAP XR
753	874857			5030	7	402			HKABV02	pCMVSPORT 2.0
754	874858			5031	59	262			HKGBD56	pSport1
755	874859			5032	2	427			HKACE03	pCMVSPORT 2.0
756	874864	(AB022914) TES101RP [Mus musculus] >sp BAA90265 BAA90265 TES101RP. Length = 250	dbj BAA90265 .1	5033	3	767	31	50	HBIOR20	pCMVSPORT 3.0
757	874865			5034	3	236			HKEAA44	ZAP Express
758	874866			5035	222	335			HKLSA63	pBluescript
759	874867			5036	491	619			HKGCI22	pSport1
760	874870			5037	796	1062			HOGDO85	pCMVSPORT 2.0
761	874871			5038	1	528			HLDXX53	pCMVSPORT 3.0
762	874873	(AF151842) CGI-84 protein [Homo sapiens] >sp AAD34079 AAD34079 CGI-84 protein. Length = 213	gb AAD34079. 1 AF1518	5039	38	859	80	80	HKAHI56	pCMVSPORT 2.0

763	874875	ORF4 [Rattus norvegicus] >pir S21348 S21348 probable pol. protein-related protein 4 - rat >sp Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF"S. Length = 275	emb CAA3764 7.1	5040	376	444	52	72	HLTBL32	Uni-ZAP XR
764	874876			5041	250	468			HLTHZ36	Uni-ZAP XR
765	874877			5042	48	158			HMEES39	Lambda ZAP II
766	874879			5043	118	378			HMKA091	pSport1
767	874880			5044	317	688			HLYAQ21	pSport1
768	874881	(AF022857) neuropilin-2(b0) [Mus musculus] >sp O35376 O35376 NEUROFILIN 2. Length = 901	gb AAC53380. 1	5045	74	490	82	84	HCRNL20	pSport1
769	874885	GTP-binding protein - mouse Length = 198	pir S39543 S39 543	5046	128	730	99	100	HSYDX40	pCMVSPORT 3.0
770	874886	(AK000178) unnamed protein product [Homo sapiens] Length = 358	dbj BAA90992 .1	5047	2	913	90	90	HWLOQ11	pSport1
771	874888	(AF129534) F-box protein Fbx4 [Homo sapiens] >sp AAF04468 AAF04468 F-box protein Fbx4. Length = 387	gb AAF04468. 1 AF1295	5048	409	1170	82	84	HMTAD91	pCMVSPORT 3.0
772	874889			5049	2	136			HOSFI36	Uni-ZAP XR
773	874890			5050	568	849			HHEYM94	pCMVSPORT 3.0
774	874891	SPIN protein [Homo sapiens] >gb AAC08315.1 (AF038969) general transcription factor 2-I [Homo sapiens] >sp O15359 O15359 SPIN PROTEIN. Length = 957	emb CAA7516 3.1	5051	2	601	87	88	HPWCL64	Uni-ZAP XR
775	874892			5052	2	538			HNTSQ62	pSport1
776	874893	ROK-alpha [Rattus norvegicus] >sp Q62868 Q62868 ROK-ALPHA. Length = 1379	gb AAB37540. 1	5053	177	395	67	71	HRDDU54	Uni-ZAP XR
777	874894			5054	1	180			HRDBA25	Uni-ZAP XR

778	874895				5055	543	758			HSRAI45	Uni-ZAP XR
779	874896				5056	338	192			HSABG91	pBluescript SK-
780	874897				5057	880	1191			HWLGN30	pSport1
781	874898				5058	2	202			HSPAL74	pSport1
782	874899				5059	149	346			HRDFM44	Uni-ZAP XR
783	874900	sin3 associated polypeptide p18 [Homo sapiens] >gb AAD41090.1 AF153608_1 (AF153608) sin3 associated polypeptide [Homo sapiens] >sp O00422 SP18_HUMAN SIN3 ASSOCIATED POLYPEPTIDE P18. Length = 153	gb AAC51322.1		5060	7	147	74	86	HCYB179	pBluescript SK-
784	874902	Cks1 protein homologue [Homo sapiens] >pir B36670 B36670 cell division control protein CKS2 - human >sp P33552 CKS2_HUMAN CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (CKS-2). Length = 79	emb CAA3870.3.1		5061	3	341	100	100	HSUBX76	Uni-ZAP XR
785	874903	cDNA EST yk425a6.3 comes from this gene; cDNA EST yk406e6.3 comes from this gene; cDNA EST yk425a6.5 comes from this gene; cDNA EST yk480c6.5 comes from this gene; cDNA EST yk406e6.5 comes from this gene [Caenorhabditis elegans] >sp CAA79619 CAA79619 F02A	emb CAA7961.9.1		5062	184	1044	24	45	HNEAF57	Uni-ZAP XR
786	874904				5063	135	317			HWLRA09	pSport1
787	874905				5064	552	941			HSUSB86	pBluescript

788	874906	bumetanide-sensitive Na-K-Cl cotransporter [Homo sapiens] >pir A57187 A57187 bumetanide-sensitive Na-K-Cl cotransporter - human >sp P55011 NKCL1_HUMAN BUMETANIDE-SENSITIVE SODIUM-(POTASSIUM)-CHLORIDE COTRANSPORTER 1 (BASOLATERAL NA-K-CL SYMPORTER). Length	gb AAC50561.1	5065	2	1027	99	99	HOSAK80	Uni-ZAP XR
789	874907	(AF049089) casein kinase I gamma 3 [Homo sapiens] >sp Q9Y6M4 Q9Y6M4 CASEIN KINASE I GAMMA 3. Length = 447	gb AAD26525.1 AF0490	5066	2	196	77	77	HE8TM43	Uni-ZAP XR
790	874908	AH antigen [Homo sapiens] >pir PC4035 PC4035 cell-cycle-dependent 350K nuclear protein - human (fragment) >sp Q13171 Q13171 AH ANTIGEN (FRAGMENT). Length = 1017	gb AAA86889.1	5067	2	235	71	77	HTTBS45	Uni-ZAP XR
791	874909			5068	24	599			HLYA114	pSport1
792	874912			5069	289	405			HODFU18	Uni-ZAP XR
793	874914			5070	22	459			HTXCZ25	Uni-ZAP XR
794	874917			5071	171	548			HWD4U63	pCMVSPORT 3.0
795	874924	homeotic protein Hox-3.6 - mouse >sp P31257 HXCA_MOUSE HOMEOBOX PROTEIN HOX-C10 (HOX-3.6). >pir B60941 B60941 homeotic protein hox 3l - human (fragment) {SUB 268-333} >sp P31312 HXCB_MOUSE HOMEOBOX PROTEIN HOX-C11 (HOX-3.7) (FRAGMENT). {SUB 268-327} >gb A	pir A56552 A56552	5072	33	647	88	92	HWHHG74	pCMVSPORT 3.0
796	874925			5073	156	407			HWLIES3	pSport1

797	874926	homeobox protein Cdx1 [Homo sapiens] >sp P47902 CDX1_HUMAN HOMEBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEBOX PROTEIN 1). >gb AAC50237.1 caudal-type homeobox protein [Homo sapiens] {SUB 63-265} >gb AAA80284.1 caudal-type homeobox protein [Homo sapiens] {SUB 1	gb AAB40602.1	5074	1	183	78	78	HWLLR30	pSport1
798	874927	artifact-warning sequence (translated ALU class B) - human Length = 301	pir B40201 B4 0201	5075	3	173	52	62	HLYCA86	pSport1
799	874928			5076	161	814			HDPTI77	pCMVSPORT 3.0
800	874929			5077	874	1050			HWBDT18	pCMVSPORT 3.0
801	874930	(AL137608) hypothetical protein [Homo sapiens] >emb CAB70840.1 (AL137608) hypothetical protein [Homo sapiens] >sp CAB70840 CAB70840 Hypothetical 46.0 kd protein (fragment). Length = 398	emb CAB70840.1	5078	2	463	31	51	HWLMV62	pSport1
802	874931	neutrophil gelatinase associated lipocalin [Homo sapiens] >sp P80188 NGAL_HUMAN NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (25 KD ALPHA-2-MICROGLOBULIN-RELATED SUBUNIT OF MMP-9) (LIPOCALIN-2) (ONCOGENE 24P3). >gb AAD14168.1 S75256_1	emb CAA5812.7.1	5079	2	763	100	100	H2MAC06	pBluescript SK-
803	874932			5080	374	547			HTNAL08	pBluescript SK-
804	874933			5081	114	341			HCQAM40	Lambda ZAP II
805	874934			5082	85	282			HWLQA72	pSport1

806	874936	TFIIIE-beta [Homo sapiens] >gb AAB20414.1 general transcription factor IIE 34 kda subunit, TFIIIE 34 kda subunit [human, Peptide, 291 aa] [Homo sapiens] >pir S29292 S29292 transcription factor TFIIIE-beta - human >sp P29084 T2EB_HUMAN TRANSCRIPTION INITIATI	emb CAA4506 9.1	5083	3	1085	93	93	H2LAD85	pBluescript SK-
807	874937			5084	388	594			HFKHN59	Uni-ZAP XR
808	874938			5085	320	619			HWLRB64	pSportl
809	874939	!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 AL U7_HUMAN	5086	1	63	93	93	HWLQB30	pSportl
810	874944			5087	1	132			HWLRS70	pSportl
811	874946			5088	1	717			HWLRO68	pSportl
812	874951			5089	2	373			HDLAZ62	pCMVSPORT 2.0
813	874957	(AF151831) CGI-73 protein [Homo sapiens] >sp Q9Y382 Q9Y382 CGI-73 PROTEIN. Length = 335	gb AAD34068. 1 AF1518	5090	294	941	31	51	HCRPS91	pSportl
814	874958	ets2 protein [Homo sapiens] >gb AAB94057.1 (AF017257) erythroblastosis virus oncogene homolog 2 protein [Homo sapiens] >pir B32066 TVHUE2 transcription factor ets-2 - human >sp P15036 ETS2_HUMAN C-ETS-2 PROTEIN. >gb AAA52411.1 ets protein [Homo sapiens]	gb AAA52412. 1	5091	3	1607	93	93	HUVFU42	Uni-ZAP XR
815	874962	keratin 18 [Homo sapiens] >gb AAA59463.1 keratin 18 precursor [Homo sapiens] >emb CAA31375.1 cytokeratin 18 [Homo sapiens] >pir S05481 S05481 keratin 18, type I, cytoskeletal - human >sp P05783 K1CR_HUMAN KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18)	gb AAA59461. 1	5092	3	1358	88	88	HDTAC50	pCMVSPORT 2.0
816	874965			5093	94	423			HWLWO06	pSportl
817	874970			5094	3	200			HWLWP88	pSportl

818	874972	tumor-associated antigen [Homo sapiens] >pir A36056 A36056 tumor-associated antigen CO-029 - human >sp P19075 CO02_HUMAN TUMOR-ASSOCIATED ANTIGEN CO-029. Length = 237	gb AAA35709.1	5095	207	929	94	94	HWLHW19	pSportl
819	874973			5096	641	883			HNTAI83	pCMVSPORT 3.0
820	874974			5097	2	310			HWLWS24	pSportl
821	874975			5098	3	431			HWLWP62	pSportl
822	874976	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	5099	1	363	81	87	HOENV16	Uni-ZAP XR
823	874977			5100	61	186			HCRPM57	pSportl
824	874978			5101	84	227			HWLQT35	pSportl
825	874979			5102	689	823			HTWBQ51	pSportl
826	874980			5103	39	209			HWLWS65	pSportl
827	874981			5104	8	175			HCRQC24	pSportl
828	874983	precursor polypeptide (AA -21 to 782) [Homo sapiens] >pir A35954 A35954 endoplasmic precursor - human >sp P14625 ENPL_HUMAN ENDOPLASMIN PRECURSOR (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (GP96 HOMOLOG) (TUMOR REJECTION ANTIGEN 1). Length = 803	emb CAA3326.1.1	5105	1	1110	93	93	HTFNM11	pSportl
829	874984			5106	748	939			HFUG95	pSportl
830	874985			5107	617	808			HSRFC02	Uni-ZAP XR
831	874989			5108	155	448			HCRPC43	pSportl
832	874990	!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 ALU7_HUMAN	5109	318	362	68	75	HMSPB24	Uni-ZAP XR
833	874991	KIAA0168 [Homo sapiens] >sp P50749 Y168_HUMAN HYPOTHETICAL PROTEIN KIAA0168. Length = 326	dbj BAA11485.1	5110	3	434	40	57	HWLWI83	pSportl

834	874992				5111	77	412			HCQB118	Lambda ZAP II
835	874993	calpain [Rattus norvegicus] Length = 703	dbj BAA03369.1		5112	438	713	80	94	HWMBE49	pSport1
836	874994	!!!! ALU SUBFAMILY SC WARNING ENTRY !!!! Length = 585	sp P39192 ALU5_HUMAN		5113	369	449	75	78	HCRPH59	pSport1
837	874995	(AK001568) unnamed protein product [Homo sapiens] Length = 718	dbj BAA91761.1		5114	1	999	98	99	HCRPJ86	pSport1
838	874996				5115	3	146			HCRPH30	pSport1
839	874997	!!!! ALU SUBFAMILY SP WARNING ENTRY !!!! Length = 593	sp P39193 ALU6_HUMAN		5116	259	378	68	77	HCRPH54	pSport1
840	874998				5117	252	347			HCRPH69	pSport1
841	874999	retrovirus-related reverse transcriptase pseudogene - human >sp P08547 LIN1_HUMAN LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. Length = 1259	pir A25313 GNHUL1		5118	330	377	45	68	HWLVX08	pSport1
842	875001	(AB002631) collectin 34 [Homo sapiens] >sp Q9Y6Z7 Q9Y6Z7 COLLECTIN 34. Length = 277	dbj BAA81747.1		5119	64	222	60	77	HKLAA30	Lambda ZAP II
843	875002				5120	346	528			HWLVW59	pSport1
844	875003	mucin 2 precursor, intestinal - human (fragments) >gb AAA59163.1 mucin [Homo sapiens] {SUB 626-1895} >gb AAA59164.1 MUC2 [Homo sapiens] {SUB 2037-3020} >gb AAA36334.1 intestinal mucin [Homo sapiens] {SUB 1916-2193} >gb AAA59861.1 mucin-like protein [H	pir A49963 A43932		5121	3	569	77	80	HWLJN18	pSport1
845	875004				5122	3	677			HCROH01	pSport1
846	875005				5123	147	260			HCRPJ81	pSport1
847	875007				5124	211	423			HETGS43	Uni-ZAP XR
848	875008	cytochrome P450 IID6 [Homo sapiens] Length = 497	gb AAA53500.1		5125	1	552	99	99	HWLRS46	pSport1
849	875009				5126	1	252			HWLRS57	pSport1

850	875011	ubiquinone-binding protein (QP) [Homo sapiens] >gb AAA60238.1 ubiquinone-binding protein precursor [Homo sapiens] >emb CAA31926.1 ubiquinone-binding protein (AA 1 - 111) [Homo sapiens] >pir A32450 A32450 ubiquinone-binding protein QP-C - human >sp P1492	gb AAA60235. 1	5127	2	373	98	98	HUSJO81	pSportl
851	875017			5128	62	247			HCRPF66	pSportl
852	875018			5129	460	606			HRMAF73	pSportl
853	875019			5130	3	185			HMSMR90	Uni-ZAP XR
854	875020			5131	281	454			HWLQM66	pSportl
855	875024			5132	146	331			HCRON47	pSportl
856	875025			5133	50	259			HWLVRV45	pSportl
857	875027			5134	818	1105			HFGAB06	Uni-ZAP XR
858	875029	!!!! ALU SUBFAMILY SC WARNING ENTRY !!!! Length = 585	sp P39192 AL U5_HUMAN	5135	128	304	82	84	HWLVA35	pSportl
859	875032	(AB014528) KIAA0628 protein [Homo sapiens] >sp O75123 O75123 KIAA0628 PROTEIN. Length = 536	dbj BAA31603 .1	5136	1	210	97	97	HCRPQ86	pSportl
860	875034	!!!! ALU SUBFAMILY SP WARNING ENTRY !!!! Length = 593	sp P39193 AL U6_HUMAN	5137	147	380	89	93	HCROZ20	pSportl
861	875035	(AF132963) CGI-29 protein [Homo sapiens] >sp Q9Y318 Q9Y318 CGI-29 PROTEIN. Length = 242	gb AAD27738. 1 AF1329	5138	66	242	100	100	HFPKD18	Uni-ZAP XR
862	875036			5139	94	261			HCR0S59	pSportl
863	875037			5140	2	226			HCROR65	pSportl
864	875038			5141	44	142			HZAAD77	pSportl
865	875042			5142	178	303			HCRPA12	pSportl
866	875044			5143	1325	1678			HMEKZ86	Lambda ZAP II
867	875045			5144	357	566			HCRPR27	pSportl
868	875046			5145	184	312			HCRPQ46	pSportl
869	875047			5146	75	236			HCRPN09	pSportl

870	875048				5147	35	205			HCRPK03	pSportl
871	875049				5148	138	440			HWLHY62	pSportl
872	875053				5149	81	509			H2CBP44	pBluescript SK-
873	875055				5150	3	242			HCROW75	pSportl
874	875056				5151	1	87			HCROW65	pSportl
875	875058	(AK000361) unnamed protein product [Homo sapiens] Length = 692	dbj BAA91111.1		5152	18	560	99	99	HPICF45	Uni-ZAP XR
876	875059				5153	170	295			HCRON87	pSportl
877	875060				5154	240	632			HIBEL82	Other
878	875061				5155	41	235			HCRPE83	pSportl
879	875062	(AJ009937) nuclear hormone receptor PRR2-A [Homo sapiens] >sp CAB55492 CAB55492 Nuclear hormone receptor PRR2-A. >emb CAB55494.1 (AJ009937) nuclear hormone receptor PRR2-B [Homo sapiens] {SUB 56-397} Length = 397	emb CAB55492.1		5156	3	95	87	90	HWLUQ22	pSportl
880	875063	homeobox protein Gsh-1 [Mus musculus] >pir S63604 S63604 homeobox protein Gsh-1 - mouse >sp P31315 GSHI_MOUSE HOMEBOX PROTEIN GSH-1. >pir A37290 A37290 homeotic protein Gsh-1 - mouse (fragment) {SUB 146-205} >sp G601819 G601819 HPX HOMEBOX PROTEIN {CLON	gb AAA96814.1		5157	1	324	65	67	HCRPE63	pSportl
881	875066	(AF195951) signal recognition particle 68 [Homo sapiens] >sp AAF24308 AAF24308 Signal recognition particle 68. Length = 619	gb AAF24308.1 AAF1959		5158	2	1315	98	99	HCRPE76	pSportl
882	875067				5159	1	825			HCRPE44	pSportl
883	875068				5160	2	439			HCRPE34	pSportl
884	875070	(AF151354) general transcription factor 3 [Homo sapiens] >sp AAF19786 AAF19786 General transcription factor 3. Length = 959	gb AAF19786.1 AAF1513		5161	1	489	96	97	HE8QV20	Uni-ZAP XR

885	875076	(AB007925) KIAA0456 protein [Homo sapiens] >sp O75044 O75044 KIAA0456 PROTEIN (FRAGMENT). >gb AAC52480.1 FBP 27 [Mus musculus] {SUB 756-806} Length = 1095	dbj BAA32301 .1	5162	2	577	69	75	HBIBQ89	Uni-ZAP XR
886	875080	(AB029036) KIAA1113 protein [Homo sapiens] >sp BAA83065 BAA83065 KIAA1113 protein (fragment). Length = 1131	dbj BAA83065 .1	5163	2	958	90	90	HFAAD07	Uni-ZAP XR
887	875081	DIA-12C protein [Homo sapiens] >emb CAB39108.1 (AL031053) dJ267M20.1 (diaphanous (Drosophila, homolog) 2) [Homo sapiens] {SUB 685-906} Length = 1096	emb CAA7586 9.1	5164	16	576	91	91	H2LAY41	pBluescript SK-
888	875088	(AL031673) dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2 type Zinc finger domains) [Homo sapiens] >sp Q9Y3M9 Q9Y3M9 dJ694B14.1 (PUTATIVE NOVEL KRAB BOX PROTEIN WITH 18 C2H2 TYPE ZINC FINGER DOMAINS) (FRAGMENT). Length = 738	emb CAB4354 8.1	5165	2	799	86	88	HDP1G12	pCMVSPORT 3.0
889	875092	(AL132964) putative protein [Arabidopsis thaliana] >sp CAB62464 CAB62464 Hypothetical 189.6 kd protein. Length = 1672	emb CAB6246 4.1	5166	2	385	42	63	HMVCZ67	pSport1
890	875093	male-enhanced antigen-2 [Mus musculus] >sp P55937 G160_MOUSE GOLGIN-160 (MALE- ENHANCED ANTIGEN-2) (MEA-2). Length = 1325	dbj BAA19612 .1	5167	2	385	56	59	HWLRF06	pSport1
891	875094	zinc finger protein (mkr5) [Mus musculus] >sp P10078 ZF28_MOUSE ZINC FINGER PROTEIN 28 (ZFP-28) (MKR5 PROTEIN) (FRAGMENT). Length = 614	gb AAA37120. 1	5168	2	424	61	66	HTNB190	pBluescript SK-
892	875099			5169	133	312			HWLUZ75	pSport1
893	875100	(AK000196) unnamed protein product [Homo sapiens] Length = 239	dbj BAA91003 .1	5170	36	497	97	99	HDTBD43	pCMVSPORT 2.0
894	875101			5171	1	243			HWLUG07	pSport1

895	875102	[Mus musculus] >pir T30250 T30250 GT1 protein - mouse >sp Q61818 Q61818 HYPOTHETICAL 196.0 KD PROTEIN. Length = 1840	dbj BAA06184.1	5172	158	3	69	69	HCRPV30	pSport1
896	875103			5173	9	332			HTPHV54	Uni-ZAP XR
897	875105			5174	172	426			HWLMY30	pSport1
898	875106			5175	29	262			HTTFJ81	Uni-ZAP XR
899	875110			5176	431	826			HDPCC41	pCMVSPORT 3.0
900	875113			5177	243	473			HINAA28	pSport1
901	875114	(AK000388) unnamed protein product [Homo sapiens] Length = 440	dbj BAA91133.1	5178	3	428	69	74	HTEBS63	Uni-ZAP XR
902	875115			5179	384	560			HCROK18	pSport1
903	875118			5180	3	317			HCROK31	pSport1
904	875121	(AK001720) unnamed protein product [Homo sapiens] Length = 605	dbj BAA91860.1	5181	3	653	86	86	HCROE24	pSport1
905	875123	spasmolytic peptide [Homo sapiens] >sp Q03403 SP HUMAN SPASMOLYTIC POLYPEPTIDE PRECURSOR (SP). Length = 129	gb AAB05397.1	5182	80	529	87	87	H2CBN19	pBluescript SK-
906	875124			5183	150	329			HDTLM04	pCMVSPORT 2.0
907	875125			5184	266	445			HOCTE49	pSport1
908	875126			5185	129	284			HWLNR78	pSport1
909	875131			5186	487	693			HCEDD96	Uni-ZAP XR
910	875133			5187	3	371			HHFHS96	Uni-ZAP XR
911	875134			5188	71	271			HWLNO90	pSport1
912	875139			5189	79	249			HE2JO22	Uni-ZAP XR
913	875143			5190	106	2			HCYB96	pBluescript SK-

914	875144	(AJ222767) ATPase subunit 6 [Cavia porcellus] >sp CAB51823 CAB51823 ATPase subunit 6. Length = 226	emb CAB5182 3.1	5191	113	169	63	73	HCQDV29	Lambda ZAP II
915	875150			5192	100	285			HCRPQ66	pSport1
916	875151	(AL035071) dJ1085F17.1.1 (ortholog of mouse DNMT3B (DNA Cytosine-5 Methyltransferase 3B1) (isoform 1)) [Homo sapiens] >gb AAD53063.1 AF156488_1 (AF156488) DNA cytosine-5 methyltransferase 3 beta 1 [Homo sapiens] >sp AAD53063 AAD53063 DNA cytosine- 5 methyl	emb CAB5307 0.1	5193	2	979	94	94	HE9RN07	Uni-ZAP XR
917	875154			5194	1	234			HDQEJ55	pCMV'Sport 3.0
918	875156			5195	2	157			HCYBJ95	pBluescript SK-
919	875157			5196	108	218			HCUDX92	ZAP Express
920	875160			5197	3	200			HCRON75	pSport1
921	875165			5198	3	116			HWLNR94	pSport1
922	875174			5199	541	846			HCRPY40	pSport1
923	875177			5200	1066	1299			HHEXW67	pCMV'Sport 3.0
924	875178			5201	1	78			HWLNH10	pSport1
925	875182	(AF170583) ets homologous factor [Homo sapiens] >sp AAF06998 AAF06998 Ets homologous factor. Length = 300	gb AAF06998. 1 AF1705	5202	133	1041	99	99	HDQEG93	pCMV'Sport 3.0
926	875190	(AB015349) HRIHFB2063 [Homo sapiens] >sp BAA88120 BAA88120 HRIHFB2063 protein (fragment). Length = 269	dbj BAA88120 .1	5203	3	341	74	88	HWLQT75	pSport1
927	875192			5204	57	194			HCRND03	pSport1

928	875194	(AF102166) intracellular chloride channel CLIC3 [Homo sapiens] >sp O95833 CLIC3_HUMAN CHLORIDE INTRACELLULAR CHANNEL PROTEIN 3. Length = 207	gb AAD16450.1	5205	3	179	100	100	HCWUO91	ZAP Express
929	875197			5206	77	208			HDTIP90	pCMVSPORT 2.0
930	875198			5207	392	538			HE9TA31	Uni-ZAP XR
931	875200			5208	264	464			HFPBV89	Uni-ZAP XR
932	875203			5209	1099	1407			HWLQZ89	pSport1
933	875205			5210	304	579			HCRMV90	pSport1
934	875206	(AF083105) HMG box factor SOX-13 [Homo sapiens] >sp O95275 O95275_HMG_BOX_FACTOR SOX-13. Length = 890	gb AAC83687.1	5211	260	1030	76	77	HNBFB35	pSport1
935	875208	(AK000010) unnamed protein product [Homo sapiens] Length = 385	dbj BAA90881.1	5212	359	577	100	100	HCQAW68	Lambda ZAP II
936	875209	!!!! ALU SUBFAMILY SC WARNING ENTRY !!!! Length = 585	sp P39192 ALU5_HUMAN	5213	196	318	57	66	HWLRR89	pSport1
937	875210			5214	170	406			HEICC11	Uni-ZAP XR
938	875211	protein involved in sexual development [Homo sapiens] >sp Q92600 Q92600_CELL DIFFERENTIATION PROTEIN RCD1. Length = 299	dbj BAA13508.1	5215	3	872	95	95	HOHAU31	pCMVSPORT 2.0
939	875214			5216	165	344			HHEVA12	pCMVSPORT 3.0
940	875215	(AK000693) unnamed protein product [Homo sapiens] Length = 452	dbj BAA91324.1	5217	1	279	98	100	HWLPE33	pSport1
941	875223			5218	339	662			HCRME38	pSport1
942	875226	(AK000572) unnamed protein product [Homo sapiens] Length = 328	dbj BAA91263.1	5219	166	582	83	84	HUSFH63	pBluescript
943	875228			5220	114	488			HMWDC28	Uni-ZAP XR

944	875236				5221	887	1183			HUVDI48	Uni-ZAP XR
945	875238				5222	209	388			HCQBE84	Lambda ZAP II
946	875239	(AF023158) tyrosine phosphatase [Homo sapiens] >sp O43183 O43183 TYROSINE PHOSPHATASE (EC 3.1.3.48). Length = 459	gb AAB88293.1		5223	2	637	84	84	HCYBI39	pBluescript SK-
947	875240				5224	221	364			HCRMW50	pSport1
948	875246				5225	612	905			HCQDF84	Lambda ZAP II
949	875253	artifact-warning sequence (translated ALU class C) - human Length = 613	pir C40201 C40201		5226	241	408	68	74	HNHOD84	Uni-ZAP XR
950	875254				5227	355	636			HACCF57	Uni-ZAP XR
951	875261				5228	1	72			HHPGU61	Uni-ZAP XR
952	875269	put. Cyt repressor (aa 1-341) [Escherichia coli] >gb AAB03066.1 CG Site No. 887 [Escherichia coli] >gb AAC76916.1 (AE000467) regulator for deo operon, udp, cdd, tsx, nupC, and nupG [Escherichia coli] >pir A24963 RPECCT cyt transcription repressor cytr -	emb CAA2731.8.1		5229	72	470	96	96	HFATS83	Uni-ZAP XR
953	875270	similar to G9a gene. [Homo sapiens] >sp Q15047 Q15047 KIAA0067 PROTEIN. Length = 1291	dbj BAA06689.1		5230	134	916	86	87	HAMFL51	pCMVSPORT 3.0
954	875271				5231	1174	1350			HPLBS64	Uni-ZAP XR
955	875275				5232	1	117			HHFGS83	Uni-ZAP XR
956	875276				5233	2	214			HCQAI83	Lambda ZAP II
957	875277				5234	128	370			HKIAB83	Uni-ZAP XR
958	875278	(AK000553) unnamed protein product [Homo sapiens] Length = 298	dbj BAA91249.1		5235	3	257	98	98	HOUAT80	Uni-ZAP XR

959	875279				5236	187	345				HCUCG82	ZAP Express
960	875280				5237	279	458				HWLMY83	pSportl
961	875281				5238	557	733				HHGDB82	Lambda ZAP II
962	875282				5239	46	207				HHEMA27	pCMVSPORT 3.0
963	875287				5240	60	269				HWLQS11	pSportl
964	875288				5241	203	559				HCRNO87	pSportl
965	875292				5242	1	438				HCRQI83	pSportl
966	875296				5243	192	503				HCQDD32	Lambda ZAP II
967	875303				5244	3	1385				HDPQA93	pCMVSPORT 3.0
968	875304				5245	2	364				HCQDT68	Lambda ZAP II
969	875305				5246	617	853				HE2RW42	Uni-ZAP XR
970	875306				5247	535	720				HAGDP04	Uni-ZAP XR
971	875307				5248	1	234				HWLRA80	pSportl
972	875308	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 ALU7_HUMAN		5249	125	364	64	70		HWLRC80	pSportl
973	875309	!!!! ALU SUBFAMILY J WARNING ENTRY !!!! Length = 591	sp P39188 ALU1_HUMAN		5250	94	273	54	64		HWBBH79	pCMVSPORT 3.0
974	875310				5251	674	880				HJMAF44	pCMVSPORT 3.0
975	875311				5252	408	569				HWLWT47	pSportl
976	875312	weak similarity to SP:YAD5_CLOAB (P33746) hypothetical protein and to PIR:C48583 stress-inducible protein STI1 [Caenorhabditis elegans] >pir T29012 T29012 hypothetical protein ZK328.7 - Caenorhabditis elegans >sp Q23468 Q23468 SIMILARITY TO SP:YAD5_CLOAB.	gb AAA91253.1		5253	3	299	33	56		HWLVG85	pSportl

977	875313	(AL137496) hypothetical protein [Homo sapiens] >emb CAB70771.1 (AL137496) hypothetical protein [Homo sapiens] >sp CAB70771 CAB70771 Hypothetical 58.1 kd protein (fragment). Length = 521	emb CAB7077 1.1	5254	2	433	98	99	HMVDQ41	pSport1
978	875316			5255	3	170			HCQCM79	Lambda ZAP II
979	875319	(AL031177) dJ889M15.3 (novel protein) [Homo sapiens] >sp O95534 O95534 DJ889M15.3 (NOVEL PROTEIN) (FRAGMENT). Length = 394	emb CAA2011 9.1	5256	145	1446	37	54	HMSGP80	Uni-ZAP XR
980	875324			5257	204	407			HCRNJ78	pSport1
981	875325			5258	31	258			HWLOY24	pSport1
982	875331	tetracycline transporter-like protein [Mus musculus] >pir JC5641 JC5641 sugar transporter protein HiAT1 - mouse >sp P70187 P70187 HIPPOCAMPUS ABUNDANT PROTEIN TRANSCRIPT 1 (TETRACYCLINE TRANSPORTER-LIKE PROTEIN). Length = 490	dbj BAA22622 .1	5259	3	317	84	86	HDQFG33	pCMV Sport 3.0
983	875332			5260	246	416			HWBCW80	pCMV Sport 3.0
984	875336			5261	2	76			HCRNL77	pSport1
985	875338			5262	2	292			H2CBI34	pBluescript SK-
986	875341			5263	15	395			HCYBD76	pBluescript SK-
987	875346			5264	372	503			HKMMQ08	pBluescript
988	875347			5265	1	381			HILCJ69	pBluescript SK-

989	875355	regulatory protein [Mus musculus] >emb CAA47648.1 npdcf-1 [Mus musculus] >pir 48691 48691 regulatory protein - mouse >sp Q64322 NPD1_MOUSE NEURAL PROLIFERATION DIFFERENTIATION AND CONTROL PROTEIN-1 PRECURSOR (NPDC-1 PROTEIN). Length = 332	gb AAA39836.1	5266	464	1138	78	82	HDPGF81	pCMVSPORT 3.0
990	875356	regulatory protein [Mus musculus] >emb CAA47648.1 npdcf-1 [Mus musculus] >pir 48691 48691 regulatory protein - mouse >sp Q64322 NPD1_MOUSE NEURAL PROLIFERATION DIFFERENTIATION AND CONTROL PROTEIN-1 PRECURSOR (NPDC-1 PROTEIN). Length = 332	gb AAA39836.1	5267	30	341	89	91	HUSGQ41	pSport1
991	875360			5268	711	968			HPMFC89	Uni-ZAP XR
992	875364			5269	429	662			HWLWK37	pSport1
993	875366	(AF050078) growth arrest specific 11 [Homo sapiens] >gb AAC69519.1 (AF050079) growth arrest specific 11 [Homo sapiens] >sp O95995 O95995 GROWTH ARREST SPECIFIC 11. Length = 478	gb AAC69518.1	5270	74	211	95	97	HSYAG49	pCMVSPORT 3.0
994	875367	!!!! ALU SUBFAMILY J WARNING ENTRY !!!! Length = 591	sp P39188 ALU1_HUMAN	5271	152	298	62	65	HAGFQ75	Uni-ZAP XR
995	875371	(AK001527) unnamed protein product [Homo sapiens] Length = 790	dbj BAA91741.1	5272	94	297	86	86	HCHMQ74	pSport1
996	875372			5273	32	220			HCQCL42	Lambda ZAP II
997	875373	apomucin [Homo sapiens] >pir A57534 A57534 mucin (clone L31) - human (fragment) >sp Q13792 Q13792 APOMUCIN (FRAGMENT). Length = 1042	emb CAA8830.7.1	5274	2	772	97	97	HHFOB15	Uni-ZAP XR
998	875377			5275	94	267			HCRMB64	pSport1
999	875378	(AJ245539) GalNAc-T5 [Homo sapiens] >sp CAB65104 CAB65104 GalNAc-T5 (fragment). Length = 668	emb CAB6510.4.1	5276	1	615	99	99	H2LAB72	pBluescript SK-

1000	875379	(AF186461) ring finger protein Fxy [Rattus norvegicus] >sp AAD56247 AAD56247 Ring finger protein Fxy. Length = 667	gb AAD56247.1 AF1864	5277	124	687	27	50	HE8OD44	Uni-ZAP XR
1001	875380			5278	274	432			HCRMZ16	pSport1
1002	875381			5279	189	365			HWLMZ75	pSport1
1003	875382			5280	252	503			HWLMT21	pSport1
1004	875384			5281	315	656			HCEMB73	Uni-ZAP XR
1005	875385			5282	485	655			HWLNF24	pSport1
1006	875388			5283	1	183			HNHNC74	Uni-ZAP XR
1007	875391			5284	269	544			HCRNF23	pSport1
1008	875397	KIAA0242 protein [Homo sapiens] >sp Q92575 Q92575 MYELOBLAST KIAA0242 (FRAGMENT). Length = 529	dbj BAA13437.1	5285	120	1790	82	82	HFXXKG78	Lambda ZAP II
1009	875402			5286	230	358			HFPFG11	Uni-ZAP XR
1010	875405			5287	153	581			HCROG59	pSport1
1011	875406			5288	77	220			HLYBH74	pSport1
1012	875410	(AL031033) C321D2.4 (novel protein) [Homo sapiens] >sp CAB53058 CAB53058 C321D2.4 (novel protein) (fragment). Length = 262	emb CAB53058.1	5289	1	696	88	88	HBGKNK79	Uni-ZAP XR
1013	875415			5290	53	328			HCQCX73	Lambda ZAP II
1014	875416			5291	111	230			HWLQG73	pSport1
1015	875417			5292	41	190			HMSIB72	Uni-ZAP XR
1016	875418			5293	158	328			HWLMC85	pSport1
1017	875419			5294	872	991			HCRNH72	pSport1
1018	875423			5295	316	462			HSDHD72	Uni-ZAP XR
1019	875425			5296	2	238			HCQAB70	Lambda ZAP II
1020	875427			5297	210	386			HCQDN71	Lambda ZAP II

1021	875428	(AC004955) supported by ESTs T61992 (NID:g665235) and W26450 (NID:g1307167) and Genscan [Homo sapiens] >sp AAD51455 AAD51455 WUGSC:H_DJ1087M19.1 protein. Length = 557	gb AAD51455.1 AC0049	5298	2	550	97	98	HCQCQ73	Lambda ZAP II
1022	875429			5299	251	454			HCQAW10	Lambda ZAP II
1023	875433			5300	2	280			HCRNE71	pSportl
1024	875434			5301	598	822			HWLNY71	pSportl
1025	875437			5302	151	396			HTXSH02	Uni-ZAP XR
1026	875440	similar to protein kinase of X.laevis, has putative transmembrane domain in central region [Homo sapiens] >sp Q14680 Q14680 KIAA0175 PROTEIN. Length = 651	dbj BAA11492.1	5303	1	816	79	83	H2CBL70	pBluescript SK-
1027	875441	(AF047441) RNA polymerase I 40kD subunit [Homo sapiens] >sp O75395 O75395 RNA POLYMERASE I 40KD SUBUNIT. Length = 342	gb AAC39892.1	5304	80	184	95	95	HNFFQ01	Uni-ZAP XR
1028	875442			5305	294	590			HCRMD70	pSportl
1029	875446			5306	133	330			HWLWX54	pSportl
1030	875452	(AL137489) hypothetical protein [Homo sapiens] >emb CAB70768.1 (AL137489) hypothetical protein [Homo sapiens] >sp CAB70768 CAB70768 Hypothetical 12.7 kd protein (fragment). Length = 116	emb CAB70768.1	5307	115	558	87	87	HD7BL01	pCMVSPORT 2.0
1031	875458			5308	1	231			HTHDF09	Uni-ZAP XR
1032	875460	(AF037448) Gry-rbp [Homo sapiens] >sp O60506 O60506 GRYP-RBP. Length = 623	gb AAC12926.1	5309	1	2112	99	99	HOHAD26	pCMVSPORT 2.0
1033	875461			5310	3	209			HWLQB70	pSportl
1034	875462	(AF086709) NAG-7 protein [Homo sapiens] >sp Q9Y6C7 Q9Y6C7 NAG-7 PROTEIN. Length = 94	gb AAD45398.1	5311	11	358	100	100	HCRNI70	pSportl
1035	875463			5312	221	520			HCHAN69	pSportl

1036	875468			5313	218	406			HDPX169	pCMVSPORT 3.0
1037	875474			5314	66	872			H2CBP05	pBluescript SK-
1038	875475			5315	1	354			HWLNO16	pSport1
1039	875477			5316	250	498			HCROC40	pSport1
1040	875478			5317	147	377			HWLWW31	pSport1
1041	875479			5318	3	197			HWLOU12	pSport1
1042	875481			5319	1	396			HPTTL69	Uni-ZAP XR
1043	875484			5320	130	273			HT3BA65	Uni-ZAP XR
1044	875486			5321	72	260			HMSHD68	Uni-ZAP XR
1045	875490			5322	456	716			HSUAE53	Uni-ZAP XR
1046	875491			5323	29	265			HTJMN69	pCMVSPORT 2.0
1047	875492			5324	3	296			HHMMMD68	pSport1
1048	875493	mucin 2 precursor, intestinal - human (fragments) >gb AAA59163.1 mucin [Homo sapiens] {SUB 626- 1895} >gb AAA59164.1 MUC2 [Homo sapiens] {SUB 2037-3020} >gb AAA36334.1 intestinal mucin [Homo sapiens] {SUB 1916-2193} >gb AAA59861.1 mucin-like protein [H	pir A49963 A4 3932	5325	1	534	97	97	HCQDM23	Lambda ZAP II
1049	875495			5326	140	292			HHEMO68	pCMVSPORT 3.0
1050	875496			5327	460	609			H2CBM67	pBluescript SK-
1051	875498			5328	21	344			HWLWJ34	pSport1
1052	875499			5329	187	387			HWLRL54	pSport1
1053	875500			5330	74	268			HCROI48	pSport1
1054	875501			5331	336	524			HCRMM67	pSport1

1055	875502	NEDD1 PROTEIN (FRAGMENT). >dbj BAA01554.1 nedd-1 protein [Mus musculus] {SUB 16-675} Length = 675	sp P33215 NE D1_MOUSE	5332	2	1213	79	88	HTFNZ86	pSport1
1056	875503			5333	205	402			HCNCD90	Lambda ZAP II
1057	875508	(AB002334) KIAA0336 [Homo sapiens] >sp O15045 O15045 KIAA0336. Length = 1583	dbj BAA20794 .1	5334	2	775	87	89	HMVDK54	pSport1
1058	875512			5335	138	317			HCQCV65	Lambda ZAP II
1059	875514			5336	2	373			HWLNY66	pSport1
1060	875515	(AB023201) KIAA0984 protein [Homo sapiens] >sp Q9Y2I9 Q9Y2I9 KIAA0984 PROTEIN (FRAGMENT). Length = 728	dbj BAA76828 .1	5337	17	424	100	100	HLYC165	pSport1
1061	875516			5338	2	361			HKAAO67	pCMVSPORT 2.0
1062	875517			5339	126	260			HCE3W64	Uni-ZAP XR
1063	875518	RAS-RELATED PROTEIN R-RAS2 (RAS-LIKE PROTEIN TC21) (TERATOCARCINOMA ONCOGENE). Length = 204	sp P17082 RR A2_HUMAN	5340	22	885	95	95	HKAKX87	pCMVSPORT 2.0
1064	875520	GATA-6 [Homo sapiens] >gb AAC50941.1 hGATA-6 [Homo sapiens] >sp Q92908 GAT6_HUMAN TRANSCRIPTION FACTOR GATA-6 (GATA BINDING FACTOR-6). Length = 449	dbj BAA22621 .1	5341	1	837	99	99	HUSGX12	pSport1
1065	875523			5342	1	165			HCNDZ15	Lambda ZAP II
1066	875525	catalase [Campylobacter jejuni] >pir 40767 40767 catalase (EC 1.11.1.6) - Campylobacter jejuni >sp Q59296 CATA_CAMJE CATALASE (EC 1.11.1.6). Length = 507	emb CAA5944 4.1	5343	306	130	84	89	HCFNM40	pSport1
1067	875527	(AK001870) unnamed protein product [Homo sapiens] Length = 278	dbj BAA91953 .1	5344	261	569	93	94	HMSGC65	Uni-ZAP XR

1068	875528				5345	3	155			HCQDN81	Lambda ZAP II
1069	875529				5346	389	676			HFICY86	pSport1
1070	875534	HsMcm6 [Homo sapiens] >sp Q14566 MCM6_HUMAN DNA REPLICATION LICENSING FACTOR MCM6 (P105MCM). Length = 821	dbj BAA12699 .1		5347	3	875	96	96	HNTSA70	pSport1
1071	875538				5348	2	100			HWLMX64	pSport1
1072	875539				5349	1	162			HTWFG63	pSport1
1073	875543				5350	2	241			HWLNY32	pSport1
1074	875544	ATPase 6 [Homo sapiens] >gb AAB58948.1 ATPase 6 [Homo sapiens] >pir A01049 PWHU6 H+- transporting ATP synthase (EC 3.6.1.34) protein 6 - human mitochondrion >sp P00846 ATP6_HUMAN ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6). Length = 226	emb CAA2403 .1		5351	175	333	71	74	HLJDL64	pCMVSPORT 1
1075	875545	(AF059531) protein arginine N-methyltransferase 3 [Homo sapiens] >sp O60678 O60678 PROTEIN ARGININE N-METHYLTRANSFERASE 3 (FRAGMENT). Length = 512	gb AAC39837. 1		5352	1	555	90	90	HHEQN62	pCMVSPORT 3.0
1076	875546				5353	193	420			HCQAF61	Lambda ZAP II
1077	875547				5354	22	207			HCQCX63	Lambda ZAP II
1078	875548				5355	411	650			HOVET54	pSport1
1079	875550	(AK000399) unnamed protein product [Homo sapiens] Length = 427	dbj BAA91139 .1		5356	108	455	99	100	HRODW53	Uni-ZAP XR
1080	875551	similar to hypothetical protein YM9959.11C of S.cerevisiae. [Homo sapiens] >sp Q14690 RRP5_HUMAN RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT). Length = 1884	dbj BAA11502 .1		5357	46	597	98	99	H2CBE60	pBluescript SK-
1081	875552				5358	88	318			HWMCK45	pSport1

1082	875553				5359	14	262			HKAF160	pCMVSPORT 2.0
1083	875554				5360	193	438			HUSXP66	pSport1
1084	875556	beta-galactosidase alpha peptide [Cloning vector pSport2] Length = 114	gb AAA67217.1		5361	328	627	98	98	HTLEY14	Uni-ZAP XR
1085	875558	(AK002174) unnamed protein product [Homo sapiens] Length = 508	dbj BAA92121.1		5362	2	1138	39	58	HOFMV44	pCMVSPORT 2.0
1086	875559	(AC002542) similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens] >sp O14577 O14577 WUGSC:H_RG114A06.1 PROTEIN. Length = 434	gb AAB70111.1		5363	3	392	84	88	HSLJN60	Uni-ZAP XR
1087	875560				5364	150	365			HCQAG54	Lambda ZAP II
1088	875563				5365	256	441			HHMMD60	pSport1
1089	875564				5366	799	1038			HWLMB59	pSport1
1090	875565	(AB033011) KIAA1185 protein [Homo sapiens] >sp BAA86499 BAA86499 KIAA1185 protein (fragment). Length = 403	dbj BAA86499.1		5367	2	1081	100	100	HUFAU68	pSport1
1091	875567	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5		5368	2	130	80	82	H2LAX58	pBluescript SK-
1092	875570				5369	524	757			HCRQD82	pSport1
1093	875572				5370	183	323			HCRPV05	pSport1
1094	875573				5371	148	330			HHECM62	pCMVSPORT 3.0
1095	875574				5372	375	542			HFOXW88	pSport1
1096	875578	(AF121775) nasopharyngeal carcinoma susceptibility protein LZ16 [Homo sapiens] >sp AAF24125 AAF24125 Nasopharyngeal carcinoma susceptibility protein LZ16. Length = 366	gb AAF24125.1 AF1217		5373	2	715	50	62	HWLXT17	pSport1

1097	875583				5374	434	667				HODAY72	Uni-ZAP XR
1098	875584				5375	3	164				HCQBI56	Lambda ZAP II
1099	875585				5376	283	438				HTTCM45	Uni-ZAP XR
1100	875587				5377	367	612				HARNM58	pCMVSPORT 3.0
1101	875588				5378	150	1019				HMIAQ09	Uni-ZAP XR
1102	875589				5379	156	332				HE9MD57	Uni-ZAP XR
1103	875590				5380	695	1150				HCQDA63	Lambda ZAP II
1104	875594				5381	337	564				HWLRO57	pSportl
1105	875596				5382	303	452				HHEQO60	pCMVSPORT 3.0
1106	875597				5383	371	769				HMUBG89	pCMVSPORT 3.0
1107	875598				5384	134	355				HDPRN70	pCMVSPORT 3.0
1108	875600				5385	234	446				HCRMC33	pSportl
1109	875604				5386	130	351				HROBR56	Uni-ZAP XR
1110	875605				5387	211	402				HWLMU33	pSportl
1111	875606	The KIAA0143 gene product is related to a putative C.elegans gene encoded on cosmid C32D5. [Homo sapiens] >sp Q14156 Y143_HUMAN HYPOTHETICAL PROTEIN KIAA0143 (FRAGMENT). Length = 885	dbj BAA09764.1	5388	1	660	92	92			HCRQC94	pSportl
1112	875608				5389	430	624				HCRMQ55	pSportl
1113	875609				5390	207	569				HSZAF81	Uni-ZAP XR

1114	875610				5391	251	397			HTJMO37	pCMVSPORT 2.0
1115	875611				5392	197	430			HKCSA54	pBluescript
1116	875612				5393	60	206			HWLQA55	pSport1
1117	875613	protein [Homo sapiens] >sp Q14288 Q14288 HYPOTHETICAL PROTEIN (FRAGMENT). Length = 641	gb AAA88038.1	5394	567	653	43	56		HWBDT63	pCMVSPORT 3.0
1118	875625			5395	97	657				H2CBQ54	pBluescript SK-
1119	875628			5396	28	252				HCQCX54	Lambda ZAP II
1120	875629			5397	135	377				HCQCG75	Lambda ZAP II
1121	875630			5398	382	630				HHEZN36	pCMVSPORT 3.0
1122	875631	TAR RNA loop binding protein [Homo sapiens] >pir S62356 S62356 TRP-185 protein - human >sp Q13395 Q13395 TAR RNA LOOP BINDING PROTEIN. Length = 1621	gb AAC50379.1	5399	1	681	89	89		HPCIS18	Other
1123	875632			5400	436	600				HISAT54	pSport1
1124	875633			5401	3	272				HLWAC54	pCMVSPORT 3.0
1125	875634	(AF072759) fatty acid transport protein 4; FATP4 [Mus musculus] >sp O88562 O88562 FATTY ACID TRANSPORT PROTEIN 4 (FATP4) (LONG- CHAIN FATTY ACID TRANSPORT PROTEIN 4) (FRAGMENT). Length = 506	gb AAC40188.1	5402	2	145	86	95		HKMAB82	Uni-ZAP XR
1126	875635	(AB028997) KIAA1074 protein [Homo sapiens] >sp BAA83026 BAA83026 KIAA1074 protein. >dbj BAA91516.1 (AK001137) unnamed protein product [Homo sapiens] {SUB 1-546} >emb CAB70706.1 (AL137351) hypothetical protein [Homo sapiens] {SUB 1337-1709} Length = 1709	dbj BAA83026.1	5403	3	302	50	67		HPVAB96	Uni-ZAP XR

1127	875636				5404	113	226			HBMSX53	Uni-ZAP XR
1128	875638				5405	2043	2228			HCFC58	pSport1
1129	875639	(AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens] >gb AAF04511.1 AF174590_1 (AF174590) F-box protein Fbl4 [Homo sapiens] >sp O95919 O95919 dJ273N12.1 (PUTATIVE PROTEIN BASED ON EST MATCHES) (FRAGMENT). >sp AAF04511 AAF04511 F-bo	emb CAB3798 .1	5406	3	87	551	89		HPMK129	Uni-ZAP XR
1130	875640	(AB032253) bromodomain adjacent to zinc finger domain 1B [Homo sapiens] >dbj BAA89210.1 (AB032253) bromodomain adjacent to zinc finger domain 1B [Homo sapiens] >sp BAA89210 BAA89210 Bromodomain adjacent to zinc finger domain 1B. Length = 1527	dbj BAA89210 .1	5407	639	93	905	93		HMWFZ60	Uni-ZAP XR
1131	875641	(AF071771) SPH-binding factor [Homo sapiens] Length = 551	gb AAC96102. 1	5408	3	91	968	91		HUCPH16	pSport1
1132	875642			5409	97		288			HCUDA52	ZAP Express
1133	875646			5410	1		81			HTWCN56	pSport1
1134	875650	(AB023416) ASC [Homo sapiens] >sp BAA87339 BAA87339 ASC protein. Length = 195	dbj BAA87339 .1	5411	85	85	699	85	85	HWLUF58	pSport1
1135	875651	(AB023416) ASC [Homo sapiens] >sp BAA87339 BAA87339 ASC protein. Length = 195	dbj BAA87339 .1	5412	8	76	481	78		HWLMI53	pSport1
1136	875653			5413	3		122			HWLMB54	pSport1
1137	875654			5414	449		655			HOEEY53	Uni-ZAP XR

1138	875658	(AL137442) hypothetical protein [Homo sapiens] >emb CAB70739.1 (AL137442) hypothetical protein [Homo sapiens] >sp CAB70739 CAB70739 Hypothetical 34.5 kd protein (fragment). Length = 316	emb CAB7073 9.1	5415	1	558	98	99	HUCQC25	pSportl
1139	875661			5416	440	556			HCRMS71	pSportl
1140	875662			5417	180	341			HWLMS13	pSportl
1141	875663			5418	282	554			HE6GF82	Uni-ZAP XR
1142	875665			5419	1	108			HSPBC14	pSportl
1143	875669			5420	132	419			HOCNE41	pSportl
1144	875672			5421	159	266			HCQBE51	Lambda ZAP II
1145	875673			5422	3	197			HWLWX40	pSportl
1146	875677	(AK000040) unnamed protein product [Homo sapiens] Length = 387	dbj BAA90899 .1	5423	65	265	88	89	HCRMB51	pSportl
1147	875678			5424	246	533			HGBBH61	Uni-ZAP XR
1148	875680	[Homo sapiens] >sp Q99770 Q99770 HYPOTHETICAL 15.4 KD PROTEIN. Length = 139	gb AAB50206. 1	5425	12	86	63	73	HCRNZ51	pSportl
1149	875681			5426	295	540			H2CAA51	pBluescript SK-
1150	875682	(AK000219) unnamed protein product [Homo sapiens] Length = 420	dbj BAA91018 .1	5427	1	504	98	98	HT3AI55	Uni-ZAP XR
1151	875683			5428	2	244			HLWBA37	pCMVSPORT 3.0
1152	875687			5429	165	332			HE2LP33	Uni-ZAP XR

1153	875688	(AB021638) X11-like protein 2 [Homo sapiens] >gb AAC72275.1 (AC005954) mint 3 [Homo sapiens]; X11gamma [Homo sapiens] >pir JG0181 JG0181 X11L2 protein - human >sp O96018 APB3 HUMAN AMYLOID BETA A4 PRECURSOR PROTEIN-BINDING FAMILY A MEMBER 3 (NEURON- SPEC	dbj BAA74430.1	5430	216	401	91	91	HCRMN10	pSport1
1154	875689			5431	707	1105			HKMMR61	pBluescript
1155	875690			5432	156	347			HUFDC50	pSport1
1156	875697			5433	44	280			HKLAB51	Lambda ZAP II
1157	875698	(AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens] >sp Q9Y6N0 Q9Y6N0 NADH:UBIQUINONE OXIDOREDUCTASE PGIV SUBUNIT. Length = 172	gb AAD42056.1 AF0449	5434	71	619	100	100	HCGBB63	pSport1
1158	875699	(AB015041) PIF1 [Caenorhabditis elegans] >pir T37310 T37310 PIF1 protein - Caenorhabditis elegans >sp O61299 O61299 PIF1. Length = 677	dbj BAA28677.1	5435	402	596	41	50	HRGDD40	Uni-ZAP XR
1159	875700	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	5436	11	154	93	93	H2LAD49	pBluescript SK-
1160	875703			5437	3	188			HMSGN49	Uni-ZAP XR
1161	875704	(AK000820) unnamed protein product [Homo sapiens] Length = 122	dbj BAA91388.1	5438	2	490	79	79	HWLMC49	pSport1
1162	875705			5439	1187	1390			HAVME52	Other
1163	875708	(AF113131) host cell factor homolog LCP [Homo sapiens] >dbj BAA91898.1 (AK001771) unnamed protein product [Homo sapiens] >sp Q9Y2U9 Q9Y2U9 HOST CELL FACTOR HOMOLOG LCP. Length = 406	gb AAD21038.1	5440	2	511	44	58	HCQDP49	Lambda ZAP II

1164	875717	(AF074264) LDL receptor-related protein 6 [Homo sapiens] >pir JE0272 JE0272 low density lipoprotein receptor-related protein 6 - human >sp O75581 O75581 LDL RECEPTOR-RELATED PROTEIN 6. Length = 1613	gb AAC33006.1	5441	216	575	81	81	HCROW44	pSportl
1165	875719			5442	101	265			HDPHF03	pCMVSPORT 3.0
1166	875722			5443	553	927			HCRMO82	pSportl
1167	875724			5444	273	1133			HFCDF47	Uni-ZAP XR
1168	875725			5445	528	698			HFICJ16	pSportl
1169	875727			5446	183	482			HWLLU74	pSportl
1170	875728			5447	470	823			HLMIDL53	Uni-ZAP XR
1171	875729			5448	10	174			HODBC46	Uni-ZAP XR
1172	875731	(AF060219) RCC1-like G exchanging factor RLG [Homo sapiens] >sp O95199 O95199 RCC1-LIKE G EXCHANGING FACTOR RLG. Length = 551	gb AAC79987.1	5449	192	485	93	98	HCYBO46	pBluescript SK-
1173	875733			5450	251	808			HCUEB32	ZAP Express
1174	875734			5451	141	260			HCRNQ45	pSportl
1175	875736			5452	520	726			HWLOO86	pSportl
1176	875737			5453	1	387			HSPME53	pSportl
1177	875738	(AJ005273) Kin17 [Homo sapiens] >sp O60870 O60870 KIN17 PROTEIN. Length = 393	emb CAA0646.2.1	5454	16	267	98	100	H2CBE48	pBluescript SK-
1178	875739			5455	145	318			HCQDJ47	Lambda ZAP II
1179	875740			5456	1	138			HDTKC01	pCMVSPORT 2.0
1180	875746			5457	3	194			HCQDI44	Lambda ZAP II

1181	875747	(AL050348) dJ447F3.2 (ubiquitin-conjugating enzyme E2 H10) [Homo sapiens] >gb AAB53362.1 cyclin-selective ubiquitin carrier protein [Homo sapiens] >sp O00762 UBCB_HUMAN_UBIQUITIN-CONJUGATING ENZYME E2 H10 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUIT	emb CAB6611 8.1	5458	112	330	75	76	HNFGP44	Uni-ZAP XR
1182	875751			5459	2	280			HWLQG44	pSport1
1183	875752			5460	58	207			HHMMD44	pSport1
1184	875753			5461	83	283			HCQAC43	Lambda ZAP II
1185	875754			5462	265	450			HWLUF33	pSport1
1186	875760			5463	321	500			HCRPE66	pSport1
1187	875761			5464	310	441			HCYBD73	pBluescript SK-
1188	875765	reverse transcriptase [Homo sapiens] Length = 361	gb AAB02291.1	5465	61	2	49	60	HWTCF43	Uni-ZAP XR
1189	875766			5466	193	366			HCRNA26	pSport1
1190	875768			5467	240	488			HCQDD42	Lambda ZAP II
1191	875769			5468	2	238			HCRNN21	pSport1
1192	875772			5469	78	812			HCRNH26	pSport1
1193	875773			5470	38	124			HDPWD42	pCMVSPORT 3.0
1194	875774			5471	1	243			HTAET42	Uni-ZAP XR
1195	875778			5472	650	808			HMCIK65	Uni-ZAP XR
1196	875779			5473	2	316			HDTGQ43	pCMVSPORT 2.0

1197	875780	GD3 synthase [Homo sapiens] >gb AAC37586.1 ganglioside-specific alpha-2, 8-polysialyltransferase [Homo sapiens] >pir A54032 A54032 alpha-N-acetylneuraminase alpha-2,8-sialyltransferase (EC 2.4.99.8) - human >sp Q92185 CAG8_HUMAN ALPHA-N-ACETYL-NEURAMINNI	emb CAA5489 1.1	5474	498	863	87	88	HT2SF78	Uni-ZAP XR
1198	875781	ZK520.1 [Caenorhabditis elegans] >pir T27880 T27880 hypothetical protein ZK520.1 - Caenorhabditis elegans >sp O46018 O46018 ZK520.1 PROTEIN. Length = 519	emb CAB0729 9.1	5475	2	712	38	61	HCRM60	pSport1
1199	875782			5476	67	492			HCRNC13	pSport1
1200	875783			5477	142	264			HCRPH74	pSport1
1201	875784			5478	92	283			HCQDW41	Lambda ZAP II
1202	875785			5479	175	318			HCRMZ22	pSport1
1203	875786			5480	220	423			HCQDE41	Lambda ZAP II
1204	875787			5481	230	532			HMKCZ06	pSport1
1205	875789			5482	908	1168			HMEGG05	Lambda ZAP II
1206	875792			5483	156	332			HNTMD41	pSport1
1207	875794	(AK002156) unnamed protein product [Homo sapiens] Length = 326	dbj BAA92113 .1	5484	2	721	95	97	HCRNJ24	pSport1
1208	875798			5485	315	455			HWABK33	pCMV Sport 3.0
1209	875800			5486	282	497			HCYBC44	pBluescript SK-
1210	875801			5487	283	507			HWLQA40	pSport1
1211	875804			5488	1	330			HWHP143	pCMV Sport 3.0
1212	875805			5489	25	390			HKCSF43	pBluescript

1213	875808					5490	462	752			HCQAD39	Lambda ZAP II
1214	875809	(AJ001714) Myosin-IXA [Homo sapiens] >sp CAA04947 CAA04947 Myosin-IXA (fragment). Length = 774	emb CAA0494 7.1	5491	207	1088	95	95	95	95	HCRNL08	pSportl
1215	875810			5492	2	256					HCRNY14	pSportl
1216	875814	(AF105376) heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3A [Homo sapiens] >sp Q9Y663 Q9Y663 HEPARAN SULFATE D-GLUCOSAMINYL 3-O-SULFOTRANSFERASE-3A (EC 2.8.2.23). Length = 406	gb AAD30208.1 AF1053	5493	3	824	52	54			HCRQG46	pSportl
1217	875815			5494	226	423					HCRQK63	pSportl
1218	875816			5495	149	499					HWLVS38	pSportl
1219	875817	(AL035461) dJ967N21.5 (novel MCM2/3/5 family member) [Homo sapiens] >sp CAB55276 CAB55276 dJ967N21.5 (novel MCM2/3/5 family member) (fragment). Length = 606	emb CAB5527 6.1	5496	44	556	91	94			HCRNT27	pSportl
1220	875819			5497	12	83					HCRMT24	pSportl
1221	875820			5498	1	222					HCRNQ33	pSportl
1222	875821			5499	22	480					HWLUO71	pSportl
1223	875822	ARG5,6 [Candida albicans] >sp P78586 AR56_CANAL ARG5,6 PROTEIN PRECURSOR [CONTAINS: N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38) (N-ACETYL-GLUTAMATE SEMIALDEHYDE DEHYDROGENASE) (NAGSA DEHYDROGENASE); ACETYLGUTAMATE KINASE (EC 2.7.2.8) (NAG K	emb CAA6738 3.1	5500	336	761	31	54			HTXRZ02	Uni-ZAP XR
1224	875824			5501	3	302					HWMO47	pSportl
1225	875825	(AF156551) putative E1-E2 ATPase [Mus musculus] >sp AAAF09449 AAAF09449 Putative E1-E2 ATPase. Length = 1187	gb AAAF09449.1 AF1565	5502	3	497	63	78			HCQCC37	Lambda ZAP II

1226	875826					5503	289	450			HUVGY13	Uni-ZAP XR
1227	875828	(AL110217) hypothetical protein [Homo sapiens] >emb CAB53677.1 (AL110217) hypothetical protein [Homo sapiens] >pir T14757 T14757 hypothetical protein DKFZp572C163.1 - human (fragment) >sp CAB53677 CAB53677 Hypothetical 80.6 kd protein (fragment). Length	emb CAB5367 7.1	5504	3	662	64	74	HPMFM59		Uni-ZAP XR	
1228	875832			5505	126	458			HCROI42		pSport1	
1229	875833	(AF192529) RPA-binding trans-activator [Homo sapiens] >sp AAF05761 AAF05761 RPA-binding trans-activator. Length = 196	gb AAF05761. 1 AF1925	5506	460	930	65	66	HACBB04		Uni-ZAP XR	
1230	875834			5507	276	410			HMMAC34		pSport1	
1231	875836			5508	49	522			HDPFA20		pCMVSPORT 3.0	
1232	875837			5509	1	162			HTGBQ40		Uni-ZAP XR	
1233	875838			5510	177	329			HDPWD53		pCMVSPORT 3.0	
1234	875839			5511	1	360			HCROZ63		pSport1	
1235	875840			5512	347	547			HWABJ67		pCMVSPORT 3.0	
1236	875841			5513	572	865			HCRMV91		pSport1	
1237	875845			5514	441	623			HNTRA39		pSport1	
1238	875846			5515	437	595			HCRPW33		pSport1	
1239	875848			5516	89	187			HFCFI37		Uni-ZAP XR	
1240	875849			5517	11	214			HCQCL72		Lambda ZAP II	
1241	875850			5518	732	1016			HCQCT09		Lambda ZAP II	
1242	875851			5519	1	123			HCRM12		pSport1	
1243	875852			5520	100	564			HCIAE18		pSport1	

1244	875855				5521	137	415			HHFHU39	Uni-ZAP XR
1245	875856				5522	121	264			HCQAW29	Lambda ZAP II
1246	875858				5523	3	509			HBMDM33	pBluescript
1247	875863				5524	2	202			HKLSD32	pBluescript
1248	875864	predicted using Genefinder; cDNA EST yk469a11.5 comes from this gene [Caenorhabditis elegans] >emb CAB01706.1 predicted using Genefinder; cDNA EST yk469a11.5 comes from this gene [Caenorhabditis elegans] >pir T21387 T21387 hypothetical protein F26A3.7 -	emb CAB0654 5.1		5525	1	516	33	50	HYACE34	pCMVSPORT 3.0
1249	875865	DNA binding protein [Homo sapiens] >sp P51523 ZN84 HUMAN ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2). >pir B32891 B32891 finger protein 2, placental - human {SUB 88-738} >sp G238102 G238102 ZINC FINGER. {SUB 71-257} Length = 738	gb AAA79359.1		5526	3	230	98	100	HNTTC18	pSport1
1250	875868	(AF191018) E2IG3 [Homo sapiens] >sp AAF09482 AAF09482 E2IG3. Length = 560	gb AAF09482.1 AF1910		5527	788	1981	82	84	H2CAA34	pBluescript SK-
1251	875871				5528	177	410			HWLQA33	pSport1
1252	875874				5529	24	263			HCQCT65	Lambda ZAP II
1253	875884				5530	2189	2653			HWHP150	pCMVSPORT 3.0
1254	875886				5531	220	408			HCRQD12	pSport1
1255	875888				5532	26	460			HNHHM31	Uni-ZAP XR
1256	875891	polypeptide BM28 [Homo sapiens] >pir S42228 S42228 replication licensing factor MCM2 - human Length = 892	emb CAA4774 9.1		5533	3	341	100	100	HCRQG23	pSport1

1257	875894	finger protein 1, placental - human >sp P51522 ZN83_HUMAN ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1). Length = 428	pir A32891 A3 2891	5534	1	540	67	79	HKLSB39	pBluescript
1258	875897	ring finger protein - fruit fly (Drosophila melanogaster) Length = 222	pir JC4296 JC4 296	5535	355	846	47	66	H2CBN05	pBluescript SK-
1259	875899			5536	60	224			HCQDT85	Lambda ZAP II
1260	875900			5537	1	192			HARAJ31	pBluescript SK-
1261	875904			5538	351	554			HORMQ35	pSport1
1262	875905			5539	3	341			HMUBG30	pCMVSPORT 3.0
1263	875906			5540	83	181			HCQAH30	Lambda ZAP II
1264	875907	(AJ131890) DNA polymerase lambda [Homo sapiens] >gb AAF27541.1 AF161019_1 (AF161019) DNA polymerase beta-N [Homo sapiens] >sp CAB65074 CAB65074 DNA polymerase lambda. >sp AAF27541 AAF27541 DNA polymerase beta-N. Length = 575	emb CAB6507 4.1	5541	1	189	93	100	HWDAAH30	pCMVSPORT 3.0
1265	875908			5542	67	252			HCQAM30	Lambda ZAP II
1266	875912	(AF151847) CGI-89 protein [Homo sapiens] >sp Q9Y397 Q9Y397 CGI-89 PROTEIN. Length = 382	gb AAD34084. 1 AF1518	5543	1	951	63	76	HAGEA31	Uni-ZAP XR
1267	875913			5544	618	845			HCROZ66	pSport1
1268	875914			5545	479	829			HDPBY50	pCMVSPORT 3.0
1269	875915			5546	1153	1353			HDTKD18	pCMVSPORT 2.0
1270	875923	(AB002371) KIAA0373 [Homo sapiens] >sp O15078 O15078 KIAA0373. Length = 1539	dbj BAA20828 .1	5547	1567	623	83	83	HHPGT16	Uni-ZAP XR

1271	875924	(AF155739) axotrophin [Mus musculus] >sp Q9WV66 Q9WV66 AXOTROPHIN. Length = 693	gb AAD38411.1 AF1557	5548	1	573	53	61	H2CBF28	pBluescript SK-
1272	875925	(AL117635) hypothetical protein [Homo sapiens] >emb CAB56025.1 (AL117635) hypothetical protein [Homo sapiens] >pir T17335 T17335 hypothetical protein DKFZp434G145.1 - human (fragment) >sp CAB56025 CAB56025 Hypothetical 21.0 kd protein (fragment). Length	emb CAB56025.1	5549	54	434	89	92	HCQDM28	Lambda ZAP II
1273	875926			5550	2	268			HUKFO71	Lambda ZAP II
1274	875927	(AJ242739) mitochondrial tryptophanyl-tRNA synthetase [Homo sapiens] >sp CAB63107 CAB63107 Mitochondrial tryptophanyl-tRNA synthetase precursor (EC 6.1.1.2). Length = 360	emb CAB63107.1	5551	1	294	87	90	HCQAT28	Lambda ZAP II
1275	875932			5552	206	427			HCYBC56	pBluescript SK-
1276	875933			5553	362	556			HAAAC11	pSport1
1277	875934			5554	148	393			HNHOI84	Uni-ZAP XR
1278	875935			5555	224	364			HRABT72	pCMVSPORT 3.0
1279	875936	(AK000070) unnamed protein product [Homo sapiens] Length = 277	dbj BAA090925.1	5556	1	336	99	99	HWLEG68	pSport1
1280	875937	(AK000070) unnamed protein product [Homo sapiens] Length = 277	dbj BAA090925.1	5557	1	456	96	98	HSIDV66	Uni-ZAP XR
1281	875938	(AF102851) dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase [Homo sapiens] >sp Q9Y672 Q9Y672 DOLICHYL-P-Glc:MAN9GLCNAC2-PP-DOLICHYL GLUCOSYLTRANSFERASE. Length = 507	gb AAD41466.1 AF1028	5558	1	507	82	82	HWAAD15	pCMVSPORT 3.0
1282	875939			5559	129	329			HUFD27	pSport1
1283	875940			5560	3	347			HWLMZ30	pSport1

1284	875941	(AF048722) ALL1 responsive protein ARP1c [Homo sapiens] Length = 324	gb AAC39718.1	5561	288	917	74	74	H2LAJ89	pBluescript SK-
1285	875942			5562	1252	1554			HSPBY20	pSport1
1286	875946			5563	512	162			HE2DS24	Uni-ZAP XR
1287	875950			5564	191	355			HSLFO26	Uni-ZAP XR
1288	875951			5565	149	289			HCQAH22	Lambda ZAP II
1289	875952			5566	22	129			HHEYK87	pCMVSPORT 3.0
1290	875954			5567	3	203			HCRQN90	pSport1
1291	875955			5568	424	672			HCQDT05	Lambda ZAP II
1292	875967			5569	101	274			HACBI44	Uni-ZAP XR
1293	875971			5570	874	1200			HHEWX30	pCMVSPORT 3.0
1294	875972	hypothetical protein - human transposon MER37 Length = 138	pir S72482 S72482	5571	368	66	77	81	HCQCL24	Lambda ZAP II
1295	875974			5572	81	200			HESNK61	Uni-ZAP XR
1296	875976	(AF126743) DNAJ domain-containing protein MCJ [Homo sapiens] >sp Q9Y5T4 Q9Y5T4 DNAJ DOMAIN-CONTAINING PROTEIN MCJ. Length = 150	gb AAD38506.1 AF1267	5573	3	179	86	88	HWLCA48	pSport1
1297	875982			5574	451	603			HUCOR05	pSport1
1298	875983			5575	201	380			HWAICT7	pCMVSPORT 3.0
1299	875984			5576	241	456			HWMBG80	pSport1
1300	875989			5577	126	317			HTXFU22	Uni-ZAP XR
1301	875990			5578	285	413			HCQDO49	Lambda ZAP II

1302	875991	70 kD tumor-specific antigen [Rattus norvegicus] >sp O35828 W70T_RAT_70_KD_WD-REPEAT TUMOR-SPECIFIC ANTIGEN (FRAGMENT). Length = 443	emb CAA7533 9.1	5579	3	431	87	90	HDPOZ22	pCMVSPORT 3.0
1303	875994	!!!! ALU SUBFAMILY SB WARNING ENTRY !!!! Length = 587	sp P39189 AL U2_HUMAN	5580	164	364	61	69	HWLQA90	pSport1
1304	875995			5581	170	367			HATBS19	Uni-ZAP XR
1305	875996			5582	289	447			HHSEJ11	Uni-ZAP XR
1306	875998			5583	244	417			HCYBA19	pBluescript SK-
1307	875999			5584	1	234			HAPQW21	Uni-ZAP XR
1308	876001			5585	107	268			HCRND16	pSport1
1309	876006			5586	193	459			HSPME68	pSport1
1310	876007			5587	194	352			HCRMC21	pSport1
1311	876008			5588	1	138			HLWCB78	pCMVSPORT 3.0
1312	876011			5589	329	502			HWLME80	pSport1
1313	876012			5590	629	862			HKTAB46	Uni-ZAP XR
1314	876013			5591	1	126			H2CBJ20	pBluescript SK-
1315	876018	(AC004983) similar to PID:g3877944 [Homo sapiens] >sp O95766 O95766 WUGSC:H_DJ1163J12.2 PROTEIN. >emb CAB43318.1 (AL050215) hypothetical protein [Homo sapiens] {SUB 88-482} Length = 482	gb AAD15546. 1	5592	2	1507	99	99	HWBDR92	pCMVSPORT 3.0
1316	876019			5593	28	213			HWMBI92	pSport1
1317	876021	(AF090915) PRO0310p1 [Homo sapiens] >sp AAF24034 AAF24034 PRO0310p1. Length = 226	gb AAF24034. 1 AF0909	5594	269	1627	92	92	HWMFU50	pSport1

1318	876022			5595	126	317			HCQCM19	Lambda ZAP II
1319	876023	cytoplasmic linker protein-170 alpha-2 [Homo sapiens] >pir A43336 A43336 microtubule-vesicle linker CLIP-170 - human Length = 1392	gb AAA35693.1	5596	178	1098	89	89	HBWCF70	ZAP Express
1320	876024			5597	87	440			HCRON30	pSport1
1321	876025			5598	85	168			HCNAK16	Lambda ZAP II
1322	876026			5599	42	242			HCQDG19	Lambda ZAP II
1323	876027			5600	117	266			HCQAD16	Lambda ZAP II
1324	876028			5601	68	220			HCQAS16	Lambda ZAP II
1325	876029	(AF045459) Etk/Bmx cytosolic tyrosine kinase [Homo sapiens] >sp O60564 O60564 ETK/BMX CYTOSOLIC TYROSINE KINASE. Length = 697	gb AAC08966.1	5602	1	429	98	98	HGBBG01	Uni-ZAP XR
1326	876030	!!!! ALU SUBFAMILY SP WARNING ENTRY !!!! Length = 593	sp P39193 ALU6_HUMAN	5603	2	130	54	56	HILBF13	pBluescript SK-
1327	876034			5604	66	314			HCQDI18	Lambda ZAP II
1328	876039	[Homo sapiens] >sp P78514 P78514 HYPOTHETICAL 48.1 KD PROTEIN (FRAGMENT). Length = 429	gb AAB61919.1	5605	3	1289	99	99	HEMGF10	Uni-ZAP XR
1329	876044			5606	7	183			HCQDG10	Lambda ZAP II
1330	876045			5607	981	1271			H2CBS17	pBluescript SK-
1331	876048	novel transcript; similar to transcription factors activation domains; linked at 5" end to AT hook motif of HMGI-C; Method: conceptual translation supplied by author [Homo sapiens] >pir J39058 J39058 hypothetical protein - human (fragment) Length = 70	gb AAA81016.1	5608	431	586	51	62	HETJT76	Uni-ZAP XR

1332	876052	beta-galactosidase alpha peptide [Cloning vector pSport1] >sp Q46478 Q46478 BETA-GALACTOSIDASE ALPHA PEPTIDE (FRAGMENT). Length = 113	gb AAA73456.2	5609	130	276	84	87	HMVBD68	pSport1
1333	876056			5610	1	126			HWLQD17	pSport1
1334	876057			5611	1	255			HCRME16	pSport1
1335	876059			5612	76	348			HCQC116	Lambda ZAP II
1336	876062			5613	252	488			HKLAB15	Lambda ZAP II
1337	876065			5614	92	748			HCYBH57	pBluescript SK-
1338	876070			5615	34	111			HCQDM08	Lambda ZAP II
1339	876078			5616	242	538			HSSEA17	Uni-ZAP XR
1340	876079			5617	409	609			HCQDG14	Lambda ZAP II
1341	876081			5618	209	451			HCQAQ14	Lambda ZAP II
1342	876082			5619	2	145			HCQBN16	Lambda ZAP II
1343	876086			5620	267	587			HWLQE13	pSport1
1344	876088			5621	26	181			HWMB501	pSport1
1345	876089			5622	97	228			HKLAA70	Lambda ZAP II
1346	876090	(AF105424) brush border myosin I [Homo sapiens] >gb AAD31189.1 AF127026_1 (AF127026) brush border myosin I [Homo sapiens] >sp AAC78645 AAC78645 Brush border myosin I. >sp AAD31189 AAD31189 Brush border myosin I. >gb AAA20900.1 myosin [Homo sapiens] {SUB	gb AAC78645.1	5623	3	305	97	97	HWLCK07	pSport1
1347	876091			5624	172	390			HISAV29	pSport1
1348	876093			5625	77	514			HWLXE78	pSport1

1349	876094	(AE000196) orf, hypothetical protein [Escherichia coli] >pir B64835 B64835 probable iron-sulfur-binding protein b0947 - Escherichia coli >sp P75863 P75863 HYPOTHETICAL 40.6 KD PROTEIN. >dbj BAA35702.1 Hypothetical protein 7.6 [Escherichia coli] {SUB 15-3	gb AAC74033.1	5626	178	2	75	75	HSLHI12	Uni-ZAP XR
1350	876095			5627	143	286			HCQCX03	Lambda ZAP II
1351	876097			5628	117	1			HCQCR12	Lambda ZAP II
1352	876098	!!!! ALU SUBFAMILY J WARNING ENTRY !!!! Length = 591	sp P39188 ALU1_HUMAN	5629	211	288	59	66	HPJBW76	Uni-ZAP XR
1353	876101			5630	1	261			HCQCD81	Lambda ZAP II
1354	876104			5631	78	356			HCYBF60	pBluescript SK-
1355	876105			5632	91	432			HCQCD09	Lambda ZAP II
1356	876107	DEIH-box RNA/DNA helicase [Arabidopsis thaliana] >sp BAA84364 BAA84364 DEIH-box RNA/DNA helicase. Length = 1538	dbj BAA84364.1	5633	631	2	42	59	HWLVY67	pSport1
1357	876108	alpha7 nicotinic acetylcholine receptor subunit [Bos taurus] >sp P54131 ACH7_BOVIN NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN PRECURSOR. Length = 499	emb CAA6380.2.1	5634	195	383	80	84	HMAKC34	Uni-ZAP XR
1358	876109			5635	272	535			HNGBJ13	Uni-ZAP XR
1359	876117			5636	1	393			HCFCP28	pSport1

1360	876118	DIF-2 protein [Homo sapiens] >emb CAA65304.1 PRG1 [Homo sapiens] >gb AAC33793.1 (AF083421) radiation-inducible immediate early response gene IEX1 [Homo sapiens] >sp P46695 IEX1_HUMAN RADIATION-INDUCIBLE IMMEDIATE-EARLY GENE IEX-1 (IMMEDIATE EARLY PROTEI	emb CAA7488.6.1	5637	2	499	90	90	HCROH40	pSport1
1361	876121			5638	1	507			HKAAK32	pCMVSPORT 2.0
1362	876123			5639	338	523			HCQDQ31	Lambda ZAP II
1363	876126	similar to Probable rabGAP domains [Caenorhabditis elegans] >pir T27026 T27026 hypothetical protein Y48E1C.3 - Caenorhabditis elegans >sp O18207 O18207 Y48E1C.3 PROTEIN. Length = 619	emb CAB0770.1.1	5640	591	1601	47	65	HHEEN22	pCMVSPORT 3.0
1364	876127			5641	73	234			HRABR73	pCMVSPORT 3.0
1365	876137			5642	329	523			HWMBX68	pSport1
1366	876139			5643	348	596			HE80F49	Uni-ZAP XR
1367	876140	putative protein [Arabidopsis thaliana] >sp O23175 O23175 HYPOTHETICAL 52.0 KD PROTEIN. Length = 462	emb CAB1678.4.1	5644	1	1221	46	55	HWLHY12	pSport1
1368	876141			5645	98	229			HCQBL07	Lambda ZAP II
1369	876142			5646	2	169			H2LAJ32	pBluescript SK-
1370	876146			5647	19	123			HSIAD07	Uni-ZAP XR
1371	876151			5648	267	584			HWLNZ56	pSport1
1372	876152			5649	154	408			HLQBA23	Lambda ZAP II
1373	876153	(AK000167) unnamed protein product [Homo sapiens] Length = 463	dbj BAA90987.1	5650	18	824	92	92	HDPQV66	pCMVSPORT 3.0

1374	876155			5651	1102	2193			HODEJ02	Uni-ZAP XR
1375	876156			5652	1	270			HWMBZ31	pSportl
1376	876166			5653	666	977			HLTCX04	Uni-ZAP XR
1377	876168			5654	412	558			HYABC06	pCMVSPORT 3.0
1378	876169			5655	308	427			HLVDI04	pSportl
1379	876170			5656	299	520			HBXFF23	ZAP Express
1380	876172			5657	510	872			HDPBG07	pCMVSPORT 3.0
1381	876174	alternatively spliced product using exon 13A [Homo sapiens] >sp P78525 P78525 MYB PROTO-ONCOGENE PROTEIN (C-MYB). Length = 666	gb AAB49034.1	5658	2	76	65	74	HCYBF02	pBluescript SK-
1382	876177			5659	16	171			HTWDI21	pSportl
1383	876179	dolichol-phosphate-mannose synthase [Homo sapiens] >emb CAB53749.1 (AL034553) dj914P20.1 (dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit) [Homo sapiens] >sp O60762 O60762 DOLICHOL-PHOSPHATE-MANNOSE SYNTHASE. >sp CAB53749 CAB53749	dbj BAA25646.1	5660	491	345	97	100	HATED01	Uni-ZAP XR
1384	876182	(AB018351) KIAA0808 protein [Homo sapiens] >sp O94900 O94900 KIAA0808 PROTEIN. Length = 526	dbj BAA34528.1	5661	564	1229	44	54	HWLVU14	pSportl
1385	876183			5662	119	262			HOVC112	pSportl
1386	876184			5663	152	433			HCYBB01	pBluescript SK-
1387	876187			5664	102	296			HCRPM32	pSportl
1388	876192	(AB002326) KIAA0328 protein [Homo sapiens] >sp BAA20786 BAA20786 KIAA0328 protein (fragment). Length = 1906	dbj BAA20786.2	5665	3	335	84	87	HLDNV31	pCMVSPORT 3.0
1389	876193			5666	1	387			HCRNN03	pSportl

1390	876198	(AB014603) KIAA0703 protein [Homo sapiens] >sp O75185 O75185 KIAA0703 PROTEIN. Length = 963	dbj BAA31678 1	5667	204	575	78	78	HTPIQ89	Uni-ZAP XR
1391	876200			5668	147	296			HWLQD01	pSport1
1392	876201			5669	80	589			HISAQ01	pSport1
1393	876206			5670	354	602			HCRMCI0	pSport1
1394	876207			5671	418	711			HWABD53	pCMVSPORT 3.0
1395	876208	No definition line found [Escherichia coli] >gb AAC76545.1 (AE000428) putative regulator [Escherichia coli] >pir S47740 S47740 probable transcription regulator (trf-kdgK intergenic region) - Escherichia coli >sp P37640 YHJB_ECOLI HYPOTHETICAL TRANSCRIPT	gb AAB18496. 1	5672	598	2	100	100	HKCSF17	pBluescript
1396	876209			5673	295	870			HTDAI12	pSport1
1397	876213			5674	302	433			HYABB57	pCMVSPORT 3.0
1398	876215			5675	152	427			HWLVN09	pSport1
1399	876220			5676	135	287			HOHAU02	pCMVSPORT 2.0
1400	876224	desmoglein 2 [Homo sapiens] >pir S38673 S38673 desmoglein 2 - human >sp Q14126 DSG2_HUMAN DESMOGLEIN 2 PRECURSOR (HDGC). Length = 1117	emb CAA8122 6.1	5677	2	1459	83	84	HCRNJ43	pSport1
1401	876226	(AF115384) LR8 [Homo sapiens] >sp Q9Y609 Q9Y609 LR8. Length = 270	gb AAD23440. 1 AF1153	5678	46	978	80	81	HWLGV14	pSport1
1402	876228	(AF038388) actin-filament binding protein Frabin [Rattus norvegicus] >sp O88387 O88387 ACTIN- FILAMENT BINDING PROTEIN FRABIN. Length = 766	gb AAC27698. 1	5679	217	510	74	81	HCYBM15	pBluescript SK-
1403	876229			5680	18	191			HTXOU56	Uni-ZAP XR
1404	876232			5681	834	995			HHFCN93	Uni-ZAP XR

1405	876236	KIAA0020 [Homo sapiens] >sp Q15397 Y020_HUMAN HYPOTHETICAL PROTEIN KIAA0020. Length = 508	dbj BAA02808 .1	5682	1	1458	92	92	H2CBC05	pBluescript SK-
1406	876238	KIAA0094 gene product is related to S.cerevisiae methionine aminopeptidase. [Homo sapiens] >sp P53582 AMP1_HUMAN PUTATIVE METHIONINE AMINOPEPTIDASE 1 (EC 3.4.11.18) (METAP 1) (PEPTIDASE M 1) (KIAA0094) (FRAGMENT). Length = 394	dbj BAA07679 .1	5683	2	640	83	87	HTEPE28	Uni-ZAP XR
1407	876239	(AC004520) similar to NFE2-related transcription factors; similar to I48694 (PID:g2137676) [Homo sapiens] >sp Q9Y4A8 Q9Y4A8 WUGSC:H_RG119C02.1 PROTEIN. >dbj BAA76288.1 (AB010812) NF-E2-related factor 3 [Homo sapiens] {SUB 295-694} Length = 694	gb AAC09039. 1	5684	1	837	94	95	HUSGL79	pSport1
1408	876259			5685	2	703			HPMFU84	Uni-ZAP XR
1409	876260			5686	260	598			HDLAD09	pCMVSPORT 2.0
1410	876261			5687	297	530			HCQAW45	Lambda ZAP II
1411	876265	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9 Y6Y5	5688	3	131	90	93	HCYAC01	pBluescript SK-
1412	876266	(AB024057) vascular Rab-GAP/TBC-containing protein [Homo sapiens] >sp O95759 O95759 VASCULAR RAB-GAP/TBC-CONTAINING PROTEIN. Length = 897	dbj BAA75489 .1	5689	233	81	100	100	HCROF86	pSport1
1413	876269			5690	398	502			H2CB183	pBluescript SK-
1414	876270			5691	9	104			H2LAW73	pBluescript SK-
1415	876274			5692	1	222			HWMCL22	pSport1

1416	876276					5693	189	338				HCRPZ42	pSport1
1417	876277					5694	441	1				HCYBM32	pBluescript SK-
1418	876278					5695	431	604				HCRPJ72	pSport1
1419	876280	Thermostable carboxypeptidase (EC 3.4.17.-). [Escherichia coli] >gb AAC74420.1 (AE000231) putative aminohydrolase (EC 3.5.1.14) [Escherichia coli] >pir E64883 E64883 probable amidohydrolase (EC 3.5.-.) ydaJ - Escherichia coli >sp P77357 YDAJ_ECOLI HYPOT	dbj BAA14940.1	5696	17	178	96	98				HKCSA58	pBluescript
1420	876281					5697	1	171				HMWFC49	Uni-ZAP XR
1421	876282					5698	368	643				HMSIE02	Uni-ZAP XR
1422	876284					5699	1	366				HCRMZ34	pSport1
1423	876300	(AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens] >sp CAB4671 CAB46717 DJ1158B12.1 (zinc finger, X-linked, duplicated A). Length = 799	emb CAB4671.7.1	5700	2	247	82	82				HTGAM27	Uni-ZAP XR
1424	876304	villin [Homo sapiens] >emb CAA31386.1 villin (AA 1 - 827) [Homo sapiens] >pir A31642 A31642 villin - human >sp P09327 VIL1_HUMAN VILLIN. {SUB 2-827} Length = 827	emb CAA0066.4.1	5701	34	981	89	89				HCYBI20	pBluescript SK-
1425	876306					5702	31	327				HNEDH18	Uni-ZAP XR
1426	876308	putative precursor (AA 1-304) [Homo sapiens] >emb CAA61579.1 uracil-DNA-glycosylase, UNG1 [Homo sapiens] >pir S05964 A60472 uracil-DNA glycosylase (EC 3.2.2.-) precursor - human >sp P13051 UNG_HUMAN URACIL-DNA GLYCOSYLASE PRECURSOR (EC 3.2.2.-) (UDG). >e	emb CAA3367.9.1	5703	2	877	96	96				HWMFQ61	pSport1

1441	876372			5718	1	408			HCQBI31	Lambda ZAP II
1442	876374			5719	190	390			HTEGD78	Uni-ZAP XR
1443	876376			5720	2	142			HCYBN59	pBluescript SK-
1444	876379			5721	1	300			HCYBC31	pBluescript SK-
1445	876380			5722	2	190			HCQBM44	Lambda ZAP II
1446	876381			5723	145	258			HKCSP75	pBluescript
1447	876382			5724	17	301			HKCSP84	pBluescript
1448	876383			5725	3	242			HPMFF45	Uni-ZAP XR
1449	876385			5726	307	459			HE2CT52	Uni-ZAP XR
1450	876386	!!!! ALU SUBFAMILY SC WARNING ENTRY !!!! Length = 585	sp P39192 ALU5_HUMAN	5727	1	114	77	80	HTNBI76	pBluescript SK-
1451	876387			5728	29	364			HE9ND38	Uni-ZAP XR
1452	876395	(AJ271079) hypothetical protein [Oenothera elata subsp. hookeri] >emb CAB67234.1 (AJ271079) hypothetical protein [Oenothera elata subsp. hookeri] >sp CAB67211 CAB67211 Hypothetical 6.7 kd protein. >sp CAB67234 CAB67234 Hypothetical 6.7 kd protein. Length	emb CAB67211.1	5729	729	538	57	68	HPIAK40	Uni-ZAP XR
1453	876397	(AB023235) KIAA1018 protein [Homo sapiens] >sp Q9Y2M0 Q9Y2M0 KIAA1018 PROTEIN. Length = 1017	dbj BAA76862.1	5730	1	189	100	100	HHPGD10	Uni-ZAP XR
1454	876398			5731	394	675			HCQBI47	Lambda ZAP II
1455	876399			5732	109	321			HE8DW67	Uni-ZAP XR

1456	876400				5733	758	1012			HONAH83	pBluescript SK-
1457	876401				5734	3	371			HHGCW95	Lambda ZAP II
1458	876402	neutral protease large subunit [Homo sapiens] Length = 166	gb AAA65999.1	5735	359	484	79	84		HCYBI75	pBluescript SK-
1459	876404	unnamed protein product [unidentified] Length = 180	emb CAB6919.5.1	5736	2	103	92	92		HCRMK04	pSport1
1460	876405			5737	1	606				H2CBF13	pBluescript SK-
1461	876408			5738	3	107				HKCSO44	pBluescript
1462	876409	reverse transcriptase [Homo sapiens] Length = 361	gb AAB02291.1	5739	405	509	38	52		HWLKU83	pSport1
1463	876418	(AK000307) unnamed protein product [Homo sapiens] Length = 325	dbj BAA91072.1	5740	1	660	98	98		HE9RM22	Uni-ZAP XR
1464	876419			5741	3	116				HCRPQ93	pSport1
1465	876420			5742	1	177				HPDDL36	pBluescript SK-
1466	876422	(AK000515) unnamed protein product [Homo sapiens] Length = 203	dbj BAA91221.1	5743	148	513	93	93		H2CBM09	pBluescript SK-
1467	876425			5744	178	375				HKCAA10	Uni-ZAP XR
1468	876426			5745	98	274				H2CBI25	pBluescript SK-
1469	876427			5746	47	397				HKISB80	pBluescript
1470	876428			5747	1	156				H2CBE84	pBluescript SK-
1471	876431	putative cytoskeletal protein=H4(D10S170) [human, thyroid, Peptide, 585 aa] [Homo sapiens] >pir I58403 I58403 H4 protein - human >sp Q16204 D170_HUMAN H4(D10S170) PROTEIN. Length = 585	gb AAC60637.1	5748	2	811	85	85		HSEBD08	pCMVSPORT 1
1472	876432			5749	123	323				HPMFM22	Uni-ZAP XR

1473	876435				5750	186	641				HDHEB14	pCMVSPORT 2.0
1474	876436				5751	181	474				HAIDH43	Uni-ZAP XR
1475	876440				5752	149	424				HJAAL27	pBluescript SK-
1476	876441				5753	754	1017				HA5AB14	pSport1
1477	876444				5754	774	857				HWLNS47	pSport1
1478	876447				5755	670	894				HE8UJ03	Uni-ZAP XR
1479	876448	(AK001452) unnamed protein product [Homo sapiens] Length = 718		dbj BAA91700.1	5756	3	1622	86	86		HDTLK03	pCMVSPORT 2.0
1480	876451	placental leucine aminopeptidase [Homo sapiens] >sp Q15145 Q15145 PLACENTAL LEUCINE AMINOPEPTIDASE. Length = 944		dbj BAA09436.1	5757	1	693	85	86		HMTBC69	pCMVSPORT 3.0
1481	876452	(AF151073) HSPC239 [Homo sapiens] Length = 293		gb AAF36159.1 AF1510	5758	87	968	100	100		HMUBP81	pCMVSPORT 3.0
1482	876458	(AF161432) HSPC314 [Homo sapiens] >sp AAF28992 AAF28992 HSPC314 (fragment). Length = 248		gb AAF28992.1 AF1614	5759	3	1295	53	55		HAPOT58	Uni-ZAP XR
1483	876459				5760	95	271				HCFLR18	pSport1
1484	876464				5761	187	483				HDPAA38	pCMVSPORT 3.0
1485	876465				5762	1	144				HCYBM66	pBluescript SK-
1486	876469				5763	327	629				HPWAY46	Uni-ZAP XR
1487	876470				5764	100	507				HLTAH77	Uni-ZAP XR
1488	876471				5765	1	504				HWLXX39	pSport1
1489	876472	rhomboid-related protein [Homo sapiens] >sp O75783 O75783 RHOMBOID-RELATED PROTEIN. Length = 438		emb CAA76629.1	5766	3	407	97	98		HPTWG85	pBluescript

1490	876473	F08C6.6 gene product [Caenorhabditis elegans] >pir T15973 T15973 hypothetical protein F08C6.6 - Caenorhabditis elegans >sp Q19202 Q19202 COSMID F08C6. Length = 296	gb AAA68725.1	5767	2	1054	50	67	HE6BS09	Uni-ZAP XR
1491	876474			5768	150	314			HERAM35	Uni-ZAP XR
1492	876475			5769	618	980			HFUG54	pSport1
1493	876476	(AF029343) protocadherin 68 [Homo sapiens] >pir T09055 T09055 protocadherin 68 - human >sp O14917 O14917 PROTOCADHERIN 68. Length = 889	gb AAB84144.1	5770	1	573	81	81	HE8CX56	Uni-ZAP XR
1494	876480	Ptx1 [Mus musculus] >sp P70314 P1X1_MOUSE PITUITARY HOMEOBOX 1 (HOMEOBOX PROTEIN P-OTX) (PITUITARY OTX-RELATED FACTOR) (HINDLIMB EXPRESSED HOMEOBOX PROTEIN BACKFOOT). >gb AAC53059.1 hindlimb expressed homeobox protein backfoot [Mus musculus] {SUB 133-315	gb AAB16860.1	5771	1	387	97	97	H2LAQ54	pBluescript SK-
1495	876481	IgG Fc receptor I [Homo sapiens] >gb AAA36049.1 Fc gamma receptor I [Homo sapiens] >pir A39878 A39878 Fc gamma (IgG) receptor I-A (high affinity) precursor - human >sp Q92663 Q92663 FC GAMMA RECEPTOR I. Length = 374	gb AAA35678.1	5772	3	1199	91	91	HWABG32	pCMVSPORT 3.0
1496	876483			5773	3	494			HMTBE05	pCMVSPORT 3.0
1497	876484	(AB030905) Heterochromatin protein 1 gamma [Homo sapiens] >gb AAB48101.1 HP1Hs-gamma [Homo sapiens] >sp Q13185 CBX3_HUMAN CHROMOBOX PROTEIN HOMOLOG 3 (HETEROCHROMATIN PROTEIN 1 HOMOLOG GAMMA) (HP1 GAMMA) (MODIFIER 2 PROTEIN). >sp BAA83340 BAA83340 Hetero	db BAA83340.1	5774	455	1006	83	83	HKABL05	pCMVSPORT 2.0

1498	876487	propionyl-CoA carboxylase [Homo sapiens] >pir S04613 A27883 propionyl-CoA carboxylase (EC 6.4.1.3) alpha chain precursor - human >sp P05165 PCCA_HUMAN PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGA	emb CAA3276 3.1	5775	65	292	100	100	HOCTA74	pSport1
1499	876490	ORF 2 (466 aa) [Mus musculus] >sp Q61787 Q61787 ORF 2. Length = 466	emb CAA2736 3.1	5776	602	772	43	55	HWLUU48	pSport1
1500	876491	galectin 3 (version 2) - human Length = 242	pir A49800 A4 9800	5777	1	831	97	97	HULAJ15	pSport1
1501	876494	(AC005326) asparagine synthetase [Homo sapiens] >sp Q15666 Q15666 ASPARAGINE SYNTHETASE. Length = 561	gb AAC62263. 1	5778	166	1860	94	94	HSYAJ64	pCMV Sport 3.0
1502	876495	UDP-GalNAc:polypeptide N- acetylglucosaminyltransferase (GalNAc-T3) [Homo sapiens] >sp Q14435 Q14435 POLYPEPTIDE N- ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N- ACETYLGALACTOSAMINYL	emb CAA6337 1.1	5779	836	1354	78	79	HETIF19	Uni-ZAP XR
1503	876496	(AK000496) unnamed protein product [Homo sapiens] Length = 239	dbj BAA91205 .1	5780	294	148	68	77	HL YEA23	pSport1
1504	876498			5781	306	494			HAPQU61	Uni-ZAP XR
1505	876499	(AF151825) CGI-67 protein [Homo sapiens] >sp Q9Y377 Q9Y377 CGI-67 PROTEIN. Length = 293	gb AAD34062. 1 AF1518	5782	465	776	83	93	HE8OT93	Uni-ZAP XR
1506	876503	(AF081281) lysophospholipase [Homo sapiens] >gb AAD26993.1 (AF077198) lysophospholipase [Homo sapiens] >sp O75608 O75608 LYSOPHOSPHOLIPASE. Length = 230	gb AAC31610. 1	5783	3	659	100	100	H2LAB08	pBluescript SK-

1507	876504	LAMP [Homo sapiens] >pir JC4776 JC4776 limbic-system-associated membrane protein precursor - human >sp Q13449 LAMP_HUMAN LIMBIC SYSTEM-ASSOCIATED MEMBRANE PROTEIN PRECURSOR (LSAMP). Length = 338	gb AAC50569.1	5784	129	1106	93	93	HISBB72	pSportl
1508	876507			5785	1	651			HCHBN47	pSportl
1509	876511			5786	572	778			HFADJ29	Uni-ZAP XR
1510	876513			5787	145	579			HWLQP42	pSportl
1511	876518			5788	116	454			HDPAG07	pCMVSPORT 3.0
1512	876524	!!!! ALU SUBFAMILY J WARNING ENTRY !!!! Length = 591	sp P39188 ALU1_HUMAN	5789	882	977	60	67	HLTAR39	Uni-ZAP XR
1513	876526			5790	72	272			HWLRF38	pSportl
1514	876530			5791	687	917			HCRNM09	pSportl
1515	876533			5792	340	699			HOBAE30	pBluescript
1516	876534			5793	240	551			HATCV09	Uni-ZAP XR
1517	876535			5794	193	300			HCRNE16	pSportl
1518	876536			5795	81	368			HCRPV63	pSportl
1519	876538	(AK002149) unnamed protein product [Homo sapiens] Length = 330	db BAA92110.1	5796	399	1058	93	93	HSKKP02	pBluescript
1520	876540			5797	3	395			HOVAN13	pSportl
1521	876543	(AL137657) hypothetical protein [Homo sapiens] >emb CAB70862.1 (AL137657) hypothetical protein [Homo sapiens] >sp CAB70862 CAB70862 Hypothetical 12.1 kd protein. Length = 106	emb CAB70862.1	5798	2	718	100	100	HWBEX78	pCMVSPORT 3.0
1522	876544			5799	3	200			HRODG74	Uni-ZAP XR
1523	876545	(AF166261) nuclear protein Sojo [Xenopus laevis] >sp AAD47086 AAD47086 Nuclear protein Sojo. Length = 676	gb AAD47086.1 AF1662	5800	1	519	39	67	HCROK30	pSportl

1524	876546	(AB007891) KIAA0431 [Homo sapiens] >pir T00061 T00061 hypothetical protein KIAA0431 - human >sp O43313 O43313 KIAA0431. Length = 667	dbj BAA24861 .1	5801	352	2508	92	92	HDABK73	pSportl
1525	876548			5802	175	342			HOGC078	pCMVSPORT 2.0
1526	876549			5803	466	645			HCRNG10	pSportl
1527	876551			5804	1	165			HWLRR08	pSportl
1528	876553	CSA protein [Homo sapiens] >pir A57090 A57090 CSA protein - human >sp Q13216 CSA_HUMAN COCKAYNE SYNDROME WD-REPEAT PROTEIN CSA. Length = 396	gb AAA82605. 1	5805	2	1102	99	99	HTEFP55	Uni-ZAP XR
1529	876557			5806	4	219			HDLAR46	pCMVSPORT 2.0
1530	876558			5807	375	1			H2CBW66	pBluescript SK-
1531	876559	connexin 26 [Homo sapiens] >pir A43424 A43424 gap junction protein Cx26 - human >sp P29033 CXB2_HUMAN GAP JUNCTION BETA-2 PROTEIN (CONNEXIN 26) (CX26). >sp AAD21314 AAD21314 Connexin 26. Length = 226	gb AAD21314. 1	5808	156	836	99	100	HOGDS65	pCMVSPORT 2.0
1532	876560	(AB035443) glycogen-debranching enzyme [Homo sapiens] >dbj BAA88405.1 (AB035443) glycogen- debranching enzyme [Homo sapiens] >sp BAA88405 BAA88405 Glycogen-debranching enzyme (EC 2.4.1.25). Length = 1532	dbj BAA88405 .1	5809	405	1043	88	88	H2CBX36	pBluescript SK-
1533	876572			5810	2	202			HSHAX43	Uni-ZAP XR
1534	876575	(AK002062) unnamed protein product [Homo sapiens] Length = 469	dbj BAA92064 .1	5811	1	780	35	49	HCRQ157	pSportl

1535	876576	homolog of Drosophila discs large protein, isoform 2 [Homo sapiens] >pir I38756 38756 homolog of Drosophila discs large protein, isoform 2 - human Length = 926	gb AAA50598.1	5812	61	1152	86	86	HCYBL73	pBluescript SK-
1536	876579	(AF132937) CGI-02 protein [Homo sapiens] >sp Q9Y2Z2 Q9Y2Z2 CGI-02 PROTEIN. Length = 618	gb AAD27712.1 AF1329	5813	320	1150	99	99	HHEGC16	pCMVSPORT 3.0
1537	876580			5814	190	297			H2CBG53	pBluescript SK-
1538	876581	AMP deaminase [Homo sapiens] >pir S68146 S68146 AMP deaminase (EC 3.5.4.6), erythrocyte, splice form 1a - human >sp AAB60408 AAB60408 AMP deaminase (EC 3.5.4.6). >dbj BAA02240.1 human erythrocyte-specific AMP deaminase [Homo sapiens] {SUB 10-776} >gb AAA5	gb AAB60408.1	5815	242	721	69	72	HCYBF23	pBluescript SK-
1539	876583			5816	723	935			HODCO80	Uni-ZAP XR
1540	876588			5817	302	370			HCYBG67	pBluescript SK-
1541	876589	(AF205889) Axin2 [Mus musculus] >sp AAF22800 AAF22800 Axin2. Length = 840	gb AAF22800.1 AF2058	5818	346	810	90	92	HCYBI10	pBluescript SK-
1542	876591	mitosin [Homo sapiens] >sp Q13246 Q13246 NUCLEAR PHOSPHOPROTEIN MITOSIN. Length = 3113	gb AAA82935.1	5819	2	952	90	90	H2CBE01	pBluescript SK-
1543	876592	glycine decarboxylase [Homo sapiens] >pir JN0124 JN0124 glycine decarboxylase (decarboxylating) (EC 1.4.4.2) - human >sp P23378 GCSP_HUMAN GLYCINE DEHYDROGENASE [DECARBOXYLATING], MITOCHONDRIAL PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAV	gb AAA36478.1	5820	2	166	90	92	HCYBI92	pBluescript SK-
1544	876595			5821	98	307			HWMCC28	pSport1

1545	876596	(AF102542) beta-1,6-N-acetylglucosaminyltransferase [Homo sapiens] >gb AAD21525.1 (AF038650) core 2/core 4 beta-1,6-N-acetylglucosaminyltransferase; core 2/4-GnT [Homo sapiens] >sp O95395 O95395 BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE. Length = 438	gb AAD10824.1	5822	353	1747	100	100	HWMAN61	pSport1
1546	876597			5823	97	291			HCQCR04	Lambda ZAP II
1547	876600			5824	294	596			HWMFE48	pSport1
1548	876601			5825	999	1184			HMTBN44	pCMVSPORT 3.0
1549	876602			5826	2	457			HCROI04	pSport1
1550	876608	hepatitis C-associated microtubular aggregate protein p44 [Homo sapiens] >sp Q14496 Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44. Length = 444	dbj BAA06043.1	5827	434	691	85	87	HTWCT64	pSport1
1551	876609	(AK000322) unnamed protein product [Homo sapiens] Length = 783	dbj BAA91085.1	5828	2	463	85	88	HETBI79	Uni-ZAP XR
1552	876610			5829	50	208			HWTBM65	Uni-ZAP XR
1553	876612			5830	536	760			HCQBN77	Lambda ZAP II
1554	876621	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens] >gb AAD50061.1 AF048686_1 (AF048686) dTDP-glucose 4,6-dehydratase like protein [Homo sapiens] >sp O95455 O95455 DTDP-D-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46). >sp AAD50061 AAD50061 DTDP-glucose 4,6-d	emb CAA0684.0.1	5831	105	1172	99	99	HKAED74	pCMVSPORT 2.0
1555	876622			5832	93	248			HCQAT20	Lambda ZAP II

1556	876630			5833	17	181				HCRMD40	pSportl
1557	876631	transcription enhancer factor TEF1 - human >sp P28347 TEF1_HUMAN TRANSCRIPTIONAL ENHANCER FACTOR TEF-1 (PROTEIN GT-IIC) (TRANSCRIPTION FACTOR 13) (NTEF-1). >gb AAB00791.1 transcription enhancer factor [Homo sapiens] {SUB 16-426} Length = 426	pir A40032 A4 0032	5834	70	762	78	79		HFIHO78	pSportl
1558	876633	(AC004030) F21856_2 [Homo sapiens] >pir T00636 T00636 hypothetical protein F21856_2 - human >sp O43360 O43360 F21856_2. Length = 679	gb AAB97620. .1	5835	3	173	64	65		HCRPG35	pSportl
1559	876637			5836	505	672				HSQFQ92	Uni-ZAP XR
1560	876638	hepatoma-derived growth factor [Mus musculus] >pir JC5662 JC5662 hepatoma-derived growth factor-related protein 2 - mouse >sp O35540 O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2. Length = 669	dbj BAA22896 .1	5837	38	1702	64	76		HUFBF32	pSportl
1561	876643	DNA topoisomerase III [Homo sapiens] >sp Q13472 TP3A_HUMAN DNA TOPOISOMERASE III ALPHA (EC 5.99.1.2). >gb AAB03695.1 DNA topoisomerase III [Homo sapiens] {SUB 26-1001} Length = 1001	gb AAB03694. .1	5838	1	681	83	83		HTXCO05	Uni-ZAP XR
1562	876645	Human giant larvae homologue [Homo sapiens] >pir S55474 S55474 Human giant larvae homolog - human >sp Q14521 Q14521 GIANT LARVAE HOMOLOGUE. Length = 1015	emb CAA6078 0.1	5839	1	762	97	97		HWMBJ09	pSportl
1563	876646			5840	225	488				HSIDP84	Uni-ZAP XR
1564	876647	(AB020684) KIAA0877 protein [Homo sapiens] >sp O94954 O94954 KIAA0877 PROTEIN (FRAGMENT). Length = 580	dbj BAA74900 .1	5841	95	388	97	100		HUSIA29	pSportl

1565	876648	(AJ009936) nuclear hormone receptor PRR1-A [Homo sapiens] >sp CAB55489 CAB55489 Nuclear hormone receptor PRR1-A. >emb CAB55491.1 (AJ009936) nuclear hormone receptor PRR1-B [Homo sapiens] {SUB 56-434} Length = 434	emb CAB55489.1	5842	3	290	100	100	HCQAG09	Lambda ZAP II
1566	876649	cyclin F [Homo sapiens] >sp P41002 CG2F_HUMAN G2/MITOTIC-SPECIFIC CYCLIN F. Length = 786	gb AAB60342.1	5843	2	475	79	79	HCR0T53	pSport1
1567	876652	(AF039023) Ran-GTP binding protein; RanBP6 [Homo sapiens] >sp O60518 O60518 RAN-GTP BINDING PROTEIN (FRAGMENT). Length = 1105	gb AAC14260.1	5844	3	215	71	74	HOENX50	Uni-ZAP XR
1568	876656	(AC005531) similar to lymphocyte early activation antigen AIM/CD69; similar to Q07108 (PID:g584906) [Homo sapiens] >sp O95043 O95043 WUGSC:H_DJ0701O16.2 PROTEIN. Length = 189	gb AAD04729.1	5845	2	412	100	100	HCEOW20	Uni-ZAP XR
1569	876657			5846	2	391			HCRMG16	pSport1
1570	876660			5847	1	420			HCEPH79	Uni-ZAP XR
1571	876666	(AF061795) dynamin-like protein Dymple isoform [Homo sapiens] >sp O60709 O60709 DYNAMIN-LIKE PROTEIN DYMPLE ISOFORM. >gb AAD22412.1 (AF107048) dynamin-like protein variant 4 [Rattus norvegicus] {SUB 448-699} Length = 699	gb AAC35283.1	5848	73	654	76	77	HFOYY56	pSport1
1572	876668			5849	555	779			HSXDG80	Uni-ZAP XR
1573	876675	(AK000294) unnamed protein product [Homo sapiens] Length = 929	dbj BAA91062.1	5850	2	724	94	94	HHEUK77	pCMVSPORT 3.0

1574	876677	protein serine/threonine kinase [Homo sapiens] >emb CAA54508.1 Cdk-activating kinase [Homo sapiens] >emb CAA55785.1 MO15/CDK-activating kinase (CAK) [Homo sapiens] >emb CAA54793.1 CDK activating kinase [Homo sapiens] >pir A54820 A54820 CDK-activating p	gb AAA36657.1	5851	23	802	100	100	HHEDO14	pCMVSPORT 3.0
1575	876680			5852	96	377			HKIMC75	Lambda ZAP II
1576	876683			5853	466	732			HWMBI36	pSport1
1577	876685	myosin-I, Myr 1b (alternatively spliced) - rat Length = 1107	pir C45439 C45439	5854	3	1634	91	93	HE8TM64	Uni-ZAP XR
1578	876687			5855	31	291			HKLSA57	pBluescript
1579	876689	(AF127577) nuclear factor RIP140 [Homo sapiens] Length = 1158	gb AAF35255.1 AF1275	5856	2	1801	91	92	HOGCV45	pCMVSPORT 2.0
1580	876690	(AF127577) nuclear factor RIP140 [Homo sapiens] Length = 1158	gb AAF35255.1 AF1275	5857	34	957	97	97	HADCX04	pSport1
1581	876693	integrin alpha6 subunit [Homo sapiens] >gb AAB24829.1 integrin subunit alpha 6 [human, Peptide Partial, 102 aa] [Homo sapiens] {SUB 703-804} Length = 1067	emb CAA4209.9.1	5858	2	1660	96	96	HCRPH70	pSport1
1582	876696	hepatocyte nuclear factor-3/fork head homolog 11B [Homo sapiens] Length = 748	gb AAC51129.1	5859	3	332	75	76	HCRQM22	pSport1
1583	876697	PDGF associated protein [Homo sapiens] >gb AAF03506.1 AC004922_3 (AC004922) PDGF associated protein [Homo sapiens] >sp Q13442 HP28_HUMAN 28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF ASSOCIATED PROTEIN). >sp AAF03506 AAF03506 PDGF associated	gb AAC50462.1	5860	2	595	61	61	HKAEB15	pCMVSPORT 2.0
1584	876701			5861	165	353			HSYAP76	pCMVSPORT 3.0

1585	876716	(AB002357) KIAA0359 [Homo sapiens] >sp O15066 KF3B_HUMAN KINESIN-LIKE PROTEIN KIF3B (MICROTUBULE PLUS END- DIRECTED KINESIN MOTOR 3B) (KIAA0359) (HH0048). Length = 747	dbj BAA20815 .1	5862	3	689	100	100	HCRMV17	pSport1
1586	876719	(AB003103) 26S proteasome subunit p55 [Homo sapiens] >pir PC6501 C6523 26s proteasom p55 protein - human >sp O00232 O00232 PROTEASOME SUBUNIT P55. Length = 456	dbj BAA19749 .1	5863	554	1447	100	100	HOEKC59	Uni-ZAP XR
1587	876722	(AB001075) galectin-2 related protein [Rattus norvegicus] >sp Q9Z144 Q9Z144 GALECTIN-2 RELATED PROTEIN. Length = 130	dbj BAA74954 .1	5864	1	306	78	92	HKCSL28	pBluescript
1588	876725	(AL031668) dJ64K7.2 (eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)) [Homo sapiens] >sp CAB43741 CAB43741 DJ64K7.2 (eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)). Length = 333	emb CAB4374 1.1	5865	120	1154	88	88	HHEFB46	pCMVSPORT 3.0
1589	876726	(AL133620) hypothetical protein [Homo sapiens] >emb CAB63746.1 (AL133620) hypothetical protein [Homo sapiens] >sp CAB63746 CAB63746 Hypothetical 115.3 kd protein. Length = 1031	emb CAB6374 6.1	5866	233	814	35	53	HWBBS84	pCMVSPORT 3.0
1590	876728	epiligrin alpha 3 subunit [Homo sapiens] >pir A55347 A55347 adhesive ligand epiligrin, alpha-3 chain form A precursor - human >sp Q16787 LMA3_HUMAN LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN 170 KD SUBUNIT) (E170). Length = 1713	gb AAA59483. 1	5867	1	1407	92	92	HSIFZ22	Uni-ZAP XR
1591	876731			5868	1	249			HCRNB80	pSport1
1592	876732			5869	234	584			HTPAY47	Uni-ZAP XR
1593	876743			5870	120	629			H2LBA37	pBluescript SK-
1594	876744			5871	90	608			HWLIP86	pSport1

1595	876745	retinoic acid receptor beta-2 - human >sp P10826 RRB2_HUMAN RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR- EPSILON), >gb AAD45688.1 AF157483_1 (AF157483) retinoic acid receptor beta 4 [Homo sapiens] {SUB 113-448} Length = 448	pir S02827 S02 827	5872	35	430	100	100	100	HGBAM79	Uni-ZAP XR
1596	876747	amphiregulin [Homo sapiens] >gb AAA51781.1 amphiregulin [Homo sapiens] >pir A34702 A34702 amphiregulin precursor - human >sp P15514 AMPR_HUMAN AMPHIREGULIN PRECURSOR (AR) (COLORECTUM CELL- DERIVED GROWTH FACTOR) (CRDGF). >gb AAA72989.1 synthetic amphireg	gb AAA51773. 1	5873	1	978	67	67	67	HKAUF85	pCMVSPORT 2.0
1597	876750			5874	1	174				HNFE067	Uni-ZAP XR
1598	876752	pS2 precursor [Homo sapiens] >emb CAA28695.1 pS2 [Homo sapiens] >emb CAA36254.1 pS2 protein [Homo sapiens] >pir A26667 A26667 pS2 protein precursor - human >sp P04155 PS2_HUMAN PS2 PROTEIN PRECURSOR (HP1.A) (BREAST CANCER ESTROGEN-INDUCIBLE PROTEIN) (PN	emb CAA2515 5.1	5875	3	281	100	100	100	H2MBA27	pBluescript SK-
1599	876753			5876	2	166				HWLMB30	pSport1
1600	876760	splicing factor [Homo sapiens] >sp Q14499 Q14499 SPLICING FACTOR. Length = 530	gb AAA16347. 1	5877	2	643	75	75	75	HHEBN60	pCMVSPORT 3.0
1601	876762			5878	989	1261				HOEMQ68	Uni-ZAP XR
1602	876764			5879	110	265				HHFCP36	Uni-ZAP XR
1603	876767	cell cycle protein p38-2G4 homolog [Homo sapiens] >sp O43846 O43846 CELL CYCLE PROTEIN P38- 2G4 HOMOLOG. Length = 394	gb AAB91536. 1	5880	743	871	94	94	97	HTXKH86	Uni-ZAP XR

1604	876771	ORF [Homo sapiens] >sp P51809 SYBL_HUMAN SYNAPTOBREVIN-LIKE PROTEIN 1. Length = 220	emb CAA6313.3.1	5881	1	393	88	88	HISCI72	pSport1
1605	876773	DDBb p48 [Homo sapiens] >sp Q92466 Q92466 DDBB P48. Length = 427	gb AAB07897.1	5882	2	679	99	99	HJACI75	pBluescript SK-
1606	876776	(AJ006487) propionyl-CoA carboxylase [Homo sapiens] >sp CAA07066 CAA07066 Propionyl-CoA carboxylase. >gb AAA60037.1 exon [Homo sapiens] {SUB 401-433} Length = 539	emb CAA07066.6.1	5883	54	1505	99	99	HTEDS58	Uni-ZAP XR
1607	876789	(AK001492) unnamed protein product [Homo sapiens] Length = 706	dbj BAA91721.1	5884	177	1208	95	95	HUVHP60	Uni-ZAP XR
1608	876791	nonspecific crossreacting antigen precursor [Homo sapiens] >pir A26902 A27681 nonspecific cross-reacting antigen precursor - human >sp Q13774 Q13774 NONSPECIFIC CROSSREACTING ANTIGEN PRECURSOR. Length = 344	gb AAA51739.1	5885	46	1140	95	95	HUFCI29	pSport1
1609	876795	(AF144756) adipocyte lipid-binding protein [Rattus norvegicus] >sp AAD37371 AAD37371 Adipocyte lipid-binding protein. Length = 150	gb AAD37371.1 AF1447	5886	2	280			HCRNO02	pSport1
1610	876798	(AF144756) adipocyte lipid-binding protein [Rattus norvegicus] >sp AAD37371 AAD37371 Adipocyte lipid-binding protein. Length = 150	gb AAD37371.1 AF1447	5887	145	390	85	88	HAUAF56	Uni-ZAP XR
1611	876802			5888	628	933			HHEUM25	pCMVSPORT 3.0
1612	876804			5889	306	458			HWLQW08	pSport1
1613	876807	(AF105036) zinc finger transcription factor GKLF [Homo sapiens] >sp AAD42165 AAD42165 Zinc finger transcription factor GKLF. Length = 470	gb AAD42165.1 AF1050	5890	1	717	93	93	HOEOP07	Uni-ZAP XR
1614	876809	mucin 2 precursor, intestinal - human (fragments) >gb AAA59163.1 mucin [Homo sapiens] {SUB 626-1895} >gb AAA59164.1 MUC2 [Homo sapiens] {SUB 2037-3020} >gb AAA36334.1 intestinal mucin [Homo sapiens] {SUB 1916-2193} >gb AAA59861.1 mucin-like protein [H	pir A49963 A43932	5891	2	808	100	100	HCQAE79	Lambda ZAP II

1615	876811	(AF034745) LNXp80 [Mus musculus] >pir T09457 T09457 numb-binding protein LNXp80 - mouse >sp O70263 O70263 LIGAND OF NUMB- PROTEIN X (LNXp80). Length = 728	gb AAC40075. 1	5892	1	681	87	93	HCQDR53	Lambda ZAP II
1616	876816			5893	209	472			HOEFO36	Uni-ZAP XR
1617	876817	thrombospondin 2 [Homo sapiens] >pir A47379 TSHUP2 thrombospondin 2 precursor - human >sp P35442 TSP2_HUMAN THROMBOSPONDIN 2 PRECURSOR. Length = 1172	gb AAA03703. 1	5894	26	1738	86	86	HFIAL22	pSport1
1618	876822			5895	607	783			HWLMN85	pSport1
1619	876823	(AL122042) hypothetical protein [Homo sapiens] >pir T34520 T34520 hypothetical protein DKFZp564J157.1 - human (fragment) >sp CAB59179 CAB59179 Hypothetical 17.9 kd protein (fragment). >emb CAB59179.2 (AL122042) hypothetical protein [Homo sapiens] {SUB 22	emb CAB5917 9.1	5896	2	529	100	100	HCGLC91	pCMVSPORT 2.0
1620	876829	(AL034423) dJ1185N5.1 (similar to C.elegans Y53C10A.5 protein) [Homo sapiens] Length = 270	emb CAB7686 4.1	5897	722	1336	97	97	HMHBJ66	Uni-ZAP XR
1621	876830	dopa decarboxylase [Homo sapiens] >gb AAA58437.1 aromatic amino acid decarboxylase [Homo sapiens] >pir A33663 DCHUA aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) - human >sp P20711 DCD_HUMAN AROMATIC- L-AMINO-ACID DECARBOXYLASE (EC 4.1.1.28) (DOPA DEC	gb AAA20894. 1	5898	1	288	92	93	HCQDG08	Lambda ZAP II
1622	876831	nidogen [Homo sapiens] Length = 1246	emb CAA5770 9.1	5899	3	296	96	98	HE8BX38	Uni-ZAP XR
1623	876836	PIG-B [Homo sapiens] >pir S71751 S71751 probable GPI mannosyl transferase PIG-B - human >sp Q92521 Q92521 PIG-B. Length = 554	dbj BAA07709 .1	5900	1194	1051	100	100	HMVCR68	pSport1

1624	876837				5901	313	573			HFCAl79	Uni-ZAP XR
1625	876842				5902	969	1217			HBIOH43	pCMVSPORT 3.0
1626	876856	cyclin [Homo sapiens] >gb AAA60040.1 proliferating cell nuclear antigen (PCNA) [Homo sapiens] >pir A27445 WMHUET proliferating cell nuclear antigen - human >sp P12004 PCNA_HUMAN PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN). Length = 261	gb AAA35736.1		5903	168	974	100	100	HOEMI36	Uni-ZAP XR
1627	876858	(AK001321) unnamed protein product [Homo sapiens] Length = 209	dbj BAA91622.1		5904	163	795	99	99	HWHPZ02	pCMVSPORT 3.0
1628	876865	human homolog of DnaJ protein [Homo sapiens] Length = 397	dbj BAA02656.1		5905	126	356	100	100	HLTAZ90	Uni-ZAP XR
1629	876866	ATP synthase subunit c precursor [Homo sapiens] >emb CAA49532.1 P1 gene for c subunit of human mitochondrial ATP synthase [Homo sapiens] >emb CAB45704.1 (AL080089) hypothetical protein [Homo sapiens] >emb CAB45704.1 (AL080089) hypothetical protein [Homo sapiens]	dbj BAA02420.1		5906	59	484	85	85	HHFUM32	pBluescript
1630	876870	KIAA0169 protein [Homo sapiens] >sp Q14675 Q14675 KIAA0169 PROTEIN (FRAGMENT). Length = 1745	dbj BAA11486.1		5907	1158	970	90	92	HHFAB62	pBluescript
1631	876873				5908	495	677			HWLWJ70	pSport1
1632	876876	retinoblastoma-binding protein mRbAp48 [Mus musculus] >pir 49366 49366 G1/S transition control protein-binding protein RbAp48 - mouse >sp Q60972 RB48_MOUSE CHROMATIN ASSEMBLY FACTOR 1 P48 SUBUNIT (CAF-1 P48 SUBUNIT) (RETINOBLASTOMA BINDING PROTEIN P48)	gb AAC52275.1		5909	1	1398	96	97	HCRPV85	pSport1
1633	876878				5910	31	231			HCE3V58	Uni-ZAP XR

1634	876882	hnRNP B1 protein [Homo sapiens] >gb AAA60271.1 hnRNP B1 protein [Homo sapiens] >pir A56845 B34504 heterogeneous nuclear ribonucleoprotein B1 - human >sp P22626 ROA2_HUMAN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 (HNRNP A2 AND HNRNP B1). >gb AAD4973	dbj BAA06031.1	5911	1	636	100	100	100	HKGBE11	pSport1
1635	876886	(AB032950) KIAA1124 protein [Homo sapiens] >sp BAA86438 BAA86438 KIAA1124 protein (fragment). Length = 1323	dbj BAA86438.1	5912	437	1591	86	90	90	HRAEG13	pCMVSPORT 3.0
1636	876888	putative [Mus musculus] >pir S15785 S15785 heat-stable antigen-related hypothetical protein HSA-C - mouse >sp Q61692 Q61692 PUTATIVE HEAT STABLE ANTIGEN. Length = 141	emb CAA3984.3.1	5913	384	500	36	43	43	HLIBZ07	pCMVSPORT 1
1637	876890	DNase protein [Homo sapiens] >gb AAB17022.1 XIB [Homo sapiens] >pir JC4633 JC4633 DNase I-like endonuclease (EC 3.1.-.-) - human >sp P49184 DRNL_HUMAN MUSCLE-SPECIFIC DNASE I-LIKE PRECURSOR (EC 3.1.21.-) (DNASE X) (XIB). Length = 302	emb CAA6203.7.1	5914	169	1131	94	94	94	HTPFB46	Uni-ZAP XR
1638	876892	!!! ALU SUBFAMILY SQ WARNING ENTRY !!! Length = 593	sp P39194 ALU7_HUMAN	5915	5	118	72	76	76	HDPSS23	pCMVSPORT 3.0
1639	876901			5916	1	1077				HCEIC29	Uni-ZAP XR
1640	876903			5917	520	765				HE9OY91	Uni-ZAP XR
1641	876904			5918	354	686				HFKFN66	Uni-ZAP XR
1642	876905	(AF078859) PTD004 [Homo sapiens] >sp Q9Y6G4 Q9Y6G4 PTD004. Length = 396	gb AAD4491.1	5919	2	1324	100	100	100	HWMFQ16	pSport1

1643	876909	membrane protein [Homo sapiens] >emb CAA42708.1 MRP-1 (motility related protein) [Homo sapiens] >gb AA80320.1 CD9 antigen [Homo sapiens] >gb AAC60586.1 CD9 antigen [human, leukocytes, Peptide, 228 aa] [Homo sapiens] >pir A46123 A40402 CD9 antigen - hu	gb AAA59982.1	5920	41	865	88	88	HCRBB01	Uni-ZAP XR
1644	876912			5921	281	625			HSAAN15	pBluescript SK-
1645	876913	CYCLIN-DEPENDENT KINASE (CDK)8 [unidentified] >emb CAA59754.1 CDK8 protein kinase [Homo sapiens] >pir I37227 I37227 cyclin- dependent kinase 8 - human >sp P49336 CDK8_HUMAN CELL DIVISION PROTEIN KINASE 8 (EC 2.7.1.-) (PROTEIN KINASE K35). Length = 464	emb CAA0358.5.1	5922	134	1006	89	89	HTEKS27	Uni-ZAP XR
1646	876920	mel-13a protein - mouse Length = 132	pir S65785 S65785	5923	231	530	70	75	HWMBA10	pSport1
1647	876921	(AF108460) ubinuclein [Homo sapiens] >gb AAF31756.1 AF108461_1 (AF108461) ubinuclein [Homo sapiens] >gb AA64188.1 VT4 [Homo sapiens] {SUB 348-691} Length = 1134	gb AAF31755.1 AF1084	5924	1	723	73	86	HCQBO58	Lambda ZAP II
1648	876923	11-beta-hydroxysteroid dehydrogenase type 2 [Homo sapiens] >pir S62789 S62789 11beta-hydroxysteroid dehydrogenase (EC 1.1.1.146) type 2 - human Length = 405	gb AAC50356.1	5925	2	991	83	83	HWLGQ64	pSport1
1649	876926			5926	309	572			HCQCV14	Lambda ZAP II
1650	876934			5927	8	127			HCR0059	pSport1
1651	876936			5928	632	970			HCRPN27	pSport1
1652	876938			5929	357	512			HCRON34	pSport1

1653	876940	heparin-binding EGF-like growth factor [Homo sapiens] >gb AAC15470.1 (AC004634) HBGF [Homo sapiens] >pir A38432 A38432 heparin-binding EGF-like growth factor precursor - human >sp Q99075 HBGF_HUMAN HEPARIN-BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF)	gb AAA35956.1	5930	2	268	81	83	HFKFH50	Uni-ZAP XR
1654	876941			5931	2	256			HCRQG66	pSport1
1655	876942	(AF149770) sentrin/SUMO-specific protease [Homo sapiens] Length = 643	gb AAF31171.1 AF1497	5932	327	791	100	100	HCROW80	pSport1
1656	876943	glutathione peroxidase-GI [Homo sapiens] Length = 190	emb CAA4839.4.1	5933	228	677	99	99	HLQER45	Lambda ZAP II
1657	876944			5934	18	218			HWADQ26	pCMVSPORT 3.0
1658	876945			5935	2	322			HLJB74	pCMVSPORT 1
1659	876946	(AF161479) HSPC130 [Homo sapiens] >sp AAF29094 AAF29094 HSPC130. Length = 473	gb AAF29094.1 AF1614	5936	486	860	91	93	HE8TT24	Uni-ZAP XR
1660	876947	aminoacylase-1 [Homo sapiens] >dbj BAA03814.1 45kDa protein [Homo sapiens] >dbj BAA03397.1 aminoacylase-1 [Homo sapiens] >pir A47488 A47488 aminoacylase (EC 3.5.1.14) - human >sp Q03154 ACY1_HUMAN AMINOACYLASE-1 (EC 3.5.1.14) (N-ACYL-L-AMINO-ACID AMIDOH	gb AAA02852.1	5937	28	696	96	98	HSSIS63	Uni-ZAP XR
1661	876949			5938	250	507			H2CAA03	pBluescript SK-
1662	876952			5939	141	530			HCROI77	pSport1
1663	876953	(AB011148) KIAA0576 protein [Homo sapiens] >pir T00341 T00341 hypothetical protein KIAA0576 - human (fragment) >sp Q9Y4E5 Q9Y4E5 KIAA0576 PROTEIN (FRAGMENT). Length = 1075	dbj BAA25502.1	5940	1	444	100	100	H2CBW39	pBluescript SK-

1664	876954	translational initiation factor eIF-2, alpha subunit [Homo sapiens] >sp P05198 IF2A_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2- ALPHA). {SUB 2-315} Length = 315	gb AAA52373.1	5941	3	806	100	100	HHBHM68	pCMVSport ₁
1665	876957	(AB024436) beta-1,4-galactosyltransferase IV [Homo sapiens] >gb AAC39735.1 (AF038662) beta-1,4-galactosyltransferase [Homo sapiens] >gb AAC72493.1 (AF022367) beta-1,4-galactosyltransferase [Homo sapiens] >sp O60513 O60513 BETA-1,4-GALACTOSYLTRANSFERASE.	dbj BAA75821.1	5942	605	1351	93	93	HSYBF36	pCMVSport _{3.0}
1666	876958			5943	221	147			HWMCE91	pSportl
1667	876959			5944	70	279			HUVFJ36	Uni-ZAP XR
1668	876961	TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA). Length = 423	sp Q92664 TF3A_HUMAN	5945	3	1229	85	86	HLYBU84	pSportl
1669	876963			5946	153	404			HWLMK65	pSportl
1670	876964	(AF114264) [Homo sapiens] >sp Q9Y2V1 Q9Y2V1 HYPOTHETICAL 53.6 KD PROTEIN. Length = 448	gb AAD29607.1 AF1142	5947	18	881	75	76	HWLPY93	pSportl
1671	876965			5948	1	294			HWMBV37	pSportl
1672	876966	(AF166331) beta crystallin A2 [Homo sapiens] >sp Q9Y562 Q9Y562 BETA CRYSTALLIN A2. >emb CAA60148.1 beta A2 crystallin [Homo sapiens] {SUB 158-185} Length = 197	gb AAD45388.1 AF1663	5949	338	751	87	87	HCDME16	pSportl
1673	876967	(AB014536) KIAA0636 protein [Homo sapiens] >gb AAD46074.2 (AF077226) copine III [Homo sapiens] >sp O75131 O75131 KIAA0636 PROTEIN. >sp AAD46074 AAD46074 Copine III. Length = 537	dbj BAA31611.1	5950	3	590	53	71	HCRQM25	pSportl
1674	876968			5951	57	428			HWMBV72	pSportl

1675	876969					5952	31	417				HCRQK24	pSportl
1676	876971					5953	293	829				HWLOK80	pSportl
1677	876975	cDNA EST EMBL:D75703 comes from this gene; cDNA EST yk513g5.3 comes from this gene; cDNA EST yk528b10.3 comes from this gene [Caenorhabditis elegans] >pir T27134 T27134 hypothetical protein Y53C12B.2 - Caenorhabditis elegans >sp O18216 O18216 Y53C12B.2 PR	emb CAB1649 1.1	5954	2	820	66	84				HNTBD04	pCMVSPORT 3.0
1678	876976	(AJ001306) PDZ domain protein [Homo sapiens] >sp O15249 O15249 PDZ DOMAIN PROTEIN. Length = 1524	emb CAA0466 6.1	5955	194	469	68	72				HWLUV59	pSportl
1679	876977	(AF125535) pp21 homolog [Homo sapiens] >sp AAF17229 AAF17229 Pp21 homolog. Length = 104	gb AAF17229. 1 AF1255	5956	1	609	100	100				HSUSF13	pBluescript
1680	876978			5957	243	473						H2CBE41	pBluescript SK-
1681	876980			5958	516	611						HWLFY03	pSportl
1682	876981			5959	3	170						HE2IX48	Uni-ZAP XR
1683	876983			5960	216	461						HNFHD27	Uni-ZAP XR
1684	876984			5961	109	339						HWLXS11	pSportl
1685	876985	(AF095791) TACC2 protein [Homo sapiens] >sp O95359 O95359 TACC2 PROTEIN (FRAGMENT). Length = 653	gb AAC64968. 1	5962	1	510	90	90				HCRPG94	pSportl
1686	876987	IMP dehydrogenase (EC 1.1.1.205) I - human >sp P20839 MD1_HUMAN INOSINE-5"- MONOPHOSPHATE DEHYDROGENASE 1 (EC 1.1.1.205) (IMP DEHYDROGENASE 1) (IMPDH-1) (IMPD 1). Length = 514	pir A35566 A3 5566	5963	2	166	100	100				HCUGO73	ZAP Express
1687	876989	KIAA0036 [Homo sapiens] >sp Q15051 Y036_HUMAN HYPOTHETICAL PROTEIN KIAA0036. Length = 598	dbj BAA04968 .1	5964	97	1575	83	85				HPMDD49	Uni-ZAP XR
1688	876990			5965	142	282						HCNSF23	pBluescript

1689	876991				5966	146	340				HKDBC15	pCMVSPORT I
1690	876992				5967	602	802				HSIGM23	Uni-ZAP XR
1691	876993				5968	498	869				HCQBN43	Lambda ZAP II
1692	876994				5969	306	566				HCQBO03	Lambda ZAP II
1693	876997				5970	335	505				HCQCF85	Lambda ZAP II
1694	876998	(AB020669) KIAA0862 protein [Homo sapiens] >sp BAA74885 BAA74885 KIAA0862 protein. Length = 582	dbj BAA74885 .1		5971	291	842	86	88		HUVFS16	Uni-ZAP XR
1695	877000	reading frame (gag?) [Spleen necrosis virus] >pir A93904 FOVDA gag polyprotein - avian spleen necrosis virus (fragment) >sp P03342 GAG_AVISN GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30] (FRAGMENT). Length =	emb CAA2451 3.1		5972	229	402	50	60		HCQBD51	Lambda ZAP II
1696	877001	!!! ALU SUBFAMILY SQ WARNING ENTRY !!! Length = 593	sp P39194 AL U7_HUMAN		5973	39	143	74	81		HCRMU18	pSport1
1697	877002				5974	1	258				HONAN63	pBluescript SK-
1698	877004				5975	332	490				HCQCU65	Lambda ZAP II
1699	877005				5976	107	187				HCRNO79	pSport1
1700	877006				5977	364	636				HCRMO22	pSport1
1701	877007	(AB014603) KIAA0703 protein [Homo sapiens] >sp O75185 O75185 KIAA0703 PROTEIN. Length = 963	dbj BAA31678 .1		5978	2	673	82	82		HFDME46	pSport1
1702	877008				5979	79	543				HCWHN82	ZAP Express

1703	877009	(AF155101) putative kruppel-related zinc finger protein NY-REN-23 antigen [Homo sapiens] >sp Q9Y5A5 Q9Y5A5 PUTATIVE KRUPPEL-RELATED ZINC FINGER PROTEIN NY-REN-23 ANTIGEN (FRAGMENT). Length = 547	gb AAD42867.1 AF1551	5980	2	271	88	89	HHPEK59	Uni-ZAP XR
1704	877010	(AF105020) putative protein O-mannosyltransferase [Homo sapiens] >sp AAF14118 AAF14118 Hypothetical 84.2 kd protein. Length = 750	gb AAF14118.1 AF1050	5981	199	360	100	100	HKCTB07	pBluescript
1705	877011			5982	38	325			HFPIZ22	Uni-ZAP XR
1706	877012			5983	494	727			HE8FB89	Uni-ZAP XR
1707	877013			5984	44	304			HCRND67	pSport1
1708	877014	(AF027571) phospholipase C-beta 4 isoform [Rattus norvegicus] >sp O88356 O88356 PHOSPHOLIPASE C-BETA 4 ISOFORM (FRAGMENT). Length = 747	gb AAC24984.1	5985	1	303	100	100	HSPA101	pSport1
1709	877015	(AK000512) unnamed protein product [Homo sapiens] Length = 335	dbj BAA91218.1	5986	3	650	100	100	HOSXA83	pBluescript
1710	877018			5987	576	776			HAVTF85	Other
1711	877019			5988	81	566			HTEPI45	Uni-ZAP XR
1712	877020			5989	262	522			HOSBX95	Uni-ZAP XR
1713	877022			5990	54	266			HSIFP30	Uni-ZAP XR
1714	877023	cytochrome P450 PCN3 [Homo sapiens] >pir A34101 A34101 cytochrome P450 3A5 - human >sp P20815 CP35_HUMAN CYTOCHROME P450 3A5 (EC 1.14.14.1) (CYP11A5) (P450-PCN3). >gb AAB00083.1 cytochrome P450 [Homo sapiens] {SUB 1-24} Length = 502	gb AAA02993.1	5991	259	909	81	85	HE9HL05	Uni-ZAP XR
1715	877024			5992	86	316			HWLMB91	pSport1

1716	877025	(AL137755) hypothetical protein [Homo sapiens]	emb CAB7090	5993	403	606	74	74	HOVEE11	pSport1
1717	877026	>emb CAB70907.1 (AL137755) hypothetical protein [Homo sapiens] >sp CAB70907 CAB70907 Hypothetical 117.6 kd protein (fragment). Length = 1027	7.1	5994	67	450			HCYBN69	pBluescript SK-
1718	877027			5995	132	287			HWLWN24	pSport1
1719	877029			5996	349	573			HOS0Z37	Uni-ZAP XR
1720	877030			5997	2	190			HCROD37	pSport1
1721	877031	(AF067806) cAMP-specific cyclic nucleotide phosphodiesterase PDE8; MMPDE8 [Mus musculus] >sp O88502 CN8A_MOUSE CAMP-SPECIFIC 3",5"-CYCLIC PHOSPHODIESTERASE 8A (EC 3.1.4.17). Length = 823	gb AAC40194.1	5998	2	679	67	75	H2LAF20	pBluescript SK-
1722	877032			5999	3	155			HCROD15	pSport1
1723	877034			6000	160	408			HS2SG18	pSport1
1724	877037	neutral protease large subunit [Homo sapiens] Length = 166	gb AAA65999.1	6001	168	605	99	99	HMCHW12	Uni-ZAP XR
1725	877043			6002	25	357			HWLVS52	pSport1
1726	877044			6003	21	215			HCRPG56	pSport1
1727	877046	(AK000488) unnamed protein product [Homo sapiens] Length = 427	dbj BAA91199.1	6004	369	1649	39	57	HTAHC75	Uni-ZAP XR
1728	877047			6005	123	326			HCRPH26	pSport1
1729	877049			6006	3	209			HWLWL67	pSport1
1730	877050			6007	288	578			HOSDU39	Uni-ZAP XR
1731	877051			6008	374	595			HCROS68	pSport1
1732	877052			6009	46	186			HWLRT47	pSport1
1733	877056			6010	175	624			HCRPN44	pSport1

1734	877057	(AL049670) hypothetical protein [Homo sapiens] >emb CAA16171.1 (AL021397) dJ69E11.3 (Yeast YPR037W and worm C02C2.6 predicted proteins LIKE) [Homo sapiens] >sp O75663 O75663 DJ69E11.3 (YEAST YPR037W AND WORM C02C2.6 PREDICTED PROTEINS LIKE). Length = 272	emb CAB4124 4.1	6011	1	237	73	75	HCRPD33	pSportl
1735	877058			6012	103	345			HCRPE57	pSportl
1736	877059	Eps8 [Mus musculus] >pir S39983 S39983 eps8 protein - mouse >sp Q08509 EPS8_MOUSE EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8. Length = 821	gb AAA16358. 1	6013	2	337	38	54	HCRNJ46	pSportl
1737	877063			6014	141	425			HWLRCS9	pSportl
1738	877065			6015	1	87			HLHCD08	Uni-ZAP XR
1739	877066			6016	136	294			HWLVE77	pSportl
1740	877067			6017	9	95			HCROJ64	pSportl
1741	877068			6018	251	484			HWLQM05	pSportl
1742	877069			6019	191	367			HCRPW24	pSportl
1743	877070			6020	186	371			HOCTA26	pSportl
1744	877071			6021	2	649			HBKDB96	pSportl
1745	877073			6022	7	135			HCRPE30	pSportl
1746	877075	beta-galactosidase alpha peptide [Cloning vector pSportl] >sp Q46478 Q46478 BETA- GALACTOSIDASE ALPHA PEPTIDE (FRAGMENT). Length = 113	gb AAA73456. 2	6023	1	165	100	100	HKGAW02	pSportl
1747	877079			6024	2	250			HCQCD93	Lambda ZAP II
1748	877080			6025	2	193			HOC7D62	pSportl
1749	877083			6026	506	832			HE8PC46	Uni-ZAP XR
1750	877087			6027	3	440			HWLQM53	pSportl
1751	877088			6028	105	770			HTLGE26	Uni-ZAP XR

1752	877092				6029	159	305				HCQCP82	pSport1
1753	877093				6030	3	221				HFEAH85	Uni-ZAP XR
1754	877094				6031	2	166				HE8QT45	Uni-ZAP XR
1755	877095	similar to beta-transducin [Caenorhabditis elegans] >pir/T16607/T16607 hypothetical protein K10B2.1 - Caenorhabditis elegans >sp Q09990 YSS1_CAEEL HYPOTHETICAL 80.3 KD TRP-ASP REPEATS CONTAINING PROTEIN K10B2.1 IN CHROMOSOME II. Length = 701	gb AAA68258.1		6032	2	442	33	56		HWLQL84	pSport1
1756	877096				6033	1	210				HCQCP82	Lambda ZAP II
1757	877097	(AC009991) protein [Arabidopsis thaliana] >sp AAF01517 AAF01517 F9F8.14 protein. Length = 701	gb AAF01517.1 AC0099		6034	3	488	39	64		HCRMW80	pSport1
1758	877098				6035	279	470				HSIGL73	Uni-ZAP XR
1759	877099				6036	338	592				HHEYT40	pCMVSPORT 3.0
1760	877101	(AK001798) unnamed protein product [Homo sapiens] Length = 298	dbj BAA91918.1		6037	527	1168	73	73		HDQHQ51	pCMVSPORT 3.0
1761	877104				6038	386	580				HODGR31	Uni-ZAP XR
1762	877105				6039	139	303				HWLWB92	pSport1
1763	877106				6040	74	235				HWLRD79	pSport1
1764	877110				6041	56	286				HWLOW72	pSport1
1765	877111				6042	112	765				HUSGT72	pSport1
1766	877112	(AF172328) [Homo sapiens] >sp AAD52585 AAD52585 Hypothetical 10.2 kd protein. Length = 95	gb AAD52585.1 AF1723		6043	136	453	96	96		HPWBM91	Uni-ZAP XR
1767	877114				6044	173	373				HWLVB03	pSport1
1768	877119				6045	218	451				HAIAM74	pCMVSPORT 3.0
1769	877120				6046	1	486				HHMME78	pSport1

1770	877121				6047	145	2			HCYBJ73	pBluescript SK-
1771	877122				6048	244	465			HCRNE77	pSport1
1772	877123				6049	201	335			HWMB94	pSport1
1773	877126				6050	601	786			HWLMS73	pSport1
1774	877129				6051	486	662			HFAMB70	Uni-ZAP XR
1775	877130				6052	139	291			HCQAK62	Lambda ZAP II
1776	877131				6053	11	277			HCQDP71	Lambda ZAP II
1777	877132				6054	1238	1513			HE9PB28	Uni-ZAP XR
1778	877133				6055	155	298			HCQCR68	Lambda ZAP II
1779	877134	sodium-D-glucose cotransporter [Homo sapiens] >sp Q92681 Q92681 SODIUM-D-GLUCOSE COTRANSPORTER. Length = 617	emb CAA5805 8.1		6056	3	167	96	98	HEPNB10	pSport1
1780	877135	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 AL U7_HUMAN		6057	71	238	73	78	HWLNY36	pSport1
1781	877137	(AF132021) myosin X [Homo sapiens] >gb AAF17363.1 AF184153_1 (AF184153) myosin X [Homo sapiens] {SUB 347-495} Length = 1540	gb AAF36524. 1 AF1320		6058	210	548	100	100	HWLRC68	pSport1
1782	877138				6059	178	309			HWLQM88	pSport1
1783	877139				6060	296	472			HWLMG40	pSport1
1784	877140				6061	1	153			HWLQO15	pSport1
1785	877142	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9 Y6Y5		6062	2	220	84	86	H2CAC59	pBluescript SK-
1786	877143				6063	257	433			HWLXJ87	pSport1
1787	877145				6064	250	447			HSDSJ26	pBluescript
1788	877146				6065	413	550			HCFBR55	pSport1

1789	877147	cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL:D68896 comes from this gene; cDNA EST yk395f9.5 comes from this gene; cDNA EST yk360f12.5 comes from this gene [Caenorhabditis elegans] >emb CAA21522.1 (AL032624) cDNA EST yk321h8.5 comes from this g	emb CAA90338.1	6066	2	409	41	68	HCRNP62	pSport1
1790	877148			6067	97	318			HCRM04	pSport1
1791	877149			6068	453	710			HGBHE60	Uni-ZAP XR
1792	877153			6069	18	263			HKAOG63	pCMVSPORT 2.0
1793	877154			6070	382	531			H2CBR38	pBluescript SK-
1794	877155			6071	2	154			HRDEW54	Uni-ZAP XR
1795	877157			6072	64	219			HBMDC60	pBluescript
1796	877163			6073	407	712			HOGDM40	pCMVSPORT 2.0
1797	877165			6074	197	307			HWLNG61	pSport1
1798	877166			6075	549	439			HCQCT53	Lambda ZAP II
1799	877167	(AK002071) unnamed protein product [Homo sapiens] Length = 528	dbj BAA92068.1	6076	1	219	82	92	HCRNV59	pSport1
1800	877168			6077	216	362			HCQDP52	Lambda ZAP II
1801	877169			6078	581	694			HFAAH06	Uni-ZAP XR
1802	877170	(AF155106) NY-REN-36 antigen [Homo sapiens] >sp Q9Y5A1 Q9Y5A1 NY-REN-36 ANTIGEN (FRAGMENT). Length = 227	gb AAD42872.1 AF1551	6079	1	909	60	60	HWLWX02	pSport1
1803	877171			6080	286	468			HCYBH52	pBluescript SK-

1804	877173	(AB018122) FGF-19 [Homo sapiens] >gb AAD45973.1 AF110400_1 (AF110400) fibroblast growth factor 19 [Homo sapiens] >sp O95750 O95750 FGF-19. >sp AAD45973 AAD45973 Fibroblast growth factor 19. Length = 216	dbj BAA75500 .1	6081	1	231	78	78	HCRNX51	pSport1
1805	877174			6082	279	148			HHEPP92	pCMVSPORT 3.0
1806	877175			6083	3	158			HCQAB45	Lambda ZAP II
1807	877176			6084	48	281			HCYBG53	pBluescript SK-
1808	877181			6085	183	383			HCQDF43	Lambda ZAP II
1809	877184			6086	674	856			HSBHU44	Uni-ZAP XR
1810	877185			6087	13	162			HLHSE50	pBluescript
1811	877187	(AB008164) ST1C2 [Homo sapiens] >gb AAC51285.1 sulfotransferase [Homo sapiens] >gb AAC00409.1 (AF026303) sulfotransferase [Homo sapiens] >sp O00338 O00338 SULFOTRANSFERASE. Length = 296	dbj BAA28346 .1	6088	1	423	97	100	HOSDV69	Uni-ZAP XR
1812	877189			6089	202	396			HCRMH42	pSport1
1813	877191			6090	758	1012			HSKZE25	Uni-ZAP XR
1814	877194	(AL023654) dJ549K18.1 (novel protein similar to GS2) [Homo sapiens] >sp CAB63061 CAB63061 dJ549K18.1 (novel protein similar to GS2) (fragment). Length = 326	emb CAB6306 1.1	6091	238	507	91	91	HCRMP38	pSport1
1815	877195			6092	213	347			HDPXD55	pCMVSPORT 3.0
1816	877200			6093	28	174			HHMMB40	pSport1

1817	877202	(AF090931) PRO0483 [Homo sapiens] >sp AAF24046 AAF24046 PRO0483. Length = 60	gb AAF24046.1 AF0909	6094	2	175	77	82	HEQAN41	pCMVSPORT 3.0
1818	877205	Ki-1/57 intracellular antigen [Homo sapiens] >sp O75804 O75804 KI-1/57 INTRACELLULAR ANTIGEN (FRAGMENT). Length = 299	gb AAC31117.1	6095	23	289	72	74	HSDZB30	pBluescript
1819	877206			6096	161	256			HWLWH56	pSportl
1820	877207			6097	120	314			HWLOT46	pSportl
1821	877208			6098	3	143			HOVCR67	pSportl
1822	877211	(AB028981) KIAA1058 protein [Homo sapiens] >sp BAA83010 BAA83010 KIAA1058 protein (fragment). Length = 1534	dbj BAA83010.1	6099	2	496	59	75	HLHSV54	pBluescript
1823	877212			6100	514	696			HSYBZ84	pCMVSPORT 3.0
1824	877213	(AL031581) /prediction=(method:"genscan", version:"1.0", score:"198.31"); /prediction=(method:"genefinder", version:"084"); /motif=(desc:"Endoplasmic reticulum targeting sequence", dbase:"PROSITE", acc:"PS00014", method:"ppsearch"); />	emb CAA2089.1.1	6101	35	502	43	60	H2LAC34	pBluescript SK-
1825	877214			6102	343	537			HCQAE29	Lambda ZAP II
1826	877215			6103	3	218			HCRMV19	pSportl
1827	877218			6104	19	429			HWLMF31	pSportl
1828	877220			6105	1	195			HFIIZ28	pSportl
1829	877222			6106	2	151			HCQDK28	Lambda ZAP II
1830	877229			6107	88	288			HHEQI29	pCMVSPORT 3.0
1831	877230			6108	363	503			HTWFA44	pSportl
1832	877231	high mobility group protein 2a [Homo sapiens] >sp O15347 O15347 HIGH MOBILITY GROUP PROTEIN 2A. Length = 200	emb CAA7114.3.1	6109	1	366	100	100	HOCMF20	pSportl
1833	877232			6110	146	391			HWMB050	pSportl

1834	877233				6111	196	297			HCQBD64	Lambda ZAP II
1835	877234				6112	417	677			HATAP30	Uni-ZAP XR
1836	877235	TB1 [Homo sapiens] >sp Q04197 Q04197 TB1 PROTEIN (FRAGMENT). Length = 434	gb AAA03587.1	6113	1	759	93	93		H2LBB51	pBluescript SK-
1837	877237			6114	327	830				H6EDT19	Uni-ZAP XR
1838	877240	(AF180919) RNA lariat debranching enzyme [Homo sapiens] >sp AAD53327 AAD53327 RNA lariat debranching enzyme. Length = 544	gb AAD53327.2	6115	3	542	98	98		HWLOW87	pSportl
1839	877242			6116	176	364				HWLMB22	pSportl
1840	877247	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	6117	3	218	85	85		H2CBA14	pBluescript SK-
1841	877250	(AF234783) tescalcin [Mus musculus] Length = 214	gb AAF40439.1	6118	1	771	96	98		HCRNM80	pSportl
1842	877251			6119	76	357				HCQCC04	Lambda ZAP II
1843	877254	heat-stable enterotoxin receptor [Homo sapiens] >pir A40940 OYHUX heat-stable enterotoxin receptor precursor - human >sp P25092 HSER_HUMAN HEAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL GUANYLATE CYCLASE) (EC 4.6.1.2) (STA RECEPTOR). Length =	gb AAA36655.1	6120	41	400	92	96		HCQCI17	Lambda ZAP II
1844	877255			6121	109	324				HFIYJ63	pSportl
1845	877256			6122	379	480				HWLOW51	pSportl
1846	877257			6123	135	341				HHFBA07	Uni-ZAP XR
1847	877258			6124	77	316				HWLDO51	pSportl
1848	877261			6125	3	278				HLSAE05	pSportl
1849	877263			6126	3	317				HCRPJ05	pSportl

1850	877264	!!!! ALU SUBFAMILY J WARNING ENTRY !!!! Length = 591	sp P39188 ALU1_HUMAN	6127	359	484	62	62	HCYBD05	pBluescript SK-
1851	877272	peptide YY [Homo sapiens] >dbj BAA02997.1 peptide YY precursor [Homo sapiens] >pir S33795 S33795 peptide YY (clone S) - human >sp P10082 PYY_HUMAN PEPTIDE YY PRECURSOR (PYY), >dbj BAA02998.1 peptide YY precursor variant [Homo sapiens] {SUB 1-90} >pir A3	gb AAA36433.1	6128	7	534	78	79	HKLSD44	pBluescript
1852	877274	BMAL1a [Homo sapiens] >sp O00327 BMAL_HUMAN BMAL1 PROTEIN (BRAIN AND MUSCLE ARNT-LIKE 1) (MEMBER OF PAS PROTEIN 3) (MOP3) (BHLH-PAS PROTEIN JAP3). Length = 583	dbj BAA19968.1	6129	856	1470	94	94	HFIXP45	pSport1
1853	877275			6130	347	535			HAQNS64	pSport1
1854	877280	cDNA EST yk552d5.3 comes from this gene [Caenorhabditis elegans] >pir T21378 T21378 hypothetical protein F25H9.7 - Caenorhabditis elegans >sp CAB02994 CAB02994 F25H9.7 protein. Length = 137	emb CAB02994.2	6131	2	250	42	63	HCQDG09	Lambda ZAP II
1855	877281	(AF014898) NADH dehydrogenase subunit 2 [Homo sapiens] >sp AAC25457 AAC25457 NADH dehydrogenase subunit 2 (fragment). Length = 347	gb AAC25457.1	6132	150	308	57	61	HCQCP81	Lambda ZAP II
1856	877282	mast cell carboxypeptidase A precursor [Homo sapiens] >gb AAA59568.1 carboxypeptidase A [Homo sapiens] >pir A43929 A43929 carboxypeptidase A (EC 3.4.17.1) CPA3 precursor - human >sp P15088 CBPC_HUMAN MAST CELL CARBOXYPEPTIDASE A PRECURSOR (EC 3.4.17.1) (gb AAA35652.1	6133	2	541	97	98	HLHEI46	Uni-ZAP XR
1857	877283			6134	221	346			HCROB02	pSport1
1858	877284	laminin A chain [Homo sapiens] Length = 2628	emb CAA41418.1	6135	2	637	100	100	HFKIN68	Uni-ZAP XR

1859	877285				6136	431	655				HWHGC93	pCMVSPORT 3.0
1860	877287	KIAA0204 protein [Homo sapiens] >sp Q92603 Q92603 KIAA0204 PROTEIN. Length = 1152	dbj BAA13195.1		6137	1	558	86	88		H2CBC75	pBluescript SK-
1861	877288				6138	3	263				H2LAW79	pBluescript SK-
1862	877289				6139	7	264				HCE2C40	Uni-ZAP XR
1863	877290	(AB032995) KIAA1169 protein [Homo sapiens] >sp BAA86483 BAA86483 KIAA1169 protein (fragment). Length = 775	dbj BAA86483.1		6140	3	1784	88	88		HMCDDH54	Uni-ZAP XR
1864	877295	interferon-induced Mx protein [Homo sapiens] >pir B33481 B33481 interferon-induced viral resistance protein MxB - human >sp P20592 MX2_HUMAN INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MXB (P78-RELATED PROTEIN). >gb AAA36459.1 p78-related protein	gb AAA36338.1		6141	3	1133	100	100		HTPFG64	Uni-ZAP XR
1865	877298				6142	47	307				H2CBQ45	pBluescript SK-
1866	877299				6143	2	130				HCQAD77	Lambda ZAP II
1867	877301				6144	136	363				HKLSB60	pBluescript
1868	877310	neuronal PAS2 [Homo sapiens] >sp Q99743 NPA2_HUMAN NEURONAL PAS DOMAIN PROTEIN 2 (NEURONAL PAS2) (MEMBER OF PAS PROTEIN 4) (MOP4). Length = 824	gb BAB47250.1		6145	143	478	97	98		HLHTC92	pBluescript
1869	877319				6146	1	225				HWLXP93	pSport1
1870	877320				6147	3	98				HUKBC55	Lambda ZAP II
1871	877321				6148	2	127				HE9FH60	Uni-ZAP XR

1872	877324				6149	1	222				HHEFC89	pCMV Sport 3.0
1873	877326	(AF034374) molybdenum cofactor biosynthesis protein C [Homo sapiens] >sp O14941 O14941 MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN C. >emb CAA11898.1 (AJ224328) MOCS1B protein [Homo sapiens] {SUB 27-249} Length = 249	gb AAB87524.1	6150	1	105	100	100			HCEOF08	Uni-ZAP XR
1874	877327			6151	305	442					HLHBZ17	Uni-ZAP XR
1875	877329			6152	1	198					HWLRP86	pSport1
1876	877331	(AF009668) polyprotein [multiple sclerosis associated retrovirus] >sp O36581 O36581 POLYPROTEIN (FRAGMENT). >gb AAB66527.1 (AF009666) protease [multiple sclerosis associated retrovirus] {SUB 1-114} Length = 768	gb AAB66528.1	6153	396	241	84	86			HISEQ81	pSport1
1877	877332			6154	346	594					HWLWA07	pSport1
1878	877333			6155	206	493					H2CBS31	pBluescript SK-
1879	877334	STM-7 [Homo sapiens] >sp Q92749 Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN). >gb AAC50916.1 type I phosphatidylinositol-4-phosphate 5-kinase beta [Homo sapiens] {SUB 112-502} >gb AAC50914.1 type I phosphati	emb CAA6322.4.1	6156	178	444	59	65			H2CBN88	pBluescript SK-
1880	877336			6157	139	246					HWLOK01	pSport1
1881	877338	(AF132818) colon Kruppel-like factor [Homo sapiens] >sp AAF18307 AAF18307 Colon Kruppel-like factor. >dbj BAA03393.1 BTEB2 [Homo sapiens] {SUB 239-457} Length = 457	gb AAF18307.1 AF1328	6158	2	1162	93	93			H2CBR23	pBluescript SK-
1882	877339	(AF131882) basic-transcription-element-binding-protein 2 [Oryctolagus cuniculus] Length = 219	gb AAF37005.1	6159	137	379	98	98			HCYBK82	pBluescript SK-

1883	877340	adenosine A2b receptor [Homo sapiens] >emb CAA48505.1 A2b adenosine receptor [Homo sapiens] >pir JC1229 JC1229 adenosine receptor A2b - human >sp P29275 AA2B_HUMAN ADENOSINE A2B RECEPTOR. Length = 332	gb AAA51598.1	6160	2	427	100	100	HCRMK82	pSport1
1884	877344			6161	559	765			HDTBO06	pCMVSPORT 2.0
1885	877346			6162	1406	1693			HEGAM94	Uni-ZAP XR
1886	877347			6163	1357	1515			HDTAH72	pCMVSPORT 2.0
1887	877351	(AF048700) gastrointestinal peptide [Homo sapiens] >sp O60575 O60575 GASTROINTESTINAL PEPTIDE. Length = 86	gb AAC05124.1	6164	2	316	90	90	HARAG42	pBluescript SK-
1888	877355	cytochrome P450 PCN3 [Homo sapiens] >pir A34101 A34101 cytochrome P450 3A5 - human >sp P20815 CP35_HUMAN CYTOCHROME P450 3A5 (EC 1.14.14.1) (CYP3A5) (P450-PCN3). >gb AAB00083.1 cytochrome P450 [Homo sapiens] {SUB 1-24} Length = 502	gb AAA02993.1	6165	99	305	100	100	HCQDL20	Lambda ZAP II
1889	877356	cytochrome P450 PCN3 [Homo sapiens] >pir A34101 A34101 cytochrome P450 3A5 - human >sp P20815 CP35_HUMAN CYTOCHROME P450 3A5 (EC 1.14.14.1) (CYP3A5) (P450-PCN3). >gb AAB00083.1 cytochrome P450 [Homo sapiens] {SUB 1-24} Length = 502	gb AAA02993.1	6166	278	514	100	100	HLQGF34	Lambda ZAP II
1890	877358	6-pyruvoyl-tetrahydropterin synthase [Homo sapiens] >dbj BAA04224.1 6-pyruvoyl-tetrahydropterin synthase [Homo sapiens] >gb AAA51541.1 6-pyruvoyltetrahydropterin synthase [Homo sapiens] >gb AAB64229.1 putative [Homo sapiens] >gb AAC16970.1 6-pyruvoyl-	dbj BAA04959.1	6167	3	359	100	100	HCDCF78	Uni-ZAP XR

1891	877361	ras-like protein [Homo sapiens] >pir D34788 TVHUC4 transforming protein ras (teratocarcinoma clone TC10) - human >sp P17081 RTCO_HUMAN GTP-BINDING PROTEIN TC10. Length = 213	gb AAA36547.1	6168	2	577	100	100	HMIBE59	Uni-ZAP XR
1892	877363			6169	141	293			HMKA86	pSport1
1893	877370	antigenic surface determinant OA3 [Homo sapiens] >pir A48997 A48997 tumor surface antigen OA3- 323 - human >sp Q08722 CD47_HUMAN LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6)	emb CAA4919.6.1	6170	1	1059	94	94	H6EDF71	Uni-ZAP XR
1894	877373	insulin-like growth factor-binding protein [Homo sapiens] >gb AAA52706.1 growth factor-binding protein-3 [Homo sapiens] >emb CAA46087.1 insulin-like growth factor binding protein 3 [Homo sapiens] >pir A36578 OHU3 insulin-like growth factor-binding prot	gb AAA52541.1	6171	8	1081	90	90	HOELC15	Uni-ZAP XR
1895	877375	(AJ002190) dihydroxyacetone phosphate acyltransferase [Homo sapiens] >gb AAC24505.1 (AF043937) peroxisomal acyl- CoA:dihydroxyacetonephosphate acyltransferase [Homo sapiens] >sp O15228 DAPT_HUMAN DIHYDROXYACETONE PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.42) (D	emb CAA0524.2.1	6172	120	539	95	95	HAIJBN08	pCMVSPORT 3.0
1896	877377	protein tyrosine phosphatase [Homo sapiens] >gb AA66496.1 protein phosphatase [Homo sapiens] >sp Q16667 CDN3_HUMAN CYCLIN- DEPENDENT KINASE INHIBITOR 3 (EC 3.1.3.48) (EC 3.1.3.16) (CDK2- ASSOCIATED DUAL SPECIFICITY PHOSPHATASE) (KINASE ASSOCIATED PHOSPHA	gb AAA60222.1	6173	31	717	91	91	HFVHT62	pBluescript

1897	877378	protein tyrosine phosphatase [Homo sapiens] >gb AA66496.1 protein phosphatase [Homo sapiens] >sp Q16667 CDN3_HUMAN CYCLIN-DEPENDENT KINASE INHIBITOR 3 (EC 3.1.3.48) (EC 3.1.3.16) (CDK2- ASSOCIATED DUAL SPECIFICITY PHOSPHATASE) (KINASE ASSOCIATED PHOSPHA	gb AAA60222.1	6174	57	605	99	99	HILBZ32	pBluescript SK-
1898	877380	microtubule associated protein [Homo sapiens] >pir 37356 37356 epithelial microtubule-associated protein, 115K - human >sp Q14244 Q14244 MICROTUBULE ASSOCIATED PROTEIN (DJ406A7.2.1) (MICROTUBULE ASSOCIATED PROTEIN E-MAP-115). >emb CAB37984.1 (AL023284)	emb CAA5208.6.1	6175	1	1782	77	77	HAPOR25	Uni-ZAP XR
1899	877384	nuclear autoantigen [Homo sapiens] >pir A37244 A37244 nuclear autoantigen Sp-100 - human Length = 480	gb AAA55537.1	6176	157	1035	84	84	HELB30	Uni-ZAP XR
1900	877387	(AK001332) unnamed protein product [Homo sapiens] Length = 682	dbj BAA91631.1	6177	2	2161	54	72	HHFMH12	Uni-ZAP XR
1901	877388	ligand for eph-related receptor tyrosine kinases [Homo sapiens] >gb AAC51203.1 putative EPH-related PTK receptor ligand LERK-8 [Homo sapiens] >sp Q15768 EFB3_HUMAN EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED	gb AAB05170.1	6178	1	81	100	100	HBXAC19	ZAP Express
1902	877390	(AC004922) similar to G10 protein; similar to AAC14190 (PID:g3064070) [Homo sapiens] >sp AAF03505 AAF03505 WUGSC:H_DJ0900K19.2 protein. Length = 144	gb AAF03505.1 AC0049	6179	499	960	100	100	HWLNV37	pSport1

1903	877393	argininosuccinate synthetase [Homo sapiens] >emb CAA25771.1 argininosuccinate synthetase (aa 1-412) [Homo sapiens] >pir A01195 AJHURS argininosuccinate synthase (EC 6.3.4.5) - human >sp P00966 ASSY_HUMAN ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLIN)	gb AAA51783.1	6180	1205	2530	96	96	HWHQH17	pCMVSPORT 3.0
1904	877396			6181	340	804			HDPFP36	pCMVSPORT 3.0
1905	877406	Rho-associated, coiled-coil containing protein kinase p160ROCK [Homo sapiens] >pir S69211 S69211 serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - human >sp Q13464 Q13464 RHO-ASSOCIATED, COILED-COIL CONTAINING PROTEIN KINASE P160ROCK	gb AAB02814.1	6182	1296	2498	93	94	HCFMY07	pSport1
1906	877408	procollagen alpha 2(V) [Homo sapiens] >pir A31427 CGHU2V collagen alpha 2(V) chain precursor - human >sp P05997 CA25_HUMAN COLLAGEN ALPHA 2(V) CHAIN PRECURSOR. >sp CAA75002 CAA75002 Procollagen alpha 2(V). >emb CAA28454.1 pro- alpha (V)collagen (AA 1099)	emb CAA75002.1	6183	3	1013	100	100	HSYBP46	pCMVSPORT 3.0
1907	877411			6184	2	313			HCRQK59	pSport1
1908	877437	multispanning membrane protein [Homo sapiens] >sp O15321 O15321 MULTISPANNING MEMBRANE PROTEIN. Length = 606	gb AAC51782.1	6185	93	314	100	100	HWLXK44	pSport1
1909	877630	(AF151877) CGI-119 protein [Homo sapiens] >sp Q9Y3C2 Q9Y3C2 CGI-119 PROTEIN. >gb AAF14868.1 AF113127_1 (AF113127) SIR protein [Homo sapiens] {SUB 21-258} Length = 258	gb AAD34114.1 AF1518	6186	1256	1657	91	91	HE8DZ94	Uni-ZAP XR
1910	877881			6187	3	662			HTELO87	Uni-ZAP XR
1911	878199			6188	245	553			HWLQL72	pSport1

1912	878207	(AK001523) unnamed protein product [Homo sapiens] Length = 165	dbj BAA91739.1	6189	572	1069	89	89	HBJL05	Uni-ZAP XR
1913	878238	similar to D. melanogaster trithorax protein [Caenorhabditis elegans] >pir T34384 T34384 hypothetical protein T26A5.7 - Caenorhabditis elegans >sp Q22795 Q22795 HYPOTHETICAL 27.6 KD PROTEIN. Length = 242	gb AAC77512.1	6190	3	272	60	73	HE2HC14	Uni-ZAP XR
1914	878274	(AF203978) MAX-like bHLHZIP protein [Homo sapiens] >sp AAF14638 AAF14638 MAX-like bHLHZIP protein. Length = 244	gb AAF14638.1 AF2039	6191	2	487	100	100	HDTHI51	pCMVSPORT 2.0
1915	878374	(AB033010) KIAA1184 protein [Homo sapiens] >sp BAA86498 BAA86498 KIAA1184 protein (fragment). Length = 380	dbj BAA86498.1	6192	2	1051	89	89	HRGDE77	Uni-ZAP XR
1916	878403	3-hydroxy-3-methylglutaryl coenzyme A synthase [Homo sapiens] >pir S45497 S45497 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), cytosolic, adrenal isoform - human >sp Q01581 HMCS_HUMAN HYDROXYMETHYLGLUTARYL-COA SYNTHASE, CYTOPLASMIC (EC 4.1.3.5) (HMG-CO	gb AA62411.1	6193	283	882	91	93	HHFHR53	Uni-ZAP XR
1917	878433	(AF096895) chemokine-like factor 1 [Homo sapiens] >sp AAF06722 AAF06722 Chemokine-like factor 1. Length = 99	gb AAF06722.1 AF0968	6194	105	443	100	100	HTPAY82	Uni-ZAP XR
1918	878436	(AK001682) unnamed protein product [Homo sapiens] Length = 242	dbj BAA91833.1	6195	85	1524	99	99	HMUBQ39	pCMVSPORT 3.0
1919	878560	(AF108139) radical fringe [Homo sapiens] >sp Q9Y644 Q9Y644 RADICAL FRINGE (FRAGMENT). Length = 191	gb AAD34321.1 AF1081	6196	331	2	98	100	HCEYN60	Uni-ZAP XR
1920	878800	ORF_f418 [Escherichia coli] >gb AAD13442.1 (AE000464) orf, hypothetical protein [Escherichia coli] >pir S40824 S40824 hypothetical 48K protein (glnA-fdhE intergenic region) - Escherichia coli >sp P32140 YIHS_ECOLI HYPOTHETICAL 47.4 KD PROTEIN IN GLNA-RBN	gb AAB03013.1	6197	223	2	100	100	HWHGF46	pCMVSPORT 3.0

1921	878909	KIAA0182 [Homo sapiens] >sp Q14687 Y182_HUMAN HYPOTHETICAL PROTEIN KIAA0182 (FRAGMENT). Length = 1157	dbj BAA11499 .1	6198	669	1421	84	85	HPMSF50	pBluescript
1922	878917	KIAA0069 [Homo sapiens] >sp Q15041 Y069_HUMAN HYPOTHETICAL PROTEIN KIAA0069 (HA1508) (FRAGMENT). Length = 226	dbj BAA06683 .1	6199	2	346	77	77	HTWEA61	pSport1
1923	878931			6200	318	506			HILBF77	pBluescript SK-
1924	879009	(AF035606) calcium binding protein [Homo sapiens] >gb AAF14336.1 U58773_1 calcium binding protein [Homo sapiens] >sp O75340 O75340 CALCIUM BINDING PROTEIN. >sp AAF14336 AAF14336 Calcium binding protein. Length = 191	gb AAC27697. 1	6201	618	1040	100	100	HTEHX05	Uni-ZAP XR
1925	879234			6202	211	903			HPHAA47	Uni-ZAP XR
1926	879386	(AF161516) HSPC167 [Homo sapiens] >sp AAF29131 AAF29131 HSPC167. Length = 586	gb AAF29131. 1 AF1615	6203	419	991	100	100	HHFJJ61	Uni-ZAP XR
1927	879484	(AF053651) cellular apoptosis susceptibility protein [Homo sapiens] >sp O75432 O75432 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN. Length = 971	gb AAC35297. 1	6204	885	2108	100	100	H2CAA49	pBluescript SK-
1928	879595			6205	3	419			HCRNW08	pSport1
1929	879661	(AF151079) HSPC245 [Homo sapiens] Length = 124	gb AAF36165. 1 AF1510	6206	158	982	100	100	HNTDJ29	pCMVSPORT 3.0
1930	879886			6207	502	762			HCRNM29	pSport1
1931	880071			6208	565	921			HTPAM76	Uni-ZAP XR
1932	880074	(AF112214) ribosomal protein L13 [Homo sapiens] >sp AAF17202 AAF17202 Ribosomal protein L13. Length = 172	gb AAF17202. 1 AF1122	6209	290	829	99	100	HCHOB95	pSport1
1933	880418			6210	1082	1339			HLSAA96	pSport1

1934	880578				6211	130	255				HBMA61	pCMVSPORT 1
1935	880649	(AF119297) neuroendocrine-specific protein-like protein 1 [Homo sapiens] >gb AAC99319.1 (AF059524) reticulon gene family protein [Homo sapiens] >gb AAD20951.1 (AF059529) reticulon gene family protein [Homo sapiens] >sp O95197 O95197 RETICULON PROTEIN. L	gb AAD26810.1 AF1192	6212	60	866	100	100			HE8QG48	Uni-ZAP XR
1936	880694	(AB001740) p27 [Homo sapiens] >sp O60232 AA27_HUMAN AUTOANTIGEN P27.1 Length = 199	dbj BAA25263.1	6213	1	618	88	88			HHENW13	pCMVSPORT 3.0
1937	880747	[Homo sapiens] >sp Q14089 Q14089 HYPOTHETICAL 40.0 KD PROTEIN (FRAGMENT). Length = 364	dbj BAA18909.1	6214	3	1751	74	77			HE8SB64	Uni-ZAP XR
1938	880927			6215	422	922					HKAEN78	pCMVSPORT 2.0
1939	880994			6216	339	527					HOSML44	Uni-ZAP XR
1940	881052	(AB020657) KIAA0850 protein [Homo sapiens] >emb CAB72329.1 (AL078644) bG279B7.1.1 (NS1-binding protein (KIAA0850, BTB/POZ domain and Kelch motifs containing protein)) [Homo sapiens] >sp Q9Y6Y0 Q9Y6Y0 KIAA0850 PROTEIN. Length = 642	dbj BAA74873.1	6217	3	1565	96	96			HTEEZ62	Uni-ZAP XR
1941	881074	Similar to a C.elegans protein in cosmid C14H10 [Homo sapiens] >sp O00236 O00236 KIAA0251 (FRAGMENT). Length = 820	dbj BAA19780.1	6218	3	1277	97	97			HOAAH52	Uni-ZAP XR
1942	881104	(AL050318) dJ977B1.3.1 (novel protein similar to putative RAB5-interacting protein (isoform 1)) [Homo sapiens] >gb AAF17201.1 AF112213_1 (AF112213) putative Rab5-interacting protein [Homo sapiens] >sp AAF17201 AAF17201 Putative Rab5-interacting protein. L	emb CAB75367.1	6219	265	654	92	92			HSDXB50	pBluescript

1943	881105	(AL050318) dJ977B1.3.1 (novel protein similar to putative RAB5-interacting protein (isoform 1)) [Homo sapiens] >gb AAAF17201.1 AF112213_1 (AF112213) putative Rab5-interacting protein [Homo sapiens] >sp AAAF17201 AAAF17201 Putative Rab5-interacting protein. L	emb CAB7536 7.1	6220	127	576	100	100	HFKMJ24	Uni-ZAP XR
1944	881219	(AC004882) similar to CAA16821 (PID:g3255952) [Homo sapiens] >sp AAAF03515 AAAF03515 WUGSC:H_DJ076B20.5 protein (fragment). Length = 620	gb AAAF03515. 1 AC0048	6221	3	2348	95	95	HEOQC11	pSport1
1945	881221	cell growth regulator CGR19 [Homo sapiens] >sp Q99675 Q99675 CELL GROWTH REGULATOR CGR19. Length = 332	gb AAC50897. 1	6222	2	1036	92	92	HWMBI22	pSport1
1946	882330			6223	1079	1477			HETDL42	Uni-ZAP XR
1947	882715	hypothetical protein [Bos taurus] >sp O18975 O18975 HYPOTHETICAL 16.6 KD PROTEIN (FRAGMENT). Length = 145	emb CAB0666 4.1	6224	1	327	72	74	HMEKW44	Lambda ZAP II
1948	882729	(AF151023) HSPC189 [Homo sapiens] Length = 222	gb AAF36109. 1 AF1510	6225	110	766	80	80	HCEDM42	Uni-ZAP XR
1949	882762			6226	1	489			HCRNZ31	pSport1
1950	883172			6227	98	652			HWMBU89	pSport1
1951	883201			6228	295	468			HUFBY15	pSport1
1952	883254	(AC003007) gene product (partial) [Homo sapiens] >sp O75201 O75201 HYPOTHETICAL 64.6 KD PROTEIN (FRAGMENT). Length = 580	gb AAC31671. 1	6229	3	695	71	71	HIBCE91	Other
1953	883371	(AJ245719) brk kinase substrate [Homo sapiens] >sp CAB65105 CAB65105 Brk kinase substrate. Length = 403	emb CAB6510 5.1	6230	3	917	85	85	HWLKF77	pSport1

1954	883753	(AB000712) CPE-receptor [Homo sapiens] >sp O14493 CLD4_HUMAN CLAUDIN-4 (CLOSTRIDIUM PERFRINGENS ENTEROTOXIN RECEPTOR) (CPE- RECEPTOR) (CPE-R). Length = 209	dbj BAA22984 .1	6231	239	868	77	77	HOGCA75	pCMVSPORT 2.0
1955	883799			6232	866	1129			HOGCI47	pCMVSPORT 2.0
1956	883945			6233	59	157			HWLUT61	pSport1
1957	883971			6234	115	303			HLTBA42	Uni-ZAP XR
1958	884038	(AF151882) CGI-124 protein [Homo sapiens] >sp Q9Y3C6 Q9Y3C6 CGI-124 PROTEIN (EC 5.2.1.8). Length = 166	gb AAD34119. 1 AF1518	6235	208	741	93	93	HHEHB82	pCMVSPORT 3.0
1959	884095	(AK000654) unnamed protein product [Homo sapiens] Length = 248	dbj BAA91309 .1	6236	432	956	46	72	HE2PR08	Uni-ZAP XR
1960	884161	(AK001845) unnamed protein product [Homo sapiens] Length = 612	dbj BAA91938 .1	6237	3	1385	99	100	HMKAN71	pSport1
1961	884168	(AF127036) calcium-activated chloride channel protein 1 [Homo sapiens] >sp AAD25487 AAD25487 Calcium-activated chloride channel protein 1. Length = 914	gb AAD25487. 1 AF1270	6238	2	2776	96	96	HSIFV30	Uni-ZAP XR
1962	884215	(AB026289) protein kinase SID6-1512 [Homo sapiens] >sp BAA85045 BAA85045 Protein kinase SID6-1512. Length = 306	dbj BAA85045 .1	6239	239	1171	81	90	HNTSY52	pSport1
1963	884379	(AF196972) JM24 protein [Homo sapiens] >sp AAF06800 AAF06800 JM24 protein (fragment). Length = 476	gb AAF06800. 1 AF1969	6240	2	775	73	75	HCR0M43	pSport1
1964	884529	(AF151908) CGI-150 protein [Homo sapiens] >sp Q9Y3E8 Q9Y3E8 CGI-150 PROTEIN. Length = 504	gb AAD34145. 1 AF1519	6241	237	683	100	100	HLWCF60	pCMVSPORT 3.0
1965	884719	(AB028859) hDj9 [Homo sapiens] >emb CAB65118.1 (AJ250137) ERj3 protein [Homo sapiens] >sp CAB65118 CAB65118 ERj3 protein precursor. >sp BAA88307 BAA88307 HDj9. Length = 358	dbj BAA88307 .1	6242	59	436	68	71	HWLKD85	pSport1

1966	885350	(AB011532) MEGF6 [Rattus norvegicus] >pir T13954 T13954 MEGF6 protein - rat >sp O88281 O88281 MEGF6. Length = 1574	dbj BAA32462 .1	6243	430	1581	45	56	HCRMX54	pSport1
1967	885476			6244	432	908			HTPHK88	Uni-ZAP XR
1968	885484	ORF4 [Rattus norvegicus] >pir S21348 S21348 probable pol. protein-related protein 4 - rat >sp Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF'S. Length = 275	emb CAA3764 7.1	6245	396	476	54	73	HCQBD35	Lambda ZAP II
1969	885511			6246	178	408			HLQFI67	Lambda ZAP II
1970	886331	(AF026124) schwannoma-associated protein [Mus musculus] >sp O35405 O35405 SCHWANNOMA- ASSOCIATED PROTEIN. Length = 488	gb AAC73069. 1	6247	3	755	37	57	HAIJBV26	pCMVSPORT 3.0
1971	886505	(AF161410) HSPC292 [Homo sapiens] >sp AAF28970 AAF28970 HSPC292 (fragment). Length = 164	gb AAF28970. 1 AF1614	6248	565	975	100	100	HBIJF90	Uni-ZAP XR
1972	886527			6249	1	375			HWLFB44	pSport1
1973	886788	(AK001350) unnamed protein product [Homo sapiens] Length = 326	dbj BAA91642 .1	6250	96	962	98	99	HCE4U96	Uni-ZAP XR
1974	886914	A33 antigen precursor [Homo sapiens] >sp Q99795 A33_HUMAN CELL SURFACE A33 ANTIGEN PRECURSOR. Length = 319	gb AAC50957. 1	6251	3	443	100	100	HWLEL48	pSport1
1975	887098	(AF161453) HSPC335 [Homo sapiens] >sp AAF29013 AAF29013 HSPC335 (fragment). Length = 159	gb AAF29013. 1 AF1614	6252	3	539	89	90	HTGBT14	Uni-ZAP XR
1976	887114	(AF067797) aquaporin 8 [Homo sapiens] >sp AAF19050 AAF19050 Aquaporin 8. Length = 261	gb AAF19050. 1	6253	297	1160	83	83	HKLRB09	pBluescript
1977	887155			6254	3	497			H2LAS29	pBluescript SK-
1978	887172	(AK000700) unnamed protein product [Homo sapiens] Length = 370	dbj BAA91327 .1	6255	505	1071	90	92	HMEKH10	Lambda ZAP II

1979	887192	urokinase [synthetic construct] >emb CAA00996.1 human u-PA cDNA insert [synthetic construct] >emb CAA01390.1 uPA [Homo sapiens] >emb CAA01559.1 pro-Urokinase [Homo sapiens] >emb CAA02215.1 u-PA [Homo sapiens] >dbj BAA00175.1 pro-urokinase precursor [emb CAA0082 9.1	6256	195	1205	95	96	HWLWR39	pSport1
1980	887280			6257	527	793			HADME31	pBluescript
1981	887399	SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3). >gb AAC62430.1 (AC005021) serum paraoxonase/arylesterase [Homo sapiens] {SUB 1-122} Length = 354	sp Q15166 PON3_HUMAN	6258	25	1134	99	99	HFVJL45	pBluescript
1982	887421	(AJ009936) nuclear hormone receptor PRR1-A [Homo sapiens] >sp CAB55489 CAB55489 Nuclear hormone receptor PRR1-A. >emb CAB55491.1 (AJ009936) nuclear hormone receptor PRR1-B [Homo sapiens] {SUB 56-434} Length = 434	emb CAB5548 9.1	6259	3	281	98	98	HWLFES6	pSport1
1983	887475			6260	218	475			HSWBP93	pCMV/Sport 3.0
1984	887535	unnamed protein product [Sus scrofa] >pir S52130 S52130 vascular endothelial growth factor - pig >sp P49151 VEGF_PIG VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF). Length = 190	emb CAA5714 3.1	6261	180	464	86	89	HSLJF91	Uni-ZAP XR
1985	887803			6262	377	757			HKLSC61	pBluescript
1986	887857	(AJ011497) Claudin-7 [Homo sapiens] >sp O95471 CLD7_HUMAN CLAUDIN-7. Length = 211	emb CAA0962 6.1	6263	319	1059	100	100	HLJEA63	pCMV/Sport 1

1987	887892	2.19 [Homo sapiens] >emb CAA39090.1 2-19 protein [Homo sapiens] >gb AA92652.1 2_19 [Homo sapiens] >pir I37095 I37095 gene 2.19 protein - human >sp P98173 219_HUMAN 2-19 PROTEIN PRECURSOR. Length = 230	emb CAA6064.5.1	6264	85	519	59	78	HWLOA40	pSport1
1988	887936	(AF131758) [Homo sapiens] >sp O95881 O95881. Length = 172	gb AAD20035.1	6265	2	199	100	100	HCQCF10	Lambda ZAP II
1989	887996	(AB006077) deleted in oral cancer 1 (doc-1, alias DORC1) [Homo sapiens] >gb AAC77831.1 (AF006484) putative oral tumor suppressor protein [Homo sapiens] >sp O14519 DOC1_HUMAN PUTATIVE ORAL CANCER SUPPRESSOR (DELETED IN ORAL CANCER-1). Length = 115	dbj BAA22937.1	6266	2	403	86	86	HAIBW90	Uni-ZAP XR
1990	888041	similar to protein kinase of X.laevis, has putative transmembrane domain in central region [Homo sapiens] >sp Q14680 Q14680 KIAA0175 PROTEIN. Length = 651	dbj BAA11492.1	6267	2	604	97	97	H2CBE03	pBluescript SK-
1991	888051	fatty acid amide hydrolase [Homo sapiens] >gb AAD13768.1 (AF098019) fatty acid amide hydrolase [Homo sapiens] >sp O00519 FAAH_HUMAN FATTY ACID AMIDE HYDROLASE (EC 3.1.-.-) (OLEAMIDE HYDROLASE). Length = 579	gb AAB58505.1	6268	2	1066	62	64	HE9Q119	Uni-ZAP XR
1992	888063	(AF073771) RNA polymerase II termination factor [Homo sapiens] >sp O75921 O75921 RNA POLYMERASE II TERMINATION FACTOR. Length = 1162	gb AAC64044.1	6269	1	399	91	91	HJACE25	pBluescript SK-
1993	888153	(AB013357) 49 kDa zinc finger protein [Mus musculus] >pir JE0367 JE0367 zinc finger protein - mouse >sp Q9Z326 Q9Z326 49 KDA ZINC FINGER PROTEIN. Length = 460	dbj BAA37094.1	6270	510	1907	80	80	HMWIR85	Uni-ZAP XR

1994	888254	glutathione S-transferase theta 2 [Homo sapiens] >pir A56847 A56847 glutathione transferase (EC 2.5.1.18) theta-2 - human >sp P30712 GTT2 HUMAN GLUTATHIONE S-TRANSFERASE THETA 2 (EC 2.5.1.18) (GST CLASS-THETA). {SUB 2-244} Length = 244	gb AAB63956.1	6271	2	334	100	100	HCRPV38	pSport1
1995	888402	(AJ271408) Fas-associated factor, FAF1 [Homo sapiens] >gb AAD27713.1 AF132938_1 (AF132938) CGI-03 protein [Homo sapiens] >sp Q9Y2Z3 Q9Y2Z3 CGI-03 PROTEIN. >sp CAB67705 CAB67705 Fas-associated factor, FAF1. >emb CAB63755.1 (AL133631) hypothetical protein	emb CAB67705.1	6272	2	2011	93	93	HSRBB92	Uni-ZAP XR
1996	888523	type I interstitial collagenase [Homo sapiens] >gb AAB36941.1 collagenase [Homo sapiens] >pir A37308 KCHUI interstitial collagenase (EC 3.4.24.7) precursor - human >sp P03956 COG1_HUMAN INTERSTITIAL COLLAGENASE PRECURSOR (EC 3.4.24.7) (MATRIX METALLOPROT	emb CAA3869.1.1	6273	2	1489	100	100	HSYEA10	pCMVSPORT 3.0
1997	888673			6274	2	286			HE2CC22	Uni-ZAP XR
1998	888708	(AL021106) /prediction=(method:"genscan", version:"1.0", score:"113.71"); /prediction=(method:"genefinder", version:"084"); /match=(desc:"LD30851.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD30851 5prime> >	emb CAA1593.9.1	6275	241	645	48	62	HOUAC22	Uni-ZAP XR
1999	888720			6276	488	964			HHECU01	pCMVSPORT 3.0
2000	888783	calcium-modulated protein S100-beta [synthetic construct] >pir A91254 BCBOIB S-100 protein beta chain - bovine {SUB 2-92} Length = 92	gb AAA72205.1	6277	111	371	40	68	H2LAP34	pBluescript SK-

2001	888950	growth factor [Mus musculus] >pir A46607 A46607 growth/differentiation factor GDF-3 precursor - mouse >sp Q07104 GDF3_MOUSE GROWTH/DIFFERENTIATION FACTOR 3 PRECURSOR (GDF-3) (VG-1-RELATED PROTEIN 2). Length = 366	gb AAA53034. 1	6278	3	1151	70	80	HNTAR08	pCMVSPORT 3.0
2002	889136			6279	311	520			HWLWH66	pSport1
2003	889263	beta-galactosidase [Expression vector pBSII- LUCINT] Length = 69	gb AAB53629. 1	6280	1924	2259	94	98	HWLCJ12	pSport1
2004	889299			6281	1329	1520			HNGEF72	Uni-ZAP XR
2005	889300	(AB011145) KIAA0573 protein [Homo sapiens] >sp O60319 O60319 KIAA0573 PROTEIN (FRAGMENT). Length = 451	dbj BAA25499. 1	6282	3	1409	97	97	HK-AEB46	pCMVSPORT 2.0
2006	889323			6283	481	996			HNHON23	Uni-ZAP XR
2007	889368	SThM [Homo sapiens] >sp Q12971 Q12971 SIALLYLTRANSFERASE STHM. Length = 374	gb AAA52228. 1	6284	3595	3176	98	98	HSKES11	Uni-ZAP XR
2008	889467	(AL096745) hypothetical protein [Homo sapiens] >emb CAB62532.1 (AL096745) hypothetical protein [Homo sapiens] >pir T12548 T12548 hypothetical protein DKFZp586D1022.1 - human >sp CAB62532 CAB62532 Hypothetical 40.6 kd protein. Length = 366	emb CAB6253 2.1	6285	3	413	99	99	HCEP05	pBluescript
2009	889494	(AF065389) tetraspan NET-4 [Homo sapiens] >gb AAF28869.1 AF121344_1 (AF121344) tetraspanin Tspan-5 [Mus musculus] >sp O60746 O60746 TETRASPAN NET-4. >sp AAF28869 AAF28869 Tetraspanin Tspan-5. Length = 268	gb AAC17120. 1	6286	2	361	74	78	HDHEA53	pCMVSPORT 2.0
2010	889700			6287	1	459			HCHAC08	pSport1
2011	889782	aldehyde dehydrogenase [Homo sapiens] Length = 517	gb AAA51693. 1	6288	140	463	100	100	HACBT96	Uni-ZAP XR

2012	889954	(AB033050) KIAA1224 protein [Homo sapiens] >sp BAA86538 BAA86538 KIAA1224 protein (fragment). Length = 635	dbj BAA86538 .1	6289	3	1025	85	92	HTLEN01	Uni-ZAP XR
2013	889962	(AF076612) chordin [Homo sapiens] >sp O95254 O95254 CHORDIN (FRAGMENT). Length = 801	gb AAC69835. 1	6290	1	705	34	47	HCROA43	pSport1
2014	889994			6291	282	446			HSLJW05	Uni-ZAP XR
2015	890666	membrane cofactor preprotein (AA -34 to 350) [Homo sapiens] >pir S01896 S01896 membrane cofactor protein precursor - human >gb AAD13968.1 S65879_1 complement system membrane cofactor protein CD46 [Homo sapiens] {SUB 1-34} Length = 384	emb CAA6867 5.1	6292	46	1308	85	85	HTPGK74	Uni-ZAP XR
2016	890698	(AL031295) dJ886K2.3(GALE (UDP-galactose-4- epimerase)) [Homo sapiens] >sp CAB40159 CAB40159 DJ886K2.3(GALE (UDP-galactose-4-epimerase)). Length = 348	emb CAB4015 9.1	6293	17	256	66	69	HHGAB64	Lambda ZAP II
2017	890753			6294	1399	1632			HOSOR86	Uni-ZAP XR
2018	890763	(AL035608) dJ479J7.2 (transmembrane 4 superfamily member 6) [Homo sapiens] >gb AAC64257.1 (AF043906) T245 protein [Homo sapiens] >gb AAC69710.1 (AF053453) tetraspan TM4SF [Homo sapiens] >gb AAD00560.1 A15 homolog [Homo sapiens] >gb AAF08365.1 AF133426_	emb CAB5568 1.1	6295	3	854	100	100	HE9RV77	Uni-ZAP XR
2019	890776	(AF079864) putative G-protein coupled receptor RA1c [Rattus norvegicus] >sp O88628 O88628 PUTATIVE G-PROTEIN COUPLED RECEPTOR RA1C. Length = 320	gb AAD12761. 1	6296	1317	2420	93	97	HPRAJ70	Uni-ZAP XR

2020	890801	(AB035207) Tob2 [Homo sapiens] >emb CAB62938.1 (AL008582) bK223H9.1 (TOB4 (BTG1 family protein)) [Homo sapiens] >sp BAA87042 BAA87042 Tob2. >sp CAB62938 CAB62938 BK223H9.1 (TOB4 (BTG1 family protein)). Length = 344	dbj BAA87042.1	6297	501	1505	65	65	HBODK52	pSport1
2021	890820	(AF009702) GABA-A receptor pi subunit [Homo sapiens] >gb AAC51357.1 GABA-A receptor pi subunit [Homo sapiens] >sp O00591 GAAP_HUMAN GAMMA-AMINOBUTYRIC-ACID RECEPTOR PI SUBUNIT PRECURSOR (GABA(A) RECEPTOR). Length = 440	gb AAC24194.1	6298	134	1516	95	95	HARNK52	pCMVSPORT 3.0
2022	890863	(AK000207) unnamed protein product [Homo sapiens] Length = 478	dbj BAA91009.1	6299	2	1210	45	64	HTLHU22	Uni-ZAP XR
2023	890945	DNA mismatch repair protein homolog [Homo sapiens] >gb AAC50285.1 hMLH1 [Homo sapiens] >pir S43085 S43085 DNA mismatch repair protein MLH1 - human >sp P40692 MLH1_HUMAN MUTL PROTEIN HOMOLOG 1 (DNA MISMATCH REPAIR PROTEIN MLH1). Length = 756	gb AAA82079.1	6300	3	2327	96	96	HWMBB29	pSport1
2024	891125	pancreatic peptidylglycine alpha-amidating monooxygenase, PAM=secretory isoform {clone PAM-15} [human, islet cell tumor cell line QGP-1, Peptide Partial, 905 aa] [Homo sapiens] >sp Q16253 Q16253 PANCREATIC PEPTIDYLGLYCINE ALPHA-AMIDATING MONOOXYGENASE (FR	gb AAB32776.1	6301	2	478	98	98	HWLND63	pSport1
2025	891264	(AK001537) unnamed protein product [Homo sapiens] Length = 129	dbj BAA91746.1	6302	1	633	100	100	HCROQ71	pSport1
2026	891305	KIAA0281 [Homo sapiens] >sp Q92556 Y281_HUMAN HYPOTHETICAL PROTEIN KIAA0281 (HA6725). Length = 247	dbj BAA13397.1	6303	227	2338	55	75	HBINP81	pCMVSPORT 3.0
2027	891896	beta-galactosidase alpha peptide [Cloning vector pSport2] Length = 114	gb AAA67217.1	6304	2	226	69	80	HDLAG89	pCMVSPORT 2.0

2028	892113	conserved hypothetical protein MTH68 - Methanobacterium thermoautotrophicum (strain Delta H) Length = 228	pir E69190 E6 9190	6305	844	1557	23	42	HE8FL95	Uni-ZAP XR
2029	892177	(AL137599) hypothetical protein [Homo sapiens] >emb CAB70835.1 (AL137599) hypothetical protein [Homo sapiens] >sp CAB70835 CAB70835 Hypothetical 45.2 kd protein (fragment). Length = 401	emb CAB7083 5.1	6306	33	1067	57	71	HHFGI59	Uni-ZAP XR
2030	892291	cathepsin D [Homo sapiens] >emb CAA28955.1 precursor polypeptide (AA -20 to 392) [Homo sapiens] >gb AAB59529.1 preprocathepsin D [Homo sapiens] >pir A25771 KHHUD cathepsin D (EC 3.4.23.5) precursor - human >sp P07339 CATD_HUMAN CATHEPSIN D PRECURSOR (EC	gb AAA51922. 1	6307	21	1232	96	96	HOFMT75	pCMVSPORT 2.0
2031	892367	!!! ALU SUBFAMILY SC WARNING ENTRY !!! Length = 585	sp P39192 AL U5_HUMAN	6308	899	1018	78	84	HWLEQ37	pSportl
2032	892558			6309	770	976			HWLDZ74	pSportl
2033	892563	MAL protein [Homo sapiens] >emb CAA53809.1 MAL [Homo sapiens] >emb CAA54100.1 MAL-a [Homo sapiens] >pir A29472 A29472 T-cell surface glycoprotein MAL, splice form a - human >sp P21145 MAL_HUMAN MYELIN AND LYMPHOCYTE PROTEIN (T-LYMPHOCYTE MATURATION-ASSO	gb AAA36196. 1	6310	1	618	39	50	HPJEB77	Uni-ZAP XR
2034	892820			6311	371	553			HNTST71	pSportl
2035	893223	(AF216312) type II membrane serine protease [Homo sapiens] Length = 423	gb AAF31436. 1 AF2163	6312	2	508	99	99	HCQDQ92	Lambda ZAP II
2036	893457			6313	88	345			HWLCU24	pSportl

2037	893827	cytochrome B [Homo sapiens] >pir A00151 CBHU ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - human mitochondrion >sp P00156 CYB_HUMAN CYTOCHROME B. >gb AAB58955.1 cytochrome b [Homo sapiens] {SUB 1-378} >gb AAA31851.1 cytochrome b [Homo s	emb CAA2403.8.1	6314	512	829	71	72	HSDJY15	Uni-ZAP XR
2038	893842			6315	86	388			HSAAR81	pBluescript SK-
2039	893866	secretory protein [Homo sapiens] >gb AAA83628.1 intestinal trefoil factor [Homo sapiens] >pir A48284 A48284 intestinal trefoil factor 3 precursor - human >sp Q07654 ITF_HUMAN INTESTINAL TREFOIL FACTOR PRECURSOR (HP1.B). Length = 80	gb AAA59981.1	6316	41	436	78	78	HNDAD16	pCMV/Sport 2.0
2040	893867	secretory protein [Homo sapiens] >gb AAA83628.1 intestinal trefoil factor [Homo sapiens] >pir A48284 A48284 intestinal trefoil factor 3 precursor - human >sp Q07654 ITF_HUMAN INTESTINAL TREFOIL FACTOR PRECURSOR (HP1.B). Length = 80	gb AAA59981.1	6317	2	316	78	78	HCNSE58	pBluescript
2041	894012	(AF023259) RNA-binding protein [Homo sapiens] >gb AAC63910.1 (AF023259) RNA-binding protein [Homo sapiens] >sp O75876 O75876 RNA-BINDING PROTEIN. Length = 411	gb AAC63910.1	6318	51	257	98	100	HSVCD79	Uni-ZAP XR
2042	894051			6319	23	310			HSIFA27	Uni-ZAP XR
2043	894121	ubiquitin carrier protein E2 - human >gb AAA58446.1 ubiquitin carrier protein [Homo sapiens] {SUB 23-247} Length = 247	pir B42856 B42856	6320	1	855	87	87	HTTKV46	Uni-ZAP XR

2044	894341	homeodomain protein [Gallus gallus] >pir B37914 B37914 homeotic protein Chox-4e - chicken (fragment) {SUB 7-99} >pir S14938 S14938 homeotic protein Hox D11 - human (fragment) {SUB 27-92} Length = 99	dbj BAA01133 .1	6321	3	122	100	100	HHGCE29	Lambda ZAP II
2045	894397	(AB037134) IRE homolog 1 [Arabidopsis thaliana] >sp BAA89784 BAA89784 IRE homolog 1 (fragment). Length = 1023	dbj BAA89784 .1	6322	2	355	54	72	HCYBE73	pBluescript SK-
2046	894631	(AL122098) hypothetical protein [Homo sapiens] >emb CAB59266.1 (AL122098) hypothetical protein [Homo sapiens] >pir T34532 T34532 hypothetical protein DKFZp434B1517.1 - human (fragment) >sp CAB59266 CAB59266 Hypothetical 71.5 kd protein (fragment). Length	emb CAB5926 6.1	6323	54	1268	86	86	HWLVS05	pSport1
2047	894806			6324	70	411			HCRMV27	pSport1
2048	894811			6325	381	620			HCR0122	pSport1
2049	894818			6326	1	102			HCQAF06	Lambda ZAP II
2050	894820	similar to [SwissProt Accession Number P23842]; start codon is not identified yet [Escherichia coli] >sp P76954 P76954 YFEA PROTEIN (FRAGMENT). Length = 771	dbj BAA16267 .1	6327	373	576	100	100	HKCSA83	pBluescript
2051	894824			6328	77	3			HSBAI04	pBluescript SK-
2052	894827			6329	253	570			HCQCD80	Lambda ZAP II
2053	894830	(AB005289) ABC transporter 7 protein [Homo sapiens] >sp O75027 ABC7_HUMAN ATP-BINDING CASSETTE TRANSPORTER 7 PRECURSOR (ABC TRANSPORTER 7 PROTEIN). Length = 752	dbj BAA28861 .1	6330	244	684	99	99	HCQCF52	Lambda ZAP II

2054	894831	(AF072816) ABC-type transporter MRP3 [Rattus norvegicus] >sp O88563 MRP3_RAT CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 2 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 3) (MRP-LIKE PROTEIN-2) (MLP-2). Length = 1522	gb AAC25416.1	6331	314	841	48	64	HCQDE22	Lambda ZAP II
2055	894832			6332	2	388			HWLVU33	pSport1
2056	894842			6333	2856	3134			HAIJAY88	pCMVSPORT 3.0
2057	894878			6334	3	230			HCRPM46	pSport1
2058	895122	MAP3K delta-1 protein kinase [Arabidopsis thaliana] >sp O23719 O23719 MAP3K DELTA-1 PROTEIN KINASE (FRAGMENT). Length = 406	emb CAA7459.1.1	6335	3	1049	39	58	HOEOQ19	Uni-ZAP XR
2059	895303	(AK000385) unnamed protein product [Homo sapiens] Length = 152	dbj BAA91131.1	6336	1468	1662	76	81	HKGBP52	pSport1
2060	895372			6337	321	632			HOUHL17	Uni-ZAP XR
2061	895675			6338	1873	2310			HDPBP40	pCMVSPORT 3.0
2062	895781			6339	337	552			HWLOI29	pSport1
2063	895927	(AB027466) spondin 2 [Homo sapiens] >sp BAA85892 BAA85892 Spondin 2. Length = 331	dbj BAA85892.1	6340	112	1266	91	91	HCRMJ47	pSport1
2064	896008	ribosomal protein L7a large subunit [Homo sapiens] >emb CAA36383.1 L7a protein [Homo sapiens] >emb CAA29889.1 PLA-X polypeptide [Homo sapiens] >emb CAA43925.1 ribosomal protein L7a [Homo sapiens] >emb CAA33117.1 ribosomal protein L7a (AA 1-266) [Rattus	gb AAA60282.1	6341	2	373	87	87	HLDXE66	pSport1
2065	897234			6342	117	446			HAIBM54	Uni-ZAP XR

2066	897524	unnamed protein product [Homo sapiens] >emb CAA93157.1 translocon-associated protein delta subunit precursor [Homo sapiens] >emb CAA92215.1 translocon-associated protein delta subunit precursor [Homo sapiens] >gb AAC51745.1 translocon-associated protei	emb CAA6221 1.1	6343	3	680	100	100	100	HSXAX45	Uni-ZAP XR
2067	897898	(AJ243320) hypothetical protein [Canis familiaris] >sp Q9XSV3 Q9XSV3 HYPOTHETICAL 20.0 KD PROTEIN. Length = 181	emb CAB4586 4.1	6344	3	707	30	47		HE8PB56	Uni-ZAP XR
2068	898087	(AF072128) claudin-2 [Mus musculus] >sp O88552 CLD2_MOUSE CLAUDIN-2. Length = 230	gb AAC27079. 1	6345	1	264	87	91		HTPGE66	Uni-ZAP XR
2069	898136			6346	190	504				HWLIL19	pSport1
2070	898157	novel ORF [Homo sapiens] >sp O00251 O00251 HYPOTHETICAL PROTEIN (FRAGMENT). Length = 68	gb AAB72234. 1	6347	688	1002	88	88		HPJEE80	Uni-ZAP XR
2071	898192			6348	111	353				HWLQX67	pSport1
2072	898355	beta-galactosidase [Expression vector pBSII- LUCINT] Length = 69	gb AAB53629. 1	6349	1810	2109	94	98		HCRNK75	pSport1
2073	898418	(AC003965) SP001LA [Homo sapiens] Length = 271	gb AAB93671. 1	6350	2	694	82	84		HOGDR01	pCMVSPORT 2.0
2074	898427	reticulocalbin [Homo sapiens] >emb CAB53067.1 (AL078612) dJ65P5.1 (reticulocalbin 1, EF-hand calcium binding domain) [Homo sapiens] >pir JC4173 JC4173 reticulocalbin precursor - human >sp Q15293 RCN1_HUMAN RETICULOCALBIN 1 PRECURSOR. >sp CAB53067 CAB5306	dbj BAA07670 .1	6351	298	1017	64	78		HHATR06	pCMVSPORT 3.0
2075	898541	(AF169677) leucine-rich repeat transmembrane protein FLRT3 [Homo sapiens] >sp AAF28461 AAF28461 Leucine-rich repeat transmembrane protein FLRT3. Length = 649	gb AAF28461. 1 AF1696	6352	424	1938	90	90		HLQDM07	Lambda ZAP II

2076	898651	(AF126484) CARD4 [Homo sapiens] >gb AAD28350.1 AF113925_1 (AF113925) Nod1 [Homo sapiens] >gb AAD43922.1 (AF149774) NOD1 protein [Homo sapiens] >sp Q9Y239 Q9Y239 NOD1 PROTEIN. Length = 953	gb AAD29125. 1 AF1264	6353	605	2761	91	91	HDPBW68	pCMVSPORT 3.0
2077	898814	(AF117754) thyroid hormone receptor-associated protein complex component TRAP240 [Homo sapiens] >sp AAD22032 AAD22032 Thyroid hormone receptor-associated protein complex component TRAP240. >dbj BAA25519.1 (AB011165) KIAA0593 protein [Homo sapiens] {SUB 1	gb AAD22032. 1	6354	1	2187	86	86	HISCJ15	pSport1
2078	898946	(AF081886) ERO1-like protein [Homo sapiens] >gb AAF06104.1 AF123887_1 (AF123887) ERO1L [Homo sapiens] {SUB 84-468} Length = 468	gb AAF35260. 1 AF0818	6355	1	1656	100	100	HCYBH77	pBluescript SK-
2079	899130	(AF117892) aspartic-like protease [Homo sapiens] >gb AAD45963.1 AF050171_1 (AF050171) aspartyl protease [Homo sapiens] >gb AAF17078.1 (AF200342) aspartyl protease 1 [Homo sapiens] >gb AAF26368.1 AF204944_1 (AF204944) transmembrane aspartic proteinase Asp	gb AAD45240. 1	6356	3	1445	92	92	HPJAS61	Uni-ZAP XR
2080	899224	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR. >emb CAA67261.1 collagen type I alpha 1 [Homo sapiens] {SUB 1-1069} >emb CAA29605.1 C- terminal propeptide domain [Homo sapiens] {SUB 1229-1454} Length = 1464	sp P02452 CA 11_HUMAN	6357	1308	2630	94	94	HCRMK25	pSport1

2081	899632	unnamed protein product [unidentified] >pir A26359 A26359 decay-accelerating factor splice form 1 precursor - human >dbj BAA22900.1 (AB003312) decay accelerating factor [Homo sapiens] {SUB 291-345} Length = 440	emb CAA0384 0.1	6358	3	1376	87	87	HNTRV11	pSport1
2082	899644	lac repressor [Cloning vector pCMVLacI] >gb AAC73448.1 (AE000141) transcriptional repressor of the lac operon [Escherichia coli] {SUB 1-360} >gb AAB61949.1 lac repressor fragment [unidentified cloning vector] {SUB 331-360} >gb AAA72793.1 lacI [unidenti	gb AAB17268. 1	6359	3	401	96	97	HWLOU33	pSport1
2083	899661	(AL050297) hypothetical protein [Homo sapiens] >emb CAB43396.1 (AL050297) hypothetical protein [Homo sapiens] >pir T08701 T08701 hypothetical protein DKFZp564N123.1 - human (fragment) >sp Q9Y3T6 Q9Y3T6 HYPOTHETICAL 50.0 KD PROTEIN (FRAGMENT). Length = 45	emb CAB4339 6.1	6360	21	1016	90	91	HAPNO50	Uni-ZAP XR
2084	899776	formate dehydrogenase [Escherichia coli] Length = 715	gb AAA23754. 1	6361	619	1392	99	99	HBSAK60	Uni-ZAP XR
2085	899866	artifact-warning sequence (translated ALU class F) - human Length = 673	pir F40201 F40 201	6362	88	201	59	70	HDPOD73	pCMVSPORT 3.0
2086	899885	SDF2 [Homo sapiens] >pir JC5106 JC5106 stromal cell-derived factor 2 precursor - human >sp Q99470 Q99470 SDF2. Length = 211	dbj BAA09312 .1	6363	233	928	91	92	HWHHQ57	pCMVSPORT 3.0
2087	899913	(AB012223) ORF2 [Canis familiaris] >sp O62658 O62658 LINE-1 ELEMENT ORF2. Length = 1275	dbj BAA25253 .1	6364	238	92	36	59	HNHFHY51	Uni-ZAP XR
2088	900015			6365	1	222			HTOHV42	Uni-ZAP XR
2089	900162	(AF157106) soluble secreted endopeptidase delta [Mus musculus] >sp AAF13153 AAF13153 Soluble secreted endopeptidase delta. Length = 742	gb AAF13153. 1 AF1571	6366	367	753	82	94	HWLXO02	pSport1

2090	900249	(AC006950) IgG Fc binding protein [AA 4671-5405] [Homo sapiens] >sp O95784 O95784 IGG FC BINDING PROTEIN (FRAGMENT). Length = 735	gb AAD15624. 1	6367	3	1409	93	93	HWLKM77	pSport1
2091	900555	(AL133620) hypothetical protein [Homo sapiens] >emb CAB63746.1 (AL133620) hypothetical protein [Homo sapiens] >sp CAB63746 CAB63746 Hypothetical 115.3 kd protein. Length = 1031	emb CAB6374 6.1	6368	29	2143	97	97	HWMCI06	pSport1
2092	900696	(AF175522) transmembrane tryptase [Homo sapiens] >gb AAF03697.1 AF175759_1 (AF175759) transmembrane tryptase [Homo sapiens] >sp AAF03695 AAF03695 Transmembrane tryptase. >sp AAF03697 AAF03697 Transmembrane tryptase. Length = 321	gb AAF03695. 1 AF1755	6369	21	902	47	57	HCRPZ48	pSport1
2093	900777	Similar to S.cerevisiae EMP70 protein precursor (S25110) [Homo sapiens] >sp Q92544 Q92544 MYELOBLAST KIAA0255. Length = 625	dbj BAA13385 .1	6370	611	1492	84	84	HCRMU04	pSport1
2094	900784	(AF106037) adipocyte-derived leucine aminopeptidase [Homo sapiens] >sp AAF07395 AAF07395 Adipocyte-derived leucine aminopeptidase. Length = 941	gb AAF07395. 1 AF1060	6371	250	3081	94	95	HHBEA82	pCMVSPORT 1
2095	900838	frizzled protein-2 - human Length = 295	pir JE0174 JE0 174	6372	2	1132	97	97	HWHGX93	pCMVSPORT 3.0
2096	900919	(AF020797) AP-mu chain family member mu1B [Homo sapiens] >sp Q9Y6Q5 Q9Y6Q5 AP-MU CHAIN FAMILY MEMBER MU1B. Length = 423	gb AAD25870. 1 AF0207	6373	3	1328	99	99	HTNAI80	pBluescript SK-

2097	900966	(AL117507) hypothetical protein [Homo sapiens] >emb CAB55969.1 (AL117507) hypothetical protein [Homo sapiens] >pir T17279 T17279 hypothetical protein DKFZp434F1935.1 - human >sp CAB55969 CAB55969 Hypothetical 39.2 kd protein. >emb CAA29963.1 hU1-70K pro	emb CAB5596 9.1	6374	1784	2824	64	64	HCRPO45	pSport1
2098	900991	(AF077030) hypothetical 43.2 kDa protein [Homo sapiens] >gb AAD34049.1 AF151812_1 (AF151812) CGI-54 protein [Homo sapiens] >sp Q9Y282 Q9Y282 CGI-54 PROTEIN. Length = 383	gb AAD27763. 1 AF0770	6375	1	1230	96	96	HWLWF60	pSport1
2099	900993	(AF147790) transmembrane mucin 12 [Homo sapiens] >sp AAD55678 AAD55678 Transmembrane mucin 12 (fragment). Length = 585	gb AAD55678. 1 AF1477	6376	3	1619	84	86	HCNCY58	Lambda ZAP II
2100	901111	(AF061022) CTH [Homo sapiens] >sp O95791 O95791 CTH. Length = 325	gb AAD17522. 1	6377	3	1097	84	85	HCNDA61	Lambda ZAP II
2101	901125	(AF127036) calcium-activated chloride channel protein 1 [Homo sapiens] >sp AAD25487 AAD25487 Calcium-activated chloride channel protein 1. Length = 914	gb AAD25487. 1 AF1270	6378	23	2629	96	96	HCNUB65	pBluescript
2102	901128	(AB002362) KIAA0364 [Homo sapiens] >gb AAC52057.1 (AF034198) IGSF1 [Homo sapiens] >pir T09402 T09402 immunoglobulin-like protein IGSF1 - human >sp O15070 O15070 KIAA0364. Length = 1327	dbj BAA20819 .1	6379	2	826	42	57	HWLRB02	pSport1
2103	901202	(AJ245620) CTL1 protein [Homo sapiens] Length = 654	emb CAB7554 1.1	6380	86	2209	93	93	HSDKL35	Uni-ZAP XR
2104	901253	GalNAc alpha-2,6-sialyltransferase I [Mus musculus] >sp CAA72137 CAA72137 GalNAc alpha-2,6- sialyltransferase I. Length = 526	emb CAA7213 7.1	6381	31	1905	65	73	HJPCX37	Uni-ZAP XR
2105	901276	(AB023172) KIAA0955 protein [Homo sapiens] >sp Q9Y2G2 Q9Y2G2 KIAA0955 PROTEIN. Length = 431	dbj BAA76799 .1	6382	259	1155	98	99	HPBEM10	pBluescript SK-

2106	901333	(AF201951) high affinity immunoglobulin epsilon receptor beta subunit [Homo sapiens] Length = 240	gb AAF17243.1 AF2019	6383	470	1288	35	49	HWBDL33	pCMVSPORT 3.0
2107	901375	regenerating protein I [Mus musculus] >pir A47148 A47148 reg I, regenerating islet cells - mouse >sp P43137 LIT1_MOUSE LITHOSTATHINE 1 PRECURSOR (PANCREATIC STONE PROTEIN 1) (PSP) (PANCREATIC THREAD PROTEIN 1) (PTP) (ISLET OF LANGERHANS REGENERATING PROTEIN)	dbj BAA03111.1	6384	172	669	36	60	H2LBA47	pBluescript SK-
2108	901415	(AF007791) secreted cement gland protein XAG-2 homolog [Homo sapiens] >gb AAC82614.1 (AF038451) secreted cement gland protein XAG-2 homolog [Homo sapiens] >gb AAF22484.1 AF088867_1 (AF088867) putative secreted protein XAG [Homo sapiens] >pir JE0350 JE035	gb AAC77358.1	6385	2	607	100	100	HCQAJ72	Lambda ZAP II
2109	901421	(AF125543) major histocompatibility complex class I protein [Monodelphis domestica] >sp AAF02448 AAF02448 Major histocompatibility complex class I protein. Length = 347	gb AAF02448.1 AF1255	6386	67	819	29	46	HETHC61	Uni-ZAP XR
2110	901472	predicted using GeneFinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans] >pir T21882 T21882 hypothetical protein F36H1.1 - Caenorhabditis elegans >sp Q20107 Q20107 F36H1.1 PROTEIN. Length = 139	emb CAA9299.4.1	6387	2	724	52	71	HTXLJ25	Uni-ZAP XR
2111	901473	2.19 [Homo sapiens] >emb CAA39090.1 2.19 protein [Homo sapiens] >gb AAA92652.1 2.19 [Homo sapiens] >pir I37095 I37095 gene 2.19 protein - human >sp P98173 P98173 HUMAN 2.19 PROTEIN PRECURSOR. Length = 230	emb CAA6064.5.1	6388	3	671	62	80	HCNAI22	Lambda ZAP II

2112	901494	(AB006781) galectin-4 [Homo sapiens] >gb AAB86590.1 galectin-4 [Homo sapiens] >gb AAC51763.1 (AF014838) galectin-4 [Homo sapiens] >sp P56470 LEG4_HUMAN GALECTIN-4 (LACTOSE-BINDING LECTIN 4) (L-36 LACTOSE BINDING PROTEIN) (L36LBP). >sp AAB86590 AAB86590	dbj BAA22165.1	6389	2	805	92	92	HSIAL77	Uni-ZAP XR
2113	901515	pre-pump-1 proteinase (AA -17 to 250) [Homo sapiens] >emb CAA77942.1 PUMP [Homo sapiens] >pir B28816 KCHUM matrilysin (EC 3.4.24.23) precursor - human >sp P09237 COG7_HUMAN MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE)	emb CAA3067.8.1	6390	3	839	100	100	HRACJ32	pCMVSPORT 3.0
2114	901567	(AK001466) unnamed protein product [Homo sapiens] Length = 202	dbj BAA91708.1	6391	2	736	92	92	HMGJ25	Uni-ZAP XR
2115	901578	G PROTEIN-COUPLED RECEPTOR CKR-L2 [Homo sapiens] >sp O15185 O15185 G PROTEIN-COUPLED RECEPTOR CKR-L2. Length = 415	emb CAB0214.3.1	6392	2	1417	80	80	HDTEO10	pCMVSPORT 2.0
2116	901621	(AL031685) dJ963K23.2 (novel protein) [Homo sapiens] >sp Q9Y508 Q9Y508 DJ963K23.2 (NOVEL PROTEIN) (FRAGMENT). Length = 228	emb CAB4602.8.1	6393	2	694	94	94	HSSGC06	Uni-ZAP XR
2117	901875	GalNAc alpha-2,6-sialyltransferase I [Mus musculus] >sp CAA72137 CAA72137 GalNAc alpha-2,6-sialyltransferase I. Length = 526	emb CAA7213.7.1	6394	32	1906	67	75	HSICN14	Uni-ZAP XR
2118	HWLMO73R	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp P39194 ALU7_HUMAN	6395	2	496	81	86	HWLMO73	pSport1
2119	HCRMU56R	!!!! ALU SUBFAMILY SX WARNING ENTRY !!!! Length = 591	sp P39195 ALU8_HUMAN	6396	25	129	75	77	HCRMU56	pSport1

2120	HWLRH49R	"TFIIA-42" [Homo sapiens] >emb CAA53151.1 TFIIA [Homo sapiens] >emb CAA54442.1 TFIIA/alpha, p55 [Homo sapiens] >gb AAF26776.1 AC010582_2 (AC010582) TFIIA- 42 [Homo sapiens] >gb AAF26776.1 AC010582_2 (AC010582) TFIIA-42 [Homo sapiens] >pir A49077 A49077	dbj BAA03604 .1	6397	2	115	75	75	HWLRH49	pSport1
2121	HKCSA70R	(AB000911) ribosomal protein [Sus scrofa] >emb CAB56794.1 ribosomal protein S18 [Homo sapiens] >emb CAA20231.1 (AL031228) dl1033B10.4 (40S ribosomal protein S18 (RPS18, KE-3)) [Homo sapiens] >gb AAA16795.1 ribosomal protein [Mus musculus] >emb CAA40750	dbj BAA19211 .1	6398	1	159	100	100	HKCSA70	pBluescript
2122	HWLOB10R	(AB001428) motor domain of KIF12 [Mus musculus] >sp O35061 O35061 MOTOR DOMAIN OF KIF12 (FRAGMENT). Length = 169	dbj BAA22388 .1	6399	2	163	93	95	HWLOB10	pSport1
2123	HCQCG26R	(AB002303) KIAA0305 [Homo sapiens] >sp O15023 O15023 KIAA0305. Length = 1539	dbj BAA20764 .1	6400	1	219	98	98	HCQCG26	Lambda ZAP II
2124	HCRNR57R	(AB002304) KIAA0306 [Homo sapiens] >sp BAA20765 BAA20765 KIAA0306 protein (fragment). Length = 1451	dbj BAA20765 .1	6401	1	303	95	95	HCRNR57	pSport1
2125	HWLUZ40R	(AF152961) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens] >sp Q9Y5B9 Q9Y5B9 CHROMATIN- SPECIFIC TRANSCRIPTION ELONGATION FACTOR FACT 140 KDA SUBUNIT. >gb AAF28231.1 (AF164924) SPT16/CDC68-like protein [Homo sapiens]	gb AAD43978. 1 AF1529	6402	2	313	79	79	HWLUZ40	pSport1
2126	H6EBJ04R			6403	332	129			H6EBJ04	Uni-ZAP XR
2127	HOENF69R	(AB011180) KIAA0608 protein [Homo sapiens] >sp O60347 O60347 KIAA0608 PROTEIN (FRAGMENT). Length = 775	dbj BAA25534 .1	6404	1	264	43	46	HOENF69	Uni-ZAP XR

2128	HCQDC8IR	(AB012725) zinc finger protein [Mus musculus] >sp O88291 O88291 ZINC FINGER PROTEIN. Length = 580	dbj BAA31522 .1	6405	169	393	76	80	HCQDC81	Lambda ZAP II
2129	HWLQY33R	(AB014519) KIAA0619 protein [Homo sapiens] >sp O75116 O75116 KIAA0619 PROTEIN. Length = 1388	dbj BAA31594 .1	6406	197	382	95	95	HWLQY33	pSport1
2130	HCRNF08R	hypothetical protein KIAA0684 - human (fragment) >sp O75169 O75169 KIAA0684 PROTEIN (FRAGMENT). Length = 903	pir T00358 T0 0358	6407	2	145	79	82	HCRNF08	pSport1
2131	HKCSZ69R	scar protein [Homo sapiens] Length = 244	gb AAA36597. 1	6408	2	313	98	98	HKCSZ69	pBluescript
2132	HCQAG23R	(AB018335) KIAA0792 protein [Homo sapiens] >sp O94886 O94886 KIAA0792 PROTEIN. Length = 807	dbj BAA34512 .1	6409	149	295	92	94	HCQAG23	Lambda ZAP II
2133	HCRQD03R	immunoglobulin heavy chain [Homo sapiens] Length = 152	gb AAA69736. 1	6410	1	573	66	75	HCRQD03	pSport1
2134	H2LAF75R	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9 Y6Y5	6411	19	180	96	96	H2LAF75	pBluescript SK-
2135	H2LAJ65R			6412	1	159			H2LAJ65	pBluescript SK-
2136	H2LAT73R	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9 Y6Y5	6413	2	202	96	96	H2LAT73	pBluescript SK-
2137	H2LAX35R	(AJ005324) glutamate permease [synthetic construct] >emb CAA06474.1 (AJ005327) glutamate permease [synthetic construct] >emb CAA06477.1 (AJ005330) glutamate permease [synthetic construct] >gb AAA24514.1 gltS [Escherichia coli] {SUB 437- 459} Length = 45	emb CAA0647 1.1	6414	1	150	93	93	H2LAX35	pBluescript SK-

2138	H2LAX79R	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	6415	3	158	96	96	H2LAX79	pBluescript SK-
2139	HCYBK85R			6416	11	127			HCYBK85	pBluescript SK-
2140	HCYBK96R	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	6417	2	154	87	87	HCYBK96	pBluescript SK-
2141	HCYBL18R	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	6418	1	120	80	86	HCYBL18	pBluescript SK-
2142	HCYBM62R	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	6419	1	123	75	80	HCYBM62	pBluescript SK-
2143	HCYBO61R	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	6420	2	112	100	100	HCYBO61	pBluescript SK-
2144	HTXPR08R	(AB020670) KIAA0863 protein [Homo sapiens] >sp O94943 O94943 KIAA0863 PROTEIN. Length = 1131	dbj BAA74886.1	6421	2	88	100	100	HTXPR08	Uni-ZAP XR

2145	HUUAQ45R	(AB021288) beta 2-microglobulin [Homo sapiens] >gb AA87972.1 beta-2-microglobulin [Pan troglodytes] >gb AA88008.1 beta-2-microglobulin [Gorilla gorilla] >gb AAD48083.1 (AF072097) beta- 2 microglobulin [Homo sapiens] >pir A90976 MGHUB2 beta-2-microglob	dbj BAA35182 .1	6422	68	322	78	78	HUUAQ45	pSportl
2146	HWLWQ51R	(AB023191) KIAA0974 protein [Homo sapiens] >sp Q9Y210 Q9Y210 KIAA0974 PROTEIN (FRAGMENT). Length = 565	dbj BAA76818 .1	6423	2	517	73	76	HWLWQ51	pSportl
2147	HKLAB44R	(AB023210) KIAA0993 protein [Homo sapiens] >sp Q9Y217 Q9Y217 KIAA0993 PROTEIN (FRAGMENT). Length = 364	dbj BAA76837 .1	6424	3	389	82	84	HKLAB44	Lambda ZAP II
2148	H2CBA06R	(AB023222) KIAA1005 protein [Homo sapiens] >sp Q9Y2K8 Q9Y2K8 KIAA1005 PROTEIN (FRAGMENT). Length = 1055	dbj BAA76849 .1	6425	1	354	100	100	H2CBA06	pBluescript SK-
2149	HWLRL41R	(AB028624) mitochondrial ATP Synthase subunit e [Homo sapiens] >sp Q9Y6W4 Q9Y6W4 MITOCHONDRIAL ATP SYNTHASE SUBUNIT E (FRAGMENT). Length = 66	dbj BAA78778 .1	6426	2	154	94	100	HWLRL41	pSportl
2150	HCNAH60R	(AC002301) Homolog of rat Zymogen granule membrane protein [Homo sapiens] >sp O60844 O60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN. Length = 167	gb AAC08708. 1	6427	2	325	80	81	HCNAH60	Lambda ZAP II
2151	HCNDF58R	(AC002301) Homolog of rat Zymogen granule membrane protein [Homo sapiens] >sp O60844 O60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN. Length = 167	gb AAC08708. 1	6428	62	328	82	86	HCNDF58	Lambda ZAP II

2152	HCRMZ60R	(AC002483) putative product from mRNA sequence CG003 from BRCA2 region; match to U50534 (NID:g1685103) [Homo sapiens] >pir T00415 T00415 hypothetical protein H_248O15.1 - human (fragment) >sp O14572 O14572 WUGSC:H_248O15.1 PROTEIN (FRAGMENT). Length = 184	gb AAC35295.1	6429	2	544	67	79	HCRMZ60	pSportl
2153	HCRNL13R	(AC002563) putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860) [Homo sapiens] >sp O14578 CTRO_HUMAN CITRON PROTEIN (FRAGMENT). >dbj BAA76793.1 (AB023166) KIAA0949 protein [Homo sapiens] {SUB 347-1286} Length = 1286	gb AAB71327.1	6430	3	236	98	100	HCRNL13	pSportl
2154	HCRMX17R	(AC003682) R27945_2 [Homo sapiens] >sp O43338 O43338 R27945_2. Length = 475	gb AAC24607.1	6431	19	204	51	65	HCRMX17	pSportl
2155	HWMB168R	(AL109657) dJ842G6.1 (novel protein) [Homo sapiens] >sp CAB65791 CAB65791 DJ842G6.1 (novel protein) (fragment). Length = 197	emb CAB65791.1	6432	3	218	100	100	HWMBJ68	pSportl
2156	HWLOV91R	(AC004475) F23858_1 [Homo sapiens] >pir T02299 T02299 hypothetical protein F23858_1 - human (fragment) >sp O60378 O60378 F23858_1 (FRAGMENT). >emb CAB70678.1 (AL137286) hypothetical protein [Homo sapiens] {SUB 217-608} Length = 608	gb AAC08052.1	6433	3	455	66	66	HWLOV91	pSportl
2157	HCRPW27R	(AC004528) R32184_3 [Homo sapiens] >sp O60392 O60392 R32184_3. Length = 529	gb AAC12681.1	6434	3	314	96	96	HCRPW27	pSportl
2158	HELGR96R	APP-binding protein 1 [Rattus norvegicus] >sp Q9Z1A5 Q9Z1A5 APP-BINDING PROTEIN 1. Length = 534	gb AAD09247.1	6435	1	249	75	79	HELGR96	Uni-ZAP XR
2159	HCRPB14R			6436	2	79			HCRPB14	pSportl
2160	HCRQM72R			6437	273	1			HCRQM72	pSportl
2161	HWLNK47R			6438	343	2			HWLNK47	pSportl

2162	HWLOI40R	unnamed protein product [unidentified] Length = 180	emb CAB6919 5.1	6439	403	212	86	93	HWLOI40	pSport1
2163	HWLMMH52R	(AL096881) hypothetical protein [Homo sapiens] >gb AAF19256.1 AC004832_1 (AC004832) similar to 45 kDa secretory protein [Rattus norvegicus]; similar to CAA10644.1 (PID:g4164418) [Homo sapiens] >sp O76054 O76054 HYPOTHETICAL 46.1 KD PROTEIN. >sp AAF19256 A	emb CAB5140 5.1	6440	3	245	100	100	HWLMMH52	pSport1
2164	H2CBU03R	(AB033044) KIAA1218 protein [Homo sapiens] >sp BAA86532 BAA86532 KIAA1218 protein (fragment). Length = 864	dbj BAA86532 .1	6441	3	353	96	96	H2CBU03	pBluescript SK-
2165	HWLUL19R	(AC005154) similar to protein U28928 (PID:g861306) [Homo sapiens] >sp O75223 O75223 WUGSC:H_DJ0777O23.1 PROTEIN. Length = 188	gb AAC23790. 1	6442	2	211	59	62	HWLUL19	pSport1
2166	HCQDR91R	(AL117583) hypothetical protein [Homo sapiens] >emb CAB56005.1 (AL117583) hypothetical protein [Homo sapiens] >pir T17315 T17315 hypothetical protein DKFZp434K058.1 - human >sp CAB56005 CAB56005 Hypothetical 12.7 kd protein. Length = 117	emb CAB5600 5.1	6443	385	146	90	90	HCQDR91	Lambda ZAP II
2167	HWMBN34R	(AC006153) similar to Aquifex aeolicus GTP- binding protein; similar to AE000771 (PID:g2984292) [Homo sapiens] >sp Q9Y6T6 Q9Y6T6 WUGSC:H_NH0120J02.1 PROTEIN (FRAGMENT). Length = 206	gb AAD15550. 1	6444	2	388	100	100	HWMBN34	pSport1
2168	HWMBN308R	(AC007228) BC37295_1 [Homo sapiens] >sp Q9Y2N9 Q9Y2N9 BC37295_1. Length = 599	gb AAD23607. 1 AC0072	6445	22	426	65	74	HWMBN308	pSport1

2169	HKCSC14R	(AF000227) putative amino acid/amine transport protein [Escherichia coli] >pir C64878 C64878 probable amino acid permease ycjJ - Escherichia coli >sp P76037 YCJJ_ECOLI_HYPOTHETICAL 50.9 KD TRANSPORT PROTEIN IN SAPA-ALDH INTERGENIC REGION. {SUB 19-479} >db	gb AAC74378.1	6446	427	14	68	70	HKCSC14	pBluescript
2170	HCRNF81R	(AF000364) heterogeneous nuclear ribonucleoprotein R [Homo sapiens] >pir T02673 T02673 heterogeneous nuclear ribonucleoprotein R - human >sp O43390 O43390 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN R. Length = 633	gb AAC39540.1	6447	1	591	88	90	HCRNF81	pSport1
2171	HOHC131R	(AF000381) non-functional folate binding protein [Homo sapiens] >sp O14597 O14597 NON-FUNCTIONAL FOLATE BINDING PROTEIN. Length = 254	gb AAB81938.1	6448	521	327	57	62	HOHC131	pCMVSPORT 2.0
2172	HSKCC10R	(AF006084) p41-Arc [Homo sapiens] >gb AAF03508.1 AC004922_5 (AC004922) P41-ARC [Homo sapiens] >sp O15143 AR41_HUMAN ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC). >sp AAF03508 AAF03508 P41-ARC. Length = 372	gb AAB64189.1	6449	34	213	72	77	HSKCC10	pBluescript
2173	HWLWU01R	(AF006621) embryonic lung protein [Homo sapiens] >sp Q9Y6R2 Q9Y6R2 EMBRYONIC LUNG PROTEIN. Length = 568	gb AAB87763.1	6450	1	246	95	95	HWLWU01	pSport1
2174	HCQDS79R	(AF007157) [Homo sapiens] >sp O43414 O43414 HYPOTHETICAL 43.1 KD PROTEIN (FRAGMENT). >gb AAC04618.1 (AC004254) similar to C. elegans hypothetical protein; similar to AF038615 (PID:g2736329) [Homo sapiens] {SUB 224-312} >emb CAB55430.1 (AL035417)	gb AAC19158.1	6451	80	571	85	92	HCQDS79	Lambda ZAP II
2175	H2CBC52R			6452	50	370			H2CBC52	pBluescript SK-

2176	HWLWU22R	(AF012023) integrin cytoplasmic domain associated protein; Icap-1a [Homo sapiens] >sp O14713 O14713 INTEGRIN CYTOPLASMIC DOMAIN ASSOCIATED PROTEIN. Length = 200	gb AAB88671.1	6453	1	342	85	85	HWLWU22	pSport1
2177	HWLMC24R	(AF051100) immunoglobulin G Fd fragment [Homo sapiens] Length = 223	gb AAD15787.1	6454	82	366	77	77	HWLMC24	pSport1
2178	HWLUR40R	(AF014118) membrane-associated kinase [Homo sapiens] >sp O14731 O14731 MEMBRANE-ASSOCIATED KINASE. Length = 499	gb AAB71843.1	6455	1	324	88	90	HWLUR40	pSport1
2179	HCQCH96R			6456	94	156			HCQCH96	Lambda ZAP II
2180	HHAOD46R	(AF014955) TFAR19 [Homo sapiens] >pir IG0192 IG0192 TFAR19 protein - human >sp O14737 TF19 HUMAN TFAR19 PROTEIN (TF-1 CELL APOPTOSIS RELATED GENE-19 PROTEIN). Length = 125	gb AAD11579.1	6457	49	432	85	85	HHAOD46	pCMVSPORT 3.0
2181	HCYBA83R	(AF017061) vasopressin-activated calcium mobilizing putative receptor protein [Homo sapiens] Length = 781	gb AAB70253.1	6458	1	489	98	99	HCYBA83	pBluescript SK-
2182	HCROZ77R	(AF018261) EH domain binding protein Epsin [Rattus norvegicus] >sp O88339 O88339 EH DOMAIN BINDING PROTEIN EPSIN. Length = 575	gb AAC33823.1	6459	1	525	67	69	HCROZ77	pSport1
2183	HWLND06R	(AF022108) putative replication initiator origin recognition complex subunit Orc4Lp [Homo sapiens] >gb AAC80282.1 (AF047598) origin recognition complex subunit 4; Orc4p [Homo sapiens] >gb AAD22110.1 (AF132596) origin recognition complex subunit 4 [Homo sapiens]	gb AAC01957.1	6460	1	213	73	79	HWLND06	pSport1
2184	HCQCP20R	(AB038463) GC36 [Homo sapiens] Length = 664	dbj BAA92137.1	6461	2	229	98	98	HCQCP20	Lambda ZAP II

2185	HCRQF71R	(AF022799) digestive tract-specific calpain; calcium-dependent cysteine proteinase [Homo sapiens] >sp O14815 O14815 DIGESTIVE TRACT-SPECIFIC CALPAIN (EC 3.4.22.17). Length = 690	gb AAB80762.1	6462	3	383	100	100	HCRQF71	pSport1
2186	HWLNF84R	(AF025459) H14A12.3 gene product [Caenorhabditis elegans] >sp O17213 O17213 H14A12.3 PROTEIN. Length = 284	gb AAB70984.1	6463	2	457	33	52	HWLNF84	pSport1
2187	HCRMF28R	(AF026977) microsomal glutathione S-transferase 3 [Homo sapiens] >sp O14880 O14880 MICROSOMAL GLUTATHIONE S-TRANSFERASE 3. Length = 152	gb AAB82609.1	6464	8	184	74	80	HCRMF28	pSport1
2188	HCROQ32R	(AF029789) GTPase-activating protein [Homo sapiens] >sp O60484 O60484 GTPASE-ACTIVATING PROTEIN. Length = 1041	gb AAC32547.1	6465	1	297	90	90	HCROQ32	pSport1
2189	HWLOW79R	(AF030339) VESPR [Homo sapiens] >pir T09074 T09074 semaphorin receptor VESPR - human >sp O60486 O60486 VESPR. Length = 1568	gb AAC18823.1	6466	2	133	100	100	HWLOW79	pSport1
2190	HCRQL67R	(AF030430) semaphorin VIa [Mus musculus] >sp O35464 O35464 SEMAPHORIN VIA PRECURSOR. Length = 888	gb AAB86408.1	6467	21	551	68	77	HCRQL67	pSport1
2191	HCRQI10R	(AL137438) hypothetical protein [Homo sapiens] >emb CAB70736.1 (AL137438) hypothetical protein [Homo sapiens] >sp CAB70736 CAB70736 Hypothetical 69.3 kd protein (fragment). Length = 596	emb CAB70736.1	6468	3	299	99	99	HCRQI10	pSport1
2192	HWLRE34R	(AF034802) liprin-beta 1 [Homo sapiens] >sp O75336 O75336 LIPRIN-BETA1. Length = 1005	gb AAC26103.1	6469	153	242	92	100	HWLRE34	pSport1

2193	HULCD94R	(AF035178) elongation factor 1 A2 [Oryctolagus cuniculus] >emb CAA50280.1 elongation factor 1 alpha-2 [Homo sapiens] >pir S35033 EFHUA2 translation elongation factor eEF-1 alpha-2 chain - human >sp Q05639 EF12_HUMAN ELONGATION FACTOR 1-ALPHA 2 (EF-1-ALPH	gb AAC39252.1	6470	119	466	82	86	HULCD94	pSport1
2194	HHMMF84R	(AF035840) NADH:ubiquinone oxidoreductase B17 subunit [Homo sapiens] >gb AAD32451.1 AF067167_1 (AF067167) NADH-ubiquinone oxidoreductase B17 subunit homolog [Homo sapiens] >sp AAD32451 AAD32451 NADH-ubiquinone oxidoreductase B17 subunit homolog. >sp O9513	gb AAC68838.1	6471	3	113	100	100	HHMMF84	pSport1
2195	HCRPO08R	(AF035940) similar to mago nashi [Homo sapiens] >gb AAD32457.1 AF067173_1 (AF067173) Mago homolog [Homo sapiens] >gb AAB66722.1 (AF007862) mm-Mago [Mus musculus] >gb AAC40044.1 (AF035939) similar to mago nashi [Mus musculus] >sp P50606 MGN_HUMAN MAGO NA	gb AAC39606.1	6472	1	267	94	100	HCRPO08	pSport1
2196	HCQAI71R	(AF037168) DnaJ homologue [Arabidopsis thaliana] >sp O49070 O49070 DNAJ HOMOLOGUE. Length = 284	gb AAB91418.1	6473	2	289	41	67	HCQAI71	Lambda ZAP II
2197	HCQCQ75R	polyubiquitin [Cricetulus griseus] >pir S21083 S21083 polyubiquitin 5 - Chinese hamster >dbj BAA03983.1 polyubiquitin [Rattus norvegicus] {SUB 77-381} >gb AAA49129.1 ubiquitin polypeptide (heat shock related) [Gallus gallus] {SUB 225-381} Length = 381	emb CAA4294.1	6474	2	298	88	93	HCQCQ75	Lambda ZAP II

2198	HWLMQ74R	(AF047471) mitotic checkpoint protein kinase [Homo sapiens] >gb AAC12729.1 (AF046078) protein kinase [Homo sapiens] >gb AAD43675.1 (AF139363) BUB1 protein [Homo sapiens] >gb AAB97855.2 (AF043294) putative mitotic checkpoint kinase [Homo sapiens] >sp O4	gb AAC03122.1	6475	90	281	73	76	HWLMQ74	pSport1
2199	HFVKA48R	(AF067168) NADH-ubiquinone oxidoreductase B22 subunit homolog [Homo sapiens] >sp AAD32452 AAD32452 NADH-ubiquinone oxidoreductase B22 subunit homolog. Length = 179	gb AAD32452.1 AF0671	6476	2	247	95	95	HFVKA48	pBluescript
2200	HLXNF14R	(AF047470) malate dehydrogenase precursor [Homo sapiens] >sp P40926 MDHM_HUMAN MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37). Length = 338	gb AAC03787.1	6477	1	144	100	100	HLXNF14	pSport1
2201	H2LAB80R	(AF047711) nGAP [Homo sapiens] >sp O95174 O95174 NGAP. >emb CAB53260.1 (AL035702) dJ593C16.1 (ras GTPase activating protein) [Homo sapiens] {SUB 41-1139} Length = 1139	gb AAD04814.1	6478	3	476	89	89	H2LAB80	pBluescript SK-
2202	HOCTC23R	(AF052788) immunoglobulin light chain variable region [Homo sapiens] Length = 116		6479	2	208			HOCTC23	pSport1
2203	HCQDO33R	(AK000460) unnamed protein product [Homo sapiens] Length = 284	gb AAC36629.1	6480	3	188	83	90	HCQDO33	Lambda ZAP II
2204	HCQDD24R	(AF061939) staufen protein [Homo sapiens] >sp O95793 O95793 STAUFEN PROTEIN. >gb AAD17530.1 (AF061938) staufen protein [Homo sapiens] {SUB 82-577} Length = 577	dbj BAA91179.1	6481	191	376	50	53	HCQDD24	Lambda ZAP II
2205	HKAFLO6R	(AF071172) HERC2 [Homo sapiens] >sp O95714 O95714 HERC2. Length = 4834	gb AAD17531.1	6482	112	465	78	83	HKAFLO6	pCMVSPORT 2.0
2206	HCRMO57R	(AF071172) HERC2 [Homo sapiens] >sp O95714 O95714 HERC2. Length = 4834	emb CAB6943.4.1	6483	43	330	59	63	HCRMO57	pSport1
2207	HCROO83R	(AF071172) HERC2 [Homo sapiens] >sp O95714 O95714 HERC2. Length = 4834	gb AAD08657.1	6484	2	250	97	97	HCROO83	pSport1

2208	HCRMW16R	(AB029013) KIAA1090 protein [Homo sapiens] >sp BAA83042 BAA83042 KIAA1090 protein. Length = 713	dbj BAA83042.1	6485	3	284	60	71	HCRMW16	pSport1
2209	HWLOO35R			6486	1	108			HWLOO35	pSport1
2210	HWLVL77R	(AF073298) small EDRK-rich factor 2 [Homo sapiens] >gb AAC63515.1 (AF073297) small EDRK-rich factor 2 [Mus musculus] >sp O75918 O75918 4F5REL. >sp O88891 O88891 4F5REL. Length = 59	gb AAC63516.1	6487	32	238	95	95	HWLVL77	pSport1
2211	HCYBH84R	(AF080000) RSK-like protein kinase RLPK [Homo sapiens] >gb AAC31171.1 (AF074393) nuclear mitogen- and stress-activated protein kinase-1 [Homo sapiens] >pir T13149 T13149 mitogen-and stress-activated protein kinase-1, nuclear - human >sp O75582 O75582 NUC	gb AAD23915.1	6488	52	408	93	94	HCYBH84	pBluescript SK-
2212	HBJMG15R	(AF080683) PITSLRE protein kinase alpha SV9 isoform [Homo sapiens] >sp O95265 O95265 PITSLRE PROTEIN KINASE ALPHA SV9 ISOFORM. Length = 755	gb AAC83664.1	6489	106	369	100	100	HBJMG15	Uni-ZAP XR
2213	H2CBH29R	(AF082556) TRF1-interacting ankyrin-related ADP-ribose polymerase [Homo sapiens] >sp O95271 O95271 TRF1-INTERACTING ANKYRIN-RELATED ADP-RIBOSE POLYMERASE. >gb AAC79842.1 (AF082557) TRF1-interacting ankyrin-related ADP-ribose polymerase [Homo sapiens] {SU	gb AAC79841.1	6490	1	459	69	85	H2CBH29	pBluescript SK-
2214	HWLMT35R	(AJ239373) immunoglobulin heavy chain variable region [Homo sapiens] >emb CAB37166.1 (AJ239373) immunoglobulin heavy chain variable region [Homo sapiens] >pir PH1429 PH1429 Ig heavy chain V region (clone VH5-2R1) - human (fragment) {SUB 1-98} Length = 12	emb CAB37166.1	6491	2	388	74	88	HWLMT35	pSport1

2215	HKCSJ59R	(AF105424) brush border myosin I [Homo sapiens] >gb AAD31189.1 AF127026_1 (AF127026) brush border myosin I [Homo sapiens] >sp AAC78645 AAC78645 Brush border myosin I. >sp AAD31189 AAD31189 Brush border myosin I. >gb AAA20900.1 myosin [Homo sapiens] {SUB	gb AAC78645. 1	6492	71	328	90	90	HKCSJ59	pBluescript
2216	HWMBG21R			6493	287	195			HWMBG21	pSport1
2217	H2LBB21R	(AF115402) Ets transcription factor ESE-2a [Homo sapiens] >sp AAD22960 AAD22960 Ets transcription factor ESE-2a. >gb AAD22961.1 AF115403_1 (AF115403) Ets transcription factor ESE-2b [Homo sapiens] {SUB 11-265} Length = 265	gb AAD22960. 1 AF1154	6494	2	406	100	100	H2LBB21	pBluescript SK-
2218	H2LAT69R	(AB015335) HRIHFB2072 [Homo sapiens] >sp BAA88116 BAA88116 HRIHFB2072 protein (fragment). >gb AAD26690.1 AF115778_1 (AF115778) short coiled coil protein SCOCO [Mus musculus] {SUB 44-125} Length = 125	dbj BAA88116 .1	6495	1	393	64	77	H2LAT69	pBluescript SK-
2219	HLWCJ40R	(AF120265) tetraspan NET-6 [Homo sapiens] >gb AAD43023.1 (AF100759) transmembrane 4 superfamily protein [Homo sapiens] >sp O95857 O95857 TETRASPAN NET-6. Length = 204	gb AAD17294. 1	6496	83	214	96	100	HLWCJ40	pCMV Sport 3.0
2220	HCQCK44R	(AF124249) SH2-containing protein Nsp1 [Homo sapiens] >sp Q9Y2X4 Q9Y2X4 SH2-CONTAINING PROTEIN NSP1. Length = 576	gb AAD28244. 1 AF1242	6497	1	387	55	62	HCQCK44	Lambda ZAP II
2221	HOGDQ57R	(AF124249) SH2-containing protein Nsp1 [Homo sapiens] >sp Q9Y2X4 Q9Y2X4 SH2-CONTAINING PROTEIN NSP1. Length = 576	gb AAD28244. 1 AF1242	6498	3	314	85	88	HOGDQ57	pCMV Sport 2.0
2222	HWLQM12R	(AB011369) RBCK2 [Rattus norvegicus] >sp Q9Z334 Q9Z334 RBCK2. Length = 260	dbj BAA33957 .1	6499	1	570	80	86	HWLQM12	pSport1
2223	HWLVX04R	(AF125099) HSPC038 protein [Homo sapiens] >sp Q9Y5V0 Q9Y5V0 HSPC038 PROTEIN. Length = 76	gb AAD39916. 1 AF1250	6500	3	260	86	86	HWLVX04	pSport1

2224	H2CBG89R	(AF126736) ubiquitin processing protease [Homo sapiens] >sp Q9Y5T5 UBPG_HUMAN_UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSIN	gb AAD20949.1	6501	9	317	38	59	H2CBG89	pBluescript SK-
2225	HWLWQ68R	(AF126743) DNAJ domain-containing protein MCJ [Homo sapiens] >sp Q9Y5T4 Q9Y5T4 DNAJ DOMAIN-CONTAINING PROTEIN MCJ. Length = 150	gb AAD38506.1 AF1267	6502	1	276	100	100	HWLWQ68	pSport1
2226	HCYBM79R	(AF127763) mitogenic oxidase [Homo sapiens] >sp Q9Y5S8 Q9Y5S8 MITOGENIC OXIDASE. Length = 564	gb AAD38133.1 AF1277	6503	52	492	100	100	HCYBM79	pBluescript SK-
2227	HMUBO33R A	(AF129075) T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) [Homo sapiens] >emb CAA85520.1 Cctq [Homo sapiens] {SUB 33-65} Length = 548	gb AAD17375.1	6504	108	518	92	93	HMUBO53	pCMVSPORT 3.0
2228	HWLOT13R	(AF129756) G5c [Homo sapiens] >sp Q95871 Q95871 NG33. Length = 148	gb AAD18080.1 AAD180	6505	2	328			HWLOT13	pSport1
2229	HWLVN81R	(AJ132584) HIRA-interacting protein HIRIP5 [Homo sapiens] >sp CAB53015 CAB53015 HIRA-interacting protein HIRIP5. Length = 196	emb CAB53015.1	6507	3	137	95	95	HWLRV71	pSport1
2231	HCRMV30R	(AF138302) decorin variant C [Homo sapiens] >sp Q9Y5N9 Q9Y5N9 DECORIN VARIANT C. Length = 212	gb AAD44714.1	6508	3	218			HCRMV30	pSport1
2232	HCROK15R	Graf protein [Homo sapiens] >sp CAA71414 CAA71414 Graf protein. Length = 759	emb CAA71414.2	6509	2	106	97	97	HCROK15	pSport1
2233	HTOAF87Ra	(AF146793) protein B [Mus musculus] >sp Q9WUP3 Q9WUP3 PROTEIN B (FRAGMENT). Length = 193	gb AAD30564.1 AF1467	6510	1	345	57	69	HTOAF87	Uni-ZAP XR
2234	HDPMJ48R		gb AAD30564.1 AF1467	6511	81	467	56	66	HDPMJ48	pCMVSPORT 3.0

2235	HWLNJ72R	(AF151820) CGI-62 protein [Homo sapiens] >sp Q9Y372 Q9Y372 CGI-62 PROTEIN. Length = 325	gb AAD34057.1 AF1518	6512	39	368	97	97	HWLNJ72	pSport1
2236	HOFME52R	(AF151852) CGI-94 protein [Homo sapiens] >sp Q9Y3A2 Q9Y3A2 CGI-94 PROTEIN. Length = 253	gb AAD34089.1 AF1518	6513	69	293	66	76	HOFME52	pCMVSPORT 2.0
2237	HCQDU46R	(AF151908) CGI-150 protein [Homo sapiens] >sp Q9Y3E8 Q9Y3E8 CGI-150 PROTEIN. Length = 504	gb AAD34145.1 AF1519	6514	89	298	74	75	HCQDU46	Lambda ZAP II
2238	HCRMG55R	(AF155108) NY-REN-41 antigen [Homo sapiens] >sp Q9Y599 Q9Y599 NY-REN-41 ANTIGEN (FRAGMENT). Length = 241	gb AAD42874.1	6515	52	417	92	92	HCRMG55	pSport1
2239	HCRNZ49R	(AJ243883) putative transcription factor [Periplaneta americana] >sp Q9Y071 Q9Y071 PUTATIVE TRANSCRIPTION FACTOR. Length = 333	emb CAB5104.1.1	6516	3	143			HCRNZ49	pSport1
2240	HASMB62R			6517	264	121	84	92	HASMB62	pSport1
2241	H2LAD43R			6518	16	108			H2LAD43	pBluescript SK-
2242	H2LAY87R	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	6519	2	121	96	96	H2LAY87	pBluescript SK-
2243	H2LAZ41R			6520	2	178			H2LAZ41	pBluescript SK-
2244	HCQCA60R			6521	2	199			HCQCA60	Lambda ZAP II
2245	HCQCB53R			6522	3	125			HCQCB53	Lambda ZAP II
2246	HCQCH45R			6523	26	229			HCQCH45	Lambda ZAP II
2247	HCQCJ70R			6524	2	109			HCQCJ70	Lambda ZAP II
2248	HCQCL32R			6525	1	99			HCQCL32	Lambda ZAP II

2249	HCQCP47R				6526	2	163			HCQCP47	Lambda ZAP II
2250	HCQDC76R				6527	2	208			HCQDC76	Lambda ZAP II
2251	HCQDH59R				6528	3	110			HCQDH59	Lambda ZAP II
2252	HCQDI82R				6529	42	245			HCQDI82	Lambda ZAP II
2253	HCQDK24R				6530	3	101			HCQDK24	Lambda ZAP II
2254	HCQDK53R				6531	3	110			HCQDK53	Lambda ZAP II
2255	HCQDL42R				6532	4	186			HCQDL42	Lambda ZAP II
2256	HCQDL82R				6533	8	154			HCQDL82	Lambda ZAP II
2257	HCQDM76R				6534	3	125			HCQDM76	Lambda ZAP II
2258	HCQDP62R				6535	3	110			HCQDP62	Lambda ZAP II
2259	HCQDR62R				6536	1	120			HCQDR62	Lambda ZAP II
2260	HCQDV85R				6537	10	195			HCQDV85	Lambda ZAP II
2261	HCQDW29R				6538	3	242			HCQDW29	Lambda ZAP II
2262	HCQDW44R	IDN4-GGTR14 PROTEIN: >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	6539	1	144	82	91	HCQDW44	Lambda ZAP II	
2263	HCRPO09R			6540	37	357			HCRPO09	pSport1	

2264	HCYBO90R	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	6541	1	204	84	84	HCYBO90	pBluescript SK-
2265	HWLVA95R	(AJ010442) immunoglobulin kappa light chain [Homo sapiens] Length = 236	emb CAA0918.1	6542	44	373			HWLVA95	pSport1
2266	HKCAA76R	(AJ010442) immunoglobulin kappa light chain [Homo sapiens] Length = 236	emb CAA0918.1	6543	1	498	85	87	HKCAA76	Uni-ZAP XR
2267	HWMCK11R	(AJ010442) immunoglobulin kappa light chain [Homo sapiens] Length = 236	emb CAA0918.1	6544	1	429	81	85	HWMCK11	pSport1
2268	HCQDA64R	(AJ223814) striatin [Homo sapiens] >sp O43815 O43815 STRIATIN. Length = 780	emb CAA1156.0.1	6545	3	473	62	65	HCQDA64	Lambda ZAP II
2269	HCRNF45R	(AJ388554) hypothetical protein [Canis familiaris] >sp Q9XSR4 Q9XSR4 HYPOTHETICAL 17.5 KD PROTEIN (FRAGMENT). Length = 174	emb CAB4685.3.1	6546	141	347	61	63	HCRNF45	pSport1
2270	HCQDC26R	(AL021683) unnamed protein product [Homo sapiens] >sp O43819 O43819 HYPOTHETICAL 29.8 KD PROTEIN ON CHROMOSOME 22. Length = 266	emb CAA1667.1.1	6547	3	269	68	81	HCQDC26	Lambda ZAP II
2271	HWLWN07R	NBK [Homo sapiens] >emb CAA18260.2 (AL022237) bK1191B2.2 (BCL2-interacting killer (apoptosis-inducing) (NBK, BP4, BIP1)) [Homo sapiens] >gb AAC50413.1 Btk [Homo sapiens] >gb AAC79124.1 apoptosis inducer Nbk [Homo sapiens] >gb AAF01156.1 (AF174424) BCL	emb CAA6201.3.1	6548	1	183	82	88	HWLWN07	pSport1
2272	HCQDU53R	ribosomal protein L3 [Homo sapiens] >emb CAA18450.1 (AL022326) dJ333H23.1 (60S Ribosomal Protein L3) [Homo sapiens] >pir S34195 S34195 ribosomal protein L3, cytosolic - human >sp P39023 RL3_HUMAN 60S RIBOSOMAL PROTEIN L3 (HIV-1 TAR RNA BINDING PROTEIN B)	emb CAA5183.9.1	6549	68	622	62	66	HCQDU53	Lambda ZAP II
2273	HCQA155R			6550	217	333			HCQA155	Lambda ZAP II

2274	HWLNK89R	(AL049946) hypothetical protein [Homo sapiens] >emb CAB43220.1 (AL049946) hypothetical protein [Homo sapiens] >pir T08678 T08678 hypothetical protein DKFZp564I1922.1 - human (fragment) >sp Q9Y3Y8 Q9Y3Y8 HYPOTHETICAL 63.9 KD PROTEIN (FRAGMENT). Length = 5	emb CAB43220.1	6551	1	99	84	84	HWLNK89	pSport1
2275	HCQCK51R	(AL050097) hypothetical protein [Homo sapiens] >emb CAB43269.1 (AL050097) hypothetical protein [Homo sapiens] >pir T08746 T08746 hypothetical protein DKFZp586B0319.1 - human (fragment) >sp Q9Y3V9 Q9Y3V9 HYPOTHETICAL 17.3 KD PROTEIN (FRAGMENT). Length = 1	emb CAB43269.1	6552	108	353	40	60	HCQCK51	Lambda ZAP II
2276	HAIDT47R	(AL050273) hypothetical protein [Homo sapiens] >emb CAB43374.1 (AL050273) hypothetical protein [Homo sapiens] >pir T08720 T08720 ribosomal protein L36 - human >sp Q9Y3U8 Q9Y3U8 60S RIBOSOMAL PROTEIN L36. Length = 105	emb CAB43374.1	6553	442	53	82	88	HAIDT47	Uni-ZAP XR
2277	HSUAK69R			6554	18	254			HSUAK69	Uni-ZAP XR
2278	HCROB90R	(AP000001) 106aa long hypothetical protein [Pyrococcus horikoshii] >pir G71244 G71244 hypothetical protein PH0217 - Pyrococcus horikoshii >sp O57956 O57956 HYPOTHETICAL 11.5 KD PROTEIN PH0217. Length = 106	dbj BAA29286.1	6555	335	129	50	61	HCROB90	pSport1
2279	HCRNI50R	(AL035461) dJ967N21.5 (novel MCM2/3/5 family member) [Homo sapiens] >sp CAB55276 CAB55276 dJ967N21.5 (novel MCM2/3/5 family member) (fragment). Length = 606	emb CAB55276.1	6556	44	577	91	94	HCRNI50	pSport1
2280	HCRPJ34R	18 kDa Alu RNA binding protein [Homo sapiens] >pir A56062 A56062 Alu RNA-binding protein - human Length = 136	gb AAA59066.1	6557	149	355	80	83	HCRPJ34	pSport1

2281	HCQBL95R					6558	124	195				HCQBL95	Lambda ZAP II
2282	HWLOR95R	3-hydroxyisobutyl-coenzyme A hydrolase [Homo sapiens] >sp Q92931 Q92931.3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE. Length = 381	gb AAC52114.1	6559	3	536	80	81				HWLOR95	pSport1
2283	HKCSI32R	40-kDa keratin protein [Homo sapiens] >pir A31370 KRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gb AAA36044.1	6560	3	260	97	97				HKCSI32	pBluescript
2284	HWLQK90R	40-kDa keratin protein [Homo sapiens] >pir A31370 KRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gb AAA36044.1	6561	2	496	91	91				HWLQK90	pSport1
2285	HCRNO08R	5"-AMP-activated protein kinase, gamma-1 subunit [Homo sapiens] >sp P54619 AAKG_HUMAN 5"-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN). Length = 331	gb AAC50495.1	6562	1	540	84	86				HCRNO08	pSport1
2286	HBGBT36R	60S ribosomal protein [Mus musculus] >sp P47963 RL13_MOUSE 60S RIBOSOMAL PROTEIN L13 (A52). {SUB 2-213} Length = 213	gb AAA69923.1	6563	1	195	84	85				HBGBT36	Uni-ZAP XR
2287	HKLSA81R	60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN 3) (FRAGMENT). Length = 132	sp Q29375 RL7A_PIG	6564	112	345	56	58				HKLSA81	pBluescript
2288	HBCJN86R	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) (FRAGMENT). Length = 93	sp Q29214 RLA0_PIG	6565	39	212	97	97				HBCJN86	pSport1
2289	HCQCO29R	(AF014364) beta actin [Cricetinae gen. sp.] >sp O35248 O35248 BETA ACTIN. Length = 295	gb AAB66488.1	6566	2	313	93	95				HCQCO29	Lambda ZAP II
2290	HWLMZ47R			6567	82	282						HWLMZ47	pSport1
2291	HCRNZ75R	alpha-1 chain precursor (AA -27 to 917) (2953 is 2nd base in codon) [Homo sapiens] Length = 944	emb CAA2907.5.1	6568	2	334	96	96				HCRNZ75	pSport1
2292	HCRPD88R	alpha-1 type III collagen [Homo sapiens] Length = 345	gb AAA52002.1	6569	2	271	98	98				HCRPD88	pSport1

2293	HCRPK90R	alpha-L fucosidase [Homo sapiens] Length = 353	gb AAA52482.1	6570	2	235	73	73	HCRPK90	pSport1
2294	HCQDC47R	alpha-N-acetylgalactosaminidase [Homo sapiens] >gb AA51677.1 alpha-N-acetylgalactosaminidase [Homo sapiens] >gb AAB06718.1 alpha-N-acetylgalactosaminidase [Homo sapiens] >emb CAB41237.1 bK250D10.5 (alpha-N-acetylgalactosaminidase) [Homo sapiens] >pir	gb AAA36351.1	6571	1	459	100	100	HCQDC47	Lambda ZAP II
2295	HCQDT07R	(AK000113) unnamed protein product [Homo sapiens] Length = 273	dbj BAA90953.1	6572	55	312	84	88	HCQDT07	Lambda ZAP II
2296	H2CBR33R	alternatively spliced form [Homo sapiens] >sp O75666 O75666 CXORF5 (71-7A) PROTEIN (71-7A). Length = 367	emb CAA7618.5.1	6573	3	242	100	100	H2CBR33	pBluescript SK-
2297	HWLXV36R	dJ408N23.5 (novel protein similar to aminopeptidase P) [Homo sapiens] >sp CAB63053 CAB63053 DJ408N23.5 (novel protein similar to aminopeptidase P) (fragment). Length = 135	emb CAB6305.3.1	6574	3	380	95	96	HWLXV36	pSport1
2298	HWLRE24R	amplaxin [Homo sapiens] >pir A48063 A48063 mammary tumor/squamous cell carcinoma-associated protein EMS1 - human >sp Q14247 SRC8_HUMAN SRC SUBSTRATE CORTACTIN (AMPLAXIN) (EMS1 ONCOGENE). Length = 550	gb AAA58455.1	6575	2	436	98	98	HWLRE24	pSport1
2299	HWMB27R	apomucin [Homo sapiens] >pir A57534 A57534 mucin (clone L31) - human (fragment) >sp Q13792 Q13792 APOMUCIN (FRAGMENT). Length = 1042	emb CAA8830.7.1	6576	1	228	79	79	HWMB27	pSport1
2300	HWMBK08R	arginine-rich protein [Homo sapiens] >pir S27956 S27956 arginine-rich protein - human >sp p55145 ARGR_HUMAN ARGinine-RICH PROTEIN. Length = 234	gb AAB08753.1	6577	2	118	97	97	HWMBK08	pSport1

2301	HKCSA84R	ARSE [Homo sapiens] >pir [37187] 37187 arylsulfatase E (EC 3.1.6.-) - human >sp P51690 ARSE_HUMAN ARYLSULFATASE E PRECURSOR (EC 3.1.6.-) (ASE). Length = 589	emb CAA5855 6.1	6578	1	231	73	73	HKCSA84	pBluescript
2302	HKCTB10R	aspartokinase II-homoserine dehydrogenase II [Escherichia coli] Length = 810	gb AAA24165. 1	6579	434	102	70	75	HKCTB10	pBluescript
2303	HCRPX81R	ataxia-telangiectasia group D-associated protein [Homo sapiens] >pir A49618 A49618 probable ataxia-telangiectasia group D protein - human >sp Q14134 Q14134 ATAXIA-TELANGIECTASIA GROUP D-ASSOCIATED PROTEIN. Length = 588	gb AAA35762. 1	6580	50	442	84	84	HCRPX81	pSport1
2304	HWLRP68R	ATP synthase subunit e [Homo sapiens] >sp P56385 ATP1_HUMAN ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34). {SUB 2-69} Length = 69	dbj BAA23322 .1	6581	1	231	69	69	HWLRP68	pSport1
2305	HCQCT96R	ATPase 6 [Homo sapiens] >gb AAB58948.1 ATPase 6 [Homo sapiens] >pir A01049 PWHU6 H+- transporting ATP synthase (EC 3.6.1.34) protein 6 - human mitochondrion >sp P00846 ATP6_HUMAN ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6). Length = 226	emb CAA2403 1.1	6582	3	176	73	77	HCQCT96	Lambda ZAP II
2306	HCQCV26R	ATPase 6 [Homo sapiens] >gb AAB58948.1 ATPase 6 [Homo sapiens] >pir A01049 PWHU6 H+- transporting ATP synthase (EC 3.6.1.34) protein 6 - human mitochondrion >sp P00846 ATP6_HUMAN ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6). Length = 226	emb CAA2403 1.1	6583	363	716	66	69	HCQCV26	Lambda ZAP II

2307	HWLXR95R	ATPase coupling factor 6 subunit [Homo sapiens] >emb CAB53667.1 (AL110183) hypothetical protein [Homo sapiens] >emb CAB53667.1 (AL110183) hypothetical protein [Homo sapiens] >pir JT0563 JT0563 coupling factor 6 precursor, mitochondrial - human >sp P1885	gb AAA51807. 1	6584	2	253	100	100	HWLXR95	pSport1
2308	HCQCV96R	ATPase subunit 6 [Homo sapiens] >dbj BAA07295.1 ATPase subunit 6 [Homo sapiens] Length = 226	dbj BAA07295 .1	6585	147	368	58	61	HCQCV96	Lambda ZAP II
2309	HEPAD45R	autoantigen [Homo sapiens] >sp Q13025 Q13025 AUTOANTIGEN. Length = 968	gb AAB51444. 1	6586	2	277	100	100	HEPAD45	Uni-ZAP XR
2310	HCRNP41R	(AB021288) beta 2-microglobulin [Homo sapiens] >gb AAA87972.1 beta-2-microglobulin [Pan troglodytes] >gb AAA88008.1 beta-2-microglobulin [Gorilla gorilla] >gb AAD48083.1 (AF072097) beta- 2 microglobulin [Homo sapiens] >pir A90976 MGHUB2 beta-2-microglob	dbj BAA35182 .1	6587	39	281	60	63	HCRNP41	pSport1
2311	HCYBK83R			6588	471	10			HCYBK83	pBluescript SK-
2312	HCRND59R	beta-adrenergic receptor kinase [Bos taurus] >pir A40088 A40088 beta-adrenergic-receptor kinase (EC 2.7.1.126) 1 - bovine >sp P21146 ARK1_BOVIN BETA-ADRENERGIC RECEPTOR KINASE 1 (EC 2.7.1.126) (BETA- ARK-1) (G- PROTEIN COUPLED RECEPTOR KINASE 2). Length =	gb AAA30384. 1	6589	2	385	96	98	HCRND59	pSport1
2313	HCRNE86R			6590	1	117			HCRNE86	pSport1
2314	HWLQZ23R			6591	1	231			HWLQZ23	pSport1
2315	HCRMA15R			6592	6	152			HCRMA15	pSport1
2316	HCRMJ42R			6593	14	244			HCRMJ42	pSport1
2317	HCRMK50R	unnamed protein product [unidentified] Length = 180	emb CAB6919 5.1	6594	24	113	100	100	HCRMK50	pSport1

2318	HCRMO88R				6595	92	352			HCRMO88	pSportl
2319	HCRNB87R				6596	354	566			HCRNB87	pSportl
2320	HCRNI95R				6597	2	97			HCRNI95	pSportl
2321	HCRNL44R				6598	1	195			HCRNL44	pSportl
2322	HCRD06R				6599	137	454			HCRD06	pSportl
2323	HCR0T10R				6600	2	211			HCR0T10	pSportl
2324	HCRPF12R				6601	25	231			HCRPF12	pSportl
2325	HCRPK22R				6602	1	96			HCRPK22	pSportl
2326	HCRPK46R				6603	29	142			HCRPK46	pSportl
2327	HCRPK48R				6604	22	153			HCRPK48	pSportl
2328	HCRQF74R	unnamed protein product [unidentified]	Length = 180	emb CAB6919 5.1	6605	1	129	100	100	HCRQF74	pSportl
2329	HCRQG02R	unnamed protein product [unidentified]	Length = 180	emb CAB6919 5.1	6606	1	171	95	100	HCRQG02	pSportl
2330	HCRQM26R				6607	23	175			HCRQM26	pSportl
2331	HCRQM90R	unnamed protein product [unidentified]	Length = 180	emb CAB6919 5.1	6608	3	104	100	100	HCRQM90	pSportl
2332	HHMMA34R				6609	14	157			HHMMA34	pSportl
2333	HHMMA44R				6610	97	219			HHMMA44	pSportl
2334	HHMMC42R				6611	26	160			HHMMC42	pSportl
2335	HHMMC86R				6612	14	154			HHMMC86	pSportl
2336	HHMMD59R				6613	6	143			HHMMD59	pSportl
2337	HHMME38R				6614	111	245			HHMME38	pSportl
2338	HHMME40R				6615	3	95			HHMME40	pSportl
2339	HHMME50R	unnamed protein product [unidentified]	Length = 180	emb CAB6919 5.1	6616	3	110	100	100	HHMME50	pSportl
2340	HHMME58R				6617	5	142			HHMME58	pSportl
2341	HHMME80R				6618	25	159			HHMME80	pSportl
2342	HHMMF60R				6619	2	136			HHMMF60	pSportl
2343	HHMMF79R				6620	3	173			HHMMF79	pSportl
2344	HOCTA39R				6621	457	582			HOCTA39	pSportl
2345	HS2AN66R				6622	161	391			HS2AN66	pSportl
2346	HULCG37R				6623	44	166			HULCG37	pSportl

2347	HWLMO16R				6624	42	146				HWLMO16	pSportl
2348	HWLMO29R				6625	24	143				HWLMO29	pSportl
2349	HWLMO44R				6626	35	142				HWLMO44	pSportl
2350	HWLMO47R				6627	31	129				HWLMO47	pSportl
2351	HWLMO84R				6628	1	177				HWLMO84	pSportl
2352	HWLMQ27R				6629	2	184				HWLMQ27	pSportl
2353	HWLMQ28R				6630	19	246				HWLMQ28	pSportl
2354	HWLMQ64R				6631	1	168				HWLMQ64	pSportl
2355	HWLMQ65R				6632	66	197				HWLMQ65	pSportl
2356	HWLNZ01R				6633	3	101				HWLNZ01	pSportl
2357	HWLNZ20R				6634	2	121				HWLNZ20	pSportl
2358	HWLNZ35R				6635	3	158				HWLNZ35	pSportl
2359	HWLNZ44R				6636	2	181				HWLNZ44	pSportl
2360	HWLNZ59R				6637	2	184				HWLNZ59	pSportl
2361	HWLOV04R	unnamed protein product [unidentified] Length = 180	emb CAB6919	5.1	6638	3	134	62	70		HWLOV04	pSportl
2362	HWLOW58R				6639	264	494				HWLOW58	pSportl
2363	HWLOZ37R				6640	322	513				HWLOZ37	pSportl
2364	HWLQF96R				6641	249	464				HWLQF96	pSportl
2365	HWLRV12R				6642	7	120				HWLRV12	pSportl
2366	HWLWE68R				6643	2	241				HWLWE68	pSportl
2367	HWLXA42R	unnamed protein product [unidentified] Length = 180	emb CAB6919	5.1	6644	3	176	100	100		HWLXA42	pSportl
2368	HWLXA48R				6645	1	132				HWLXA48	pSportl
2369	HWLXA94R				6646	10	186				HWLXA94	pSportl
2370	HWLXI52R				6647	1	114				HWLXI52	pSportl
2371	HWMBR11R				6648	2	136				HWMBR11	pSportl
2372	HWMBR26R				6649	3	278				HWMBR26	pSportl
2373	HWMBR49R	unnamed protein product [unidentified] Length = 180	emb CAB6919	5.1	6650	48	260	100	100		HWMBR49	pSportl
2374	HWMBR53R				6651	3	194				HWMBR53	pSportl
2375	HWMBR56R				6652	1	156				HWMBR56	pSportl
2376	HWMBR18R				6653	1	117				HWMBR18	pSportl

2377	HWMB36R			6654	2	187				HWMB36	pSportl
2378	HWMB38R			6655	5	223				HWMB38	pSportl
2379	HWMBW16R			6656	86	394				HWMBW16	pSportl
2380	HCRMH48R			6657	95	421				HCRMH48	pSportl
2381	HCRMY75R			6658	3	254				HCRMY75	pSportl
2382	HCRNZ66R			6659	3	305				HCRNZ66	pSportl
2383	HCRJ91R			6660	8	283				HCRJ91	pSportl
2384	HCRPR59R			6661	26	202				HCRPR59	pSportl
2385	HCRPY45R			6662	218	430				HCRPY45	pSportl
2386	HCRQG95R	unnamed protein product [unidentified] Length = 180 emb CAB6919 5.1		6663	3	185	82	86		HCRQG95	pSportl
2387	HHMMC37R			6664	13	144				HHMMC37	pSportl
2388	HHMMC68R			6665	3	137				HHMMC68	pSportl
2389	HHMMD73R			6666	2	160				HHMMD73	pSportl
2390	HHMMF44R			6667	2	154				HHMMF44	pSportl
2391	HTWEL13RA			6668	2	157				HTWEL13	pSportl
2392	HWLMT48R			6669	343	480				HWLMT48	pSportl
2393	HWLQK72R			6670	17	103				HWLQK72	pSportl
2394	HWLUI68R			6671	3	476				HWLUI68	pSportl
2395	HWLVY86R			6672	234	464				HWLVY86	pSportl
2396	HE2JQ95R			6673	2	232				HE2JQ95	Uni-ZAP XR
2397	HCRMH46R			6674	65	334				HCRMH46	pSportl
2398	HWLMW81R			6675	3	191				HWLMW81	pSportl
2399	HWLND45R			6676	91	501				HWLND45	pSportl
2400	HWLWG95R			6677	23	298				HWLWG95	pSportl
2401	HCQCX19R	beta-hexosaminidase beta-subunit [Homo sapiens] >pir A31250 A31250 beta-N-acetylhexosaminidase (EC 3.2.1.52) beta chain precursor - human >sp P07686 HEXB_HUMAN BETA- HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-BETA- GLUCOSAMINIDASE) (BETA-N	gb AAA52645.1	6678	3	143	65	73		HCQCX19	Lambda ZAP II

2402	HCRQO33R	bHLH protein MesP2 [Mus musculus] >sp O08574 O08574 MESODERM POSTERIOR 2 (BHLH PROTEIN MESP2). Length = 370	gb AAB51199.1	6679	2	442	59	63	HCRQO33	pSport1
2403	HCRNT56R	BN51 protein [Homo sapiens] >pir A43700 A43700 BN51 protein - human >sp P05423 BN51_HUMAN BN51 PROTEIN. Length = 395	gb AAA51838.1	6680	1	516	78	79	HCRNT56	pSport1
2404	HCRPR45R	branched-chain alpha-keto acid dehydrogenase E1 alpha subunit [human, Peptide, 443 aa] [Homo sapiens] Length = 443	gb AAB20222.1	6681	3	167	100	100	HCRPR45	pSport1
2405	HCRMJ70R	C protein (AA 1-159) [Homo sapiens] >pir S01387 S01387 U1 snRNP protein C - human >sp P09234 RU1C_HUMAN U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (U1-C). Length = 159	emb CAA3103.7.1	6682	2	169	100	100	HCRMJ70	pSport1
2406	HWLMM72R	C10 [Homo sapiens] >sp Q99622 Q99622 CHROMOSOME 12P13 SEQUENCE; HTGS PHASE 3, COMPLETE SEQUENCE. Length = 126	gb AAB51329.1	6683	80	385	81	87	HWLMM72	pSport1
2407	HCRMD32R	CAG-isl 7 [Homo sapiens] >sp P50914 RL14_HUMAN 60S RIBOSOMAL PROTEIN L14 (CAG-ISL 7). {SUB 2-213} Length = 213	gb AAC16021.1	6684	2	292	73	75	HCRMD32	pSport1
2408	HCRQC71R	calpactin I light chain [Bos taurus] >gb AAA58404.1 calpactin I light chain [Homo sapiens] >gb AAA58426.1 cellular ligand of annexin II [Homo sapiens] >pir JC1139 JC1139 calpactin I light chain - human >pir B28489 B28489 calpactin I light chain - bovine	gb AAA30423.1	6685	1	261	98	98	HCRQC71	pSport1
2409	HWMCH04R	carbonic anhydrase II [Homo sapiens] >gb AAA51909.1 carbonic anhydrase II [Homo sapiens] >gb AAA51911.1 carbonic anhydrase II [Homo sapiens] >emb CAA68426.1 carbonic anhydrase II (AA 1-260) [Homo sapiens] >pir A27175 CRHU2 carbonate dehydratase (EC 4.2	gb AAA51908.1	6686	3	320	81	84	HWMCH04	pSport1

2410	HCQDH40R					6687	2	331				HCQDH40	Lambda ZAP II
2411	HKAHM80R	CDC37 homolog [Homo sapiens] >gb AAB63979.1 CDC37 homolog [Homo sapiens] >pir G02313 G02313 CDC37 homolog - human >sp Q16543 Q16543 CDC37 HOMOLOG. Length = 378	gb AAB04798.1	6688	2	388	85	85				HKAHM80	pCMVSPORT 2.0
2412	H2CBM60R	CDP-DIACYLGLYCEROL--SERINE O-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.8) (PHOSPHATIDYLTRANSFERASE). [Escherichia coli] >dbj BAA16473.1 CDP-DIACYLGLYCEROL--SERINE O-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.8) (PHOSPHATIDYLTRANSFERASE). [Escherichia coli] >sp P7	dbj BAA16470.1	6689	2	532	99	99				H2CBM60	pBluescript SK-
2413	HCQAN45R	chaperonin (HSP60) [Homo sapiens] >sp G242370 G242370 P60, 60-KDA HEAT SHOCK PROTEIN, HSP60. {SUB 27-55} >pir A56868 A56868 heat shock protein 60 - bovine (fragment) {SUB 27-48} Length = 573	gb AAA36022.1	6690	3	281	66	69				HCQAN45	Lambda ZAP II
2414	HWMCI76R			6691	3	317						HWMCI76	pSport1
2415	HWLXR73R			6692	3	341						HWLXR73	pSport1
2416	HWLOI59R	tat interactive protein [Homo sapiens] Length = 482	gb AAB02683.1	6693	2	646	80	82				HWLOI59	pSport1
2417	HWLUX53R	cpn10 protein [Bos taurus] >gb AAA50953.1 chaperonin 10 [Homo sapiens] >emb CAA53455.1 heat shock protein 10 [Homo sapiens] >emb CAB75425.1 (AJ250915) chaperonin 10, Hsp10 protein [Homo sapiens] >pir S47532 S47532 chaperonin groES - human >pir A56682 A	emb CAA4928.8.1	6694	1	282	87	87				HWLUX53	pSport1

2418	HCRNB29R	cyclophilin C, Cyp-C [human, kidney, Peptide, 212 aa] [Homo sapiens] >pir A54204 A54204 peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human >sp P45877 CYPC_HUMAN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN C).	gb AAB31350.1	6695	1	336	100	100	HCRNB29	pSport1
2419	HARMO20R	cytochrome oxidase III [Homo sapiens] >pir A00482 OTHU3 cytochrome-c oxidase (EC 1.9.3.1) chain III - human mitochondrion >gb AAB63452.1 (AF004341) cytochrome c oxidase subunit III [Homo sapiens] {SUB 167-261} Length = 261	emb CAA2403.2.1	6696	153	275	60	64	HARMO20	pCMVSPORT 3.0
2420	HCQCQ58R	cytochrome c oxidase subunit 3 [Homo sapiens] >dbj BAA77671.1 cytochrome c oxidase subunit 3 [Homo sapiens] >sp P00414 COX3_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1). >sp BAA77671 BAA77671 Cytochrome c oxidase subunit 3 (fragment). >gb AAB5	dbj BAA77671.1	6697	158	280	64	65	HCQCQ58	Lambda ZAP II
2421	HCQDQ11R	cytochrome c oxidase subunit 3 [Homo sapiens] >dbj BAA77671.1 cytochrome c oxidase subunit 3 [Homo sapiens] >sp P00414 COX3_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1). >sp BAA77671 BAA77671 Cytochrome c oxidase subunit 3 (fragment). >gb AAB5	dbj BAA77671.1	6698	272	550	72	75	HCQDQ11	Lambda ZAP II
2422	HCQDM81R	cytochrome oxidase III [Homo sapiens] >pir A00482 OTHU3 cytochrome-c oxidase (EC 1.9.3.1) chain III - human mitochondrion >gb AAB63452.1 (AF004341) cytochrome c oxidase subunit III [Homo sapiens] {SUB 167-261} Length = 261	emb CAA2403.2.1	6699	129	251	71	72	HCQDM81	Lambda ZAP II

2423	HCQCU09R	cytochrome oxidase subunit I [Hyllobates lar] >dbj BAA07496.1 Cytochrome C oxidase subunit 1 (COXI) [Hyllobates syndactylus] >dbj BAA07496.1 Cytochrome C oxidase subunit 1 (COXI) [Hyllobates syndactylus] >pir J37049 J37049 cytochrome-c oxidase (EC 1.9.3.1)	emb CAA6763 0.1	6700	70	186	83	89	HCQCU09	Lambda ZAP II
2424	HHS GT23R	cytochrome oxidase subunit II [Homo sapiens] >gb AA20844.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA20845.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA20847.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA31850.1 cytochrome	gb AA20843. 1	6701	165	284	51	55	HHS GT23	Uni-ZAP XR
2425	HCQDA11R	cytochrome oxidase subunit II [Homo sapiens] >gb AA20844.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA20845.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA20847.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA31850.1 cytochrome	gb AA20843. 1	6702	165	284	59	62	HCQDA11	Lambda ZAP II
2426	HFIJB15R	cytochrome oxidase subunit II [Homo sapiens] >gb AA20844.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA20845.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA20847.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA31850.1 cytochrome	gb AA20843. 1	6703	326	517	84	87	HFIJB15	pSport1
2427	HACCH14R	cytochrome oxidase subunit II [Homo sapiens] >gb AA20844.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA20845.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA20847.1 cytochrome oxidase subunit II [Homo sapiens] >gb AA31850.1 cytochrome	gb AA20843. 1	6704	100	267	63	67	HACCH14	Uni-ZAP XR

2428	HWLNH49R	cytochrome P450 PCN3 [Homo sapiens] >pir A34101 A34101 cytochrome P450 3A5 - human >sp P20815 CP35_HUMAN CYTOCHROME P450 3A5 (EC 1.14.14.1) (CYP3A5) (P450-PCN3). >gb AAB00083.1 cytochrome P450 [Homo sapiens] {SUB 1-24} Length = 502	gb AAA02993.1	6705	267	401	68	74	HWLNH49	pSport1
2429	HWLRO11R	cytochrome P450 reductase [EC 1.6.2.4] [human, placenta, Peptide Partial, 676 aa] [Homo sapiens] Length = 676	gb AAB21814.1	6706	2	190	98	98	HWLRO11	pSport1
2430	HCRMP82R	cytochrome P450-IIB [Homo sapiens] >gb AAF32444.1 AC023172_1 (AC023172) CYP2B6 [Homo sapiens] >pir A32969 A32969 cytochrome P450 2B6 - human >sp P20813 CPB6_HUMAN CYTOCHROME P450 2B6 (EC 1.14.14.1) (CYP2B6) (P450 IIB1). >gb AAD25924.1 AF081569_1 (AF08156	gb AAA52144.1	6707	2	475	90	90	HCRMP82	pSport1
2431	HCRPV08R	KERATIN TYPE II CYTOSKELETAL 8 (FRAGMENT). Length = 116	sp Q29386 Q29386	6708	3	269	55	57	HCRPV08	pSport1
2432	HWMBB77R	macrophage inflammatory protein-2beta precursor [Homo sapiens] >pir JH0282 J38290 GRO-gamma precursor - human >sp P19876 MI2B_HUMAN MACROPHAGE INFLAMMATORY PROTEIN-2- BETA PRECURSOR (MIP2-BETA) (GROWTH REGULATED PROTEIN GAMMA) (GRO- GAMMA). >gb AAA03454.1	emb CAA3780.9.1	6709	2	415	76	76	HWMBB77	pSport1
2433	HHEPL48R	cytotoxic ligand TRAIL receptor [Homo sapiens] >sp O00220 O00220 CYTOTOXIC LIGAND TRAIL RECEPTOR. Length = 468	gb AAC51226.1	6710	2	229	70	70	HHEPL48	pCMV/Sport 3.0
2434	HCRPT53R	DAP-3 [Homo sapiens] >sp P51398 DAP3_HUMAN DEATH-ASSOCIATED PROTEIN 3 (DAP-3). Length = 398	emb CAA5853.5.1	6711	3	179	100	100	HCRPT53	pSport1
2435	HA5BV11R	death associated protein 5 [Homo sapiens] Length = 907	emb CAA6185.7.1	6712	3	314	58	60	HA5BV11	pSport1

2436	HCQCD92R	decay-accelerating factor precursor [Homo sapiens] Length = 376	gb AAA52167.1	6713	2	130	57	67	HCQCD92	Lambda ZAP II
2437	HTXJU67R	(AF064768) diacylglycerol kinase alpha [Homo sapiens] Length = 210	gb AAC34803.1	6714	23	124	90	90	HTXJU67	Uni-ZAP XR
2438	HWMCL33R	diacylglycerol kinase [Homo sapiens] >sp P52824 KDG_HUMAN DIACYLGLYCEROL KINASE, DELTA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK- DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE). Length = 942	gb AAA98749.1	6715	2	367	88	89	HWMCL33	pSport1
2439	HCRMM56R	dJ142L7.3 (Connective tissue growth factor (NOV, GIG) LIKE protein) [Homo sapiens]		6716	2	250			HCRMM56	pSport1
2440	HCQCO67R	>gb AAD31517.1 AF143679_1 (AF143679) lost in inflammatory breast cancer tumor suppressor protein [Homo sapiens] >sp O95958 O95958 DJ142L7.3 (CONNECTIVE TISSUE GROWTH FACTOR	emb CAB1655.6.1	6717	3	209	73	79	HCQCO67	Lambda ZAP II
2441	HCRPQ41R	DOCK180 protein [Homo sapiens] >sp Q14185 Q14185 DOCK180 PROTEIN. Length = 1865	dbj BAA09454.1	6718	3	320	45	65	HCRPQ41	pSport1
2442	HWLVI33R	dodecenoyl-CoA delta-isomerase [Homo sapiens] >pir A55723 A55723 dodecenoyl-CoA Delta-isomerase (EC 5.3.3.8) precursor, mitochondrial - human >sp P42126 D3D2_HUMAN 3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR (EC 5.3.3.8) (DODECENOYL-COA DELTA-1	emb CAA8106.6.1	6719	2	298	65	70	HWLVI33	pSport1
2443	HWMBA55R	dynamitin [Homo sapiens] >sp Q13561 DYNC_HUMAN DYNACTIN, 50 KD ISOFORM (50 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DYNAMITIN). Length = 406	gb AAC50423.1	6720	3	404	53	54	HWMBA55	pSport1
2444	HCYBK79R			6721	11	217			HCYBK79	pBluescript SK-

2445	HCRPS75R	elongation factor 2 [Homo sapiens] >emb CAA77750.1 human elongation factor 2 [Homo sapiens] >pir S18294 EFHU2 translation elongation factor eEF-2 - human >sp P13639 EF2_HUMAN ELONGATION FACTOR 2 (EF-2). >gb AAA50388.1 elongation factor 2 [Homo sapiens]	emb CAA3582 9.1	6722	2	328	85	88	HCRPS75	pSport1
2446	HCRMJ60R	endoglin [Homo sapiens] Length = 625	emb CAA5089 1.1	6723	81	230	77	78	HCRMJ60	pSport1
2447	HCRPV09R	endoneurine precursor [Homo sapiens] >pir B26448 NZHU endoneurine - human >sp P07108 ACBP_HUMAN ACYL-COA- BINDING PROTEIN (ACBP) (DIAZEPAM BINDING INHIBITOR) (DBI) (ENDOZEPINE) (EP). {SUB 2-87} Length = 87	gb AAA35788. 1	6724	1	318	100	100	HCRPV09	pSport1
2448	HCRON89R	enhancer protein [Homo sapiens] >pir S4533 S4533 enhancer protein - human Length = 199	gb AAA50464. 1	6725	2	361	80	80	HCRON89	pSport1
2449	HAAAT79R	epithelial glycoprotein (EGP) precursor [Homo sapiens] Length = 314	gb AAA35723. 1	6726	1	579	99	99	HAAAT79	pSport1
2450	HLDDP53R	ERD-2-like protein, ELP-1 - human >emb CAA45277.1 KDEL receptor [Homo sapiens] {SUB 3-214} Length = 214	pir A42286 A4 2286	6727	28	486	98	98	HLDDP53	pCMVSPORT 3.0
2451	HWLME23R	FAST kinase [Homo sapiens] >pir J37386 J37386 FAST kinase - human >sp Q14296 Q14296 FAST KINASE. Length = 549	emb CAA6044 8.1	6728	3	407	53	53	HWLME23	pSport1
2452	HWLVP88R	fau [Homo sapiens] >emb CAA46714.1 fau 1 [Homo sapiens] >pir JC1278 JC1278 ubiquitin-like protein / ribosomal protein S30, cytosolic - human >sp P35544 UBIM_HUMAN UBIQUITIN-LIKE PROTEIN FUBI. {SUB 1-74} Length = 133	emb CAA4671 6.1	6729	3	473	77	79	HWLVP88	pSport1

2453	HCROF57R	fibroblast activation protein [Homo sapiens] >sp Q12884 Q12884 FIBROBLAST ACTIVATION PROTEIN: >gb AAF21600.1 (AF007822) cytoplasmic Seprase truncated isoform [Homo sapiens] {SUB 522-760} Length = 760	gb AAB49652.1	6730	2	493	96	96	HCROF57	pSport1
2454	HMWAM77R	FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS). >gb AAA35852.1 foly polyglutamate synthetase [Homo sapiens] {SUB 43-587} >gb AAA87568.1 foly polyglutamate synthetase [Homo sapiens] {SUB 1	sp Q05932 FO LC_HUMAN	6731	1	78	57	60	HMWAM77	Uni-ZAP XR
2455	HCQCO75R	git protein - phage lambda >sp P03762 SIEB_LAMBD SUPERINFECTION EXCLUSION PROTEIN B. >emb CAA23982.1 reading frame GIT [bacteriophage lambda] {SUB 5- 183} >emb CAA41524.1 git [bacteriophage lambda] {SUB 6-67} Length = 183	pir 43010 QQ BPGL	6732	264	82	46	52	HCQCO75	Lambda ZAP II
2456	HCQCR94R	glutathione peroxidase-GI [Homo sapiens] Length = 190	emb CAA4839 4.1	6733	1	114	95	95	HCQCR94	Lambda ZAP II
2457	HNBTG35R	(AF134895) glyoxylate reductase [Homo sapiens] >gb AAD45886.1 AF146018 1 (AF146018) hydroxypyruvate reductase [Homo sapiens] >gb AAD46517.1 AF146689 1 (AF146689) hydroxypyruvate reductase [Homo sapiens] >sp AAD45886 AAD45886 Hydroxypyruvate reductase. >sp	gb AAF00111. 1 AF1348	6734	1	285	91	92	HNBTG35	pSport1
2458	HCROE12R			6735	10	105			HCROE12	pSport1

2459	HCQAB69R	gro protein [Homo sapiens] >emb CAA31027.1 MGSA preprotein (AA -34 to 73) [Homo sapiens] >emb CAA38361.1 melanoma growth stimulatory activity preprotein [Homo sapiens] >pir S13669 A28414 melanoma growth-stimulatory activity precursor - human >sp P09341	gb AAA35933.1	6736	118	408	84	86	HCQAB69	Lambda ZAP II
2460	HCQAR52R	gro protein [Homo sapiens] >emb CAA31027.1 MGSA preprotein (AA -34 to 73) [Homo sapiens] >emb CAA38361.1 melanoma growth stimulatory activity preprotein [Homo sapiens] >pir S13669 A28414 melanoma growth-stimulatory activity precursor - human >sp P09341	gb AAA35933.1	6737	2	103	82	82	HCQAR52	Lambda ZAP II
2461	HCQAM84R	growth-regulating protein [Homo sapiens] >pir A56008 A56008 growth-regulating protein BB1 - human >sp P50290 BB1_HUMAN GROWTH- REGULATING PROTEIN BB1. Length = 57	gb AAA18898.1	6738	184	131	63	70	HCQAM84	Lambda ZAP II
2462	HWLMG29R	GTP binding protein [Mus musculus] >pir A39611 A39611 probable GTP-binding protein - mouse >sp P23249 MV10_MOUSE PROTEIN MOV-10. >emb CAA53453.1 gb 110 /Mov 10 locus [Mus musculus] {SUB 1-45} Length = 1004	emb CAA3680.3.1	6739	7	204	98	100	HWLMG29	pSport1
2463	HCQCF55R	alpha subunit (aa 1-394) [Bos taurus] >sp P04896 GBAS_BOVIN GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (ADENYLATE CYCLASE- STIMULATING G ALPHA PROTEIN). Length = 394	emb CAA2713.7.1	6740	2	274	100	100	HCQCF55	Lambda ZAP II
2464	HCRMV87R	GTP_BINDING PROTEIN (FRAGMENT). Length = 92	sp Q29222 Q29222	6741	260	328	83	88	HCRMV87	pSport1
2465	HWLWB88R			6742	1	108			HWLWB88	pSport1

2466	HODGF21R	(AF028832) Hsp89-alpha-delta-N [Homo sapiens] >sp O75322 O75322 HSP89-ALPHA-DELTA-N. Length = 539	gb AAC25497. 1	6743	3	242	94	94	HODGF21	Uni-ZAP XR
2467	HWLMC42R	non-histone protein HMG2 precursor [Sus scrofa] >pir A34719 A34719 nonhistone chromosomal protein HMG-2 - pig >sp P17741 HMG2_PIG HIGH MOBILITY GROUP PROTEIN HMG2 (HMG-2). {SUB 2-210} Length = 210	gb AAA31051. 1	6744	7	255	80	93	HWLMC42	pSport1
2468	HCRQJ58R	histamine H1 receptor [Homo sapiens] >dbj BAA03319.1 histamine H1 receptor [Homo sapiens] >emb CAA54182.1 histamine H1 receptor [Homo sapiens] >emb CAA84380.1 Human histamine H1 receptor [Homo sapiens] >gb AAB95156.1 (AF026261) histamine H1 receptor [dbj BAA05840 .1	6745	29	478	93	93	HCRQJ58	pSport1
2469	HCRQC27R	histone H2A variant (AA 1-141) [Drosophila melanogaster] >emb CAA33555.1 histone H2A [Drosophila melanogaster] >pir S08118 S08118 histone H2A.vD - fruit fly (Drosophila melanogaster) >sp P08985 H2AV_DROME HISTONE H2A VARIANT. {SUB 2-141} >gb AAA72378.1	emb CAA3037 0.1	6746	135	224	81	89	HCRQC27	pSport1
2470	HWLXR58R	HMG-1 [Homo sapiens] >sp Q14321 Q14321 HMG- 1. Length = 215	dbj BAA09924 .1	6747	1	384	100	100	HWLXR58	pSport1
2471	HMWHX32R	HsMcm6 [Homo sapiens] >sp Q14566 MCM6 HUMAN DNA REPLICATION LICENSING FACTOR MCM6 (P105MCM). Length = 821	dbj BAA12699 .1	6748	1	180	100	100	HMWHX32	Uni-ZAP XR
2472	HCROW95R	HTF4a 5'-region hypothetical 13K protein - human Length = 117	pir A56611 A5 6611	6749	317	3	83	84	HCROW95	pSport1
2473	HCYBO60R	HU-K4 [Homo sapiens] >sp Q92853 Q92853 HU- K4. Length = 437	gb AAB16799. 1	6750	25	387	74	76	HCYBO60	pBluescript SK-

2474	HE2BG62R	human gamma-glutamyl hydrolase [Homo sapiens] >gb AAF03360.1 (AF147083) gamma-glutamyl hydrolase [Homo sapiens] >sp Q92820 GGH_HUMAN GAMMA- GLUTAMYL HYDROLASE PRECURSOR (EC 3.4.19.9) (GAMMA-GLU-X CARBOXYPEPTIDASE) (CONJUGASE) (GH). >sp AAF03360 AAF03360 G	gb AAC05579. 1	6751	187	336	88	94	HE2BG62	Uni-ZAP XR
2475	HCRMW12R	human homolog of DnaJ protein [Homo sapiens] Length = 397	dbj BAA02656 .1	6752	2	496	92	92	HCRMW12	pSport1
2476	HRDEK90R	human protein homologous to DROER protein [Homo sapiens] >gb AAC51172.1 enhancer of rudimentary homolog [Homo sapiens] >dbj BAA11118.1 Mer [Mus musculus] >gb AAC53105.1 enhancer of rudimentary homolog [Mus musculus] >gb AAF28892.1 AF124330_1 (AF124330)	dbj BAA12865 .1	6753	18	188	57	62	HRDEK90	Uni-ZAP XR
2477	HHBEF23R	hypothetical 18K protein - goldfish mitochondrion Length = 166	pir JC1348 JC1 348	6754	186	269	47	52	HHBEF23	pCMVSPORT 1
2478	HWLVF61R	HYPOTHETICAL PROTEIN (FRAGMENT). Length = 122	sp Q16465 YZ A1_HUMAN	6755	382	2	90	90	HWLVF61	pSport1
2479	HKCSR28R	hypothetical protein [Escherichia coli] >gb AAC73592.1 (AE000155) putative ATP- binding component of a transport system [Escherichia coli] >pir A64780 A64780 probable ABC transport protein ybbL - Escherichia coli >sp P77279 YBBL_ECOLI HYPOTHETICAL ABC TRAN	gb AAB40244. 1	6756	8	190	100	100	HKCSR28	pBluescript
2480	HWMBP47R	(AL021682) unnamed protein product [Homo sapiens] >sp O43788 O43788 CDNA MAPPING TO 22Q13. Length = 287	emb CAA1667 0.1	6757	1	171	84	84	HWMBP47	pSport1
2481	HWMBG58R	(AF106966) I3 protein [Homo sapiens] >sp O95415 O95415 I3 PROTEIN. Length = 125	gb AAD05167. 1	6758	446	333	91	91	HWMBG58	pSport1

2482	HCRMF92R	IEF 7442 [Homo sapiens] >gb AAC50231.1 retinoblastoma-binding protein RbAp46 [Homo sapiens] >gb AAC36349.1 (AF090306) retinoblastoma binding protein [Rattus norvegicus] >pir I39181 I39181 G1/S transition control protein-binding protein RbAp46 - human >s	emb CAA5136 0.1	6759	240	368	67	74	HCRMF92	pSport1
2483	HWLQF89R	IEF 7442 [Homo sapiens] >gb AAC50231.1 retinoblastoma-binding protein RbAp46 [Homo sapiens] >gb AAC36349.1 (AF090306) retinoblastoma binding protein [Rattus norvegicus] >pir I39181 I39181 G1/S transition control protein-binding protein RbAp46 - human >s	emb CAA5136 0.1	6760	3	263	92	92	HWLQF89	pSport1
2484	HWLOG90R	(AF103261) immunoglobulin heavy chain variable region [Homo sapiens] Length = 117 Ig kappa chain Am37 precursor - human Length = 216	gb AAD30821.1	6761	49	501	75	79	HWLOG90	pSport1
2485	HWLRV24R	Ig kappa chain V-J-C region - human {SUB 1-136} >emb CAA61443.1 immunoglobulin anti-F(ab')2 variable region light chain [Homo sapiens] {SUB 21-132} Length = 137	pir JE0241 JE0241	6762	2	241	81	81	HWLRV24	pSport1
2486	HWMCC54R	Ig kappa light chain (V1C) [Homo sapiens] >pir S40357 S40357 Ig kappa chain V-J-C region - human {SUB 1-136} >emb CAA61443.1 immunoglobulin anti-F(ab')2 variable region light chain [Homo sapiens] {SUB 21-132} Length = 137	emb CAA5113 5.1	6763	3	395	90	94	HWMCC54	pSport1
2487	HWLNK85R	(AF018265) immunoglobulin lambda light chain [synthetic construct] Length = 236	gb AAF21612.1	6764	2	208	84	86	HWLNK85	pSport1
2488	HCQAV48R	IG light chain variable region (VJ) [Homo sapiens] >pir S38643 S38643 Ig kappa chain V region - human (fragment) >pir S46369 S46369 IG light chain variable region (VJ) - human {SUB 6-134} >pir A25521 A25521 Ig kappa chain V region (321) - human (fragment)	emb CAA8169 4.1	6765	1	243	78	78	HCQAV48	Lambda ZAP II
2489	HWMCM79R	immunoglobulin kappa-chain [Homo sapiens] Length = 104	gb AAA02610.1	6766	78	209	55	62	HWMCM79	pSport1

2490	HCQAS76R	immunoglobulin variable chain lambda [Homo sapiens] >pir S04519 S04519 Ig lambda chain precursor V-II region (2.1) - human (fragment) Length = 118	emb CAA3277 0.1	6767	3	170	74	76	HCQAS76	Lambda ZAP II
2491	HKLRA71R	(AF038143) immunoglobulin lambda-2b light chain variable region [Ovis aries] Length = 118	gb AAB94909. 1	6768	2	223	47	55	HKLRA71	pBluescript
2492	HWMCI58R	IgG [Homo sapiens] Length = 476	gb AAA02914. 1	6769	2	508	70	83	HWMCI58	pSport1
2493	HWLMJ20R	immunoglobulin gamma heavy chain [Homo sapiens] Length = 134	emb CAA6740 6.1	6770	2	247	69	79	HWLMJ20	pSport1
2494	HWLMZ25R	(AB019438) immunoglobulin heavy chain variable region [Homo sapiens] Length = 119	dbj BAA75031 .1	6771	1	423	91	95	HWLMZ25	pSport1
2495	HKLRB13R	(AJ010444) immunoglobulin kappa light chain [Homo sapiens] Length = 210	emb CAA0918 3.1	6772	3	356	85	91	HKLRB13	pBluescript
2496	HWLMU79R	immunoglobulin kappa light chain [Homo sapiens] Length = 236	emb CAA6506 1.1	6773	3	443	88	95	HWLMU79	pSport1
2497	HKLSA25R	immunoglobulin kappa light chain variable region [Homo sapiens] Length = 106	gb AAA71907. 1	6774	1	477	57	68	HKLSA25	pBluescript
2498	HWLNN06R	(AF018265) immunoglobulin lambda light chain [synthetic construct] Length = 236	gb AAF21612. 1	6775	2	484	74	76	HWLNN06	pSport1
2499	HWLMM42R	immunoglobulin lambda heavy chain [Homo sapiens] >gb AAF14196.1 (AF107231) immunoglobulin heavy chain variable region [Homo sapiens] {SUB 20-147} Length = 477	emb CAA7503 2.1	6776	242	433	75	75	HWLMM42	pSport1
2500	HWMBC38R	(AF063771) immunoglobulin lambda light chain variable region [Homo sapiens] Length = 108	gb AAC16848. 1	6777	3	455	70	80	HWMBC38	pSport1
2501	HWLVU11R	immunoglobulin lambda-chain subgroup II [Homo sapiens] >dbj BAA20002.1 V1-5 [Homo sapiens] {SUB 20-118} Length = 118	gb AAB00166. 1	6778	1	402	69	69	HWLVU11	pSport1
2502	HCQAM96R	This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal [Homo sapiens] Length = 139	gb AAA52938. 1	6779	1	174	38	50	HCQAM96	Lambda ZAP II

2503	HCQCE43R			6780	133	26			HCQCE43	Lambda ZAP II
2504	HCQCG90R			6781	139	2			HCQCG90	Lambda ZAP II
2505	HCQCK29R			6782	107	3			HCQCK29	Lambda ZAP II
2506	HCQCU15R			6783	97	2			HCQCU15	Lambda ZAP II
2507	HCQDW78R			6784	134	24			HCQDW78	Lambda ZAP II
2508	HCQDW90R			6785	109	2			HCQDW90	Lambda ZAP II
2509	HCYBM34R			6786	109	2			HCYBM34	pBluescript SK-
2510	HCYBM57R			6787	134	6			HCYBM57	pBluescript SK-
2511	HKLAA14R			6788	148	2			HKLAA14	Lambda ZAP II
2512	HCQCK49R			6789	114	22			HCQCK49	Lambda ZAP II
2513	HWLMU27R	initiation factor 4D [Homo sapiens] >gb AAA86989.1 eIF-5A [Homo sapiens] >pir B31486 FIHUA translation initiation factor eIF-5A - human >sp P10159 IF5A_HUMAN INITIATION FACTOR 5A (EIF-5A) (EIF-4D) (REV BINDING FACTOR). {SUB 2-154} Length = 154	gb AAA58453.1	6790	2	139	97	97	HWLMU27	pSport1
2514	HWLUR23R	insulin-like growth factor binding protein 5 [Homo sapiens] >gb AAA72051.1 [Human insulin-like growth factor binding protein 5 (IGFBP5) gene], gene product [Homo sapiens] >gb AAC09368.1 (AF055033) insulin-like growth factor binding protein 5 [Homo sapie	gb AAA53505.1	6791	43	366	95	95	HWLUR23	pSport1
2515	HWLRQ41R	interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human Length = 739	pir A46159 A46159	6792	53	211	86	88	HWLRQ41	pSport1

2516	HWLOC77R	inter feron-gamma [Homo sapiens] >gb AAA53230.1 inter feron-gamma [Homo sapiens] >gb AAF02217.1 AF078829_1 (AF078829) protease activator PA28 alpha [Homo sapiens] >pir A54859 A54859 proteasome activator PA28 alpha chain - human >sp Q06323 IGUP_HUMAN INTE	gb AAA16521. 1	6793	1	294	100	100	HWLOC77	pSport1
2517	HDDNQ21R	inter feron-inducible protein [Homo sapiens] >sp P13164 IN9_HUMAN INTERFERON- INDUCIBLE PROTEIN 9-27 (LEU-13 ANTIGEN). Length = 125	emb CAA5933 7.1	6794	1	408	98	98	HDDNQ21	pSport1
2518	HCQDS58R	Interleukin 15 [Homo sapiens] >emb CAA62616.1 inter leukin-15 [Homo sapiens] >sp P40933 IL15_HUMAN INTERLEUKIN-15 PRECURSOR (IL-15). Length = 162	gb AAA21551. 1	6795	298	384	58	66	HCQDS58	Lambda ZAP II
2519	HCQDA89R	IP63 protein [Rattus norvegicus] >sp O55160 O55160 IP63 PROTEIN. Length = 571	emb CAA6770 5.1	6796	187	330	74	82	HCQDA89	Lambda ZAP II
2520	HCQCO43R	J (tail:host specificity;1132) [bacteriophage lambda] >pii D43009 QSBPL host specificity protein J - phage lambda >sp P03749 VHSJ_LAMBD HOST SPECIFICITY PROTEIN J. Length = 1132	gb AAA96553. 1	6797	1	180	96	98	HCQCO43	Lambda ZAP II
2521	HCQCG73R	KHS1 [Homo sapiens] >sp Q9Y4K4 Q9Y4K4 KHS1. Length = 846	gb AAB48435. 1	6798	2	328	97	97	HCQCG73	Lambda ZAP II
2522	HWLQA92R	KIAA0007 [Homo sapiens] >sp Q92577 Q92577 MYELOBLAST KIAA0007 (FRAGMENT). Length = 459	dbj BAA13441 .1	6799	2	208	65	69	HWLQA92	pSport1
2523	HCROO70R	KIAA0036 [Homo sapiens] >sp Q15051 Y036_HUMAN HYPOTHETICAL PROTEIN KIAA0036. Length = 598	dbj BAA04968 .1	6800	252	413	86	88	HCROO70	pSport1
2524	HCRNL15R			6801	108	233			HCRNL15	pSport1
2525	HCRQM41R	KIAA0061 [Homo sapiens] >sp Q15037 Q15037 KIAA0061 PROTEIN (FRAGMENT). Length = 903	dbj BAA06543 .1	6802	3	524	98	98	HCRQM41	pSport1

2526	H2LAA02R	KIAA0158 gene product is related to Drosophila Df176 protein. [Homo sapiens] >gb AAB92377.1 (AF038404) homolog of Nedd5; hNedd5 [Homo sapiens] >sp Q15019 NED5_HUMAN NEDD5 PROTEIN HOMOLOG (KIAA0158). >gb AAD12225.1 (AC005104) KIAA0158; similar to human N	dbj BAA09928.1	6803	122	487	98	98	H2LAA02	pBluescript SK-
2527	H2CBC43R	kinesin-like spindle protein HKSP [Homo sapiens] >pir G02157 G02157 kinesin-like spindle protein HKSP - human Length = 1056	gb AAA86132.1	6804	65	409	82	83	H2CBC43	pBluescript SK-
2528	HCQDU29R			6805	17	73			HCQDU29	Lambda ZAP II
2529	HWMBH25R	lactate dehydrogenase B [Homo sapiens] >emb CAA68701.1 lactate dehydrogenase B (AA 1 - 334) [Homo sapiens] >pir S02795 DEHULH L-lactate dehydrogenase (EC 1.1.1.27) chain H - human >sp P07195 LDHH_HUMAN L-LACTATE DEHYDROGENASE H CHAIN (EC 1.1.1.27) (LDH-B	emb CAA3203.3.1	6806	3	440	96	96	HWMBH25	pSport1
2530	HWMBW89R			6807	3	527			HWMBW89	pSport1
2531	HCYBK06R			6808	11	148			HCYBK06	pBluescript SK-
2532	HWMCL19R	Ig kappa light chain (VJC) [Homo sapiens] >emb CAB75876.1 (AJ272080) immunoglobulin light chain variable region [Homo sapiens] {SUB 14-131; >gb AAD16547.1 (AF103376) immunoglobulin kappa light chain variable region [Homo sapiens] {SUB 22-122} >pir S3409	emb CAA5112.0.1	6809	3	275	95	98	HWMCL19	pSport1
2533	HCRM39R	lumican [Homo sapiens] >sp P51884 LUM_HUMAN LUMICAN PRECURSOR (LUM) (KERATAN SULFATE PROTEOGLYCAN). Length = 338	gb AAA85268.1	6810	3	413	65	65	HCRM39	pSport1

2534	HWMBJ73R	lymphocyte antigen [Homo sapiens] >gb AAA59613.1 HLA-A31 precursor [Homo sapiens] >gb AAB05976.1 lymphocyte antigen [Homo sapiens] >pir J72170 J72170 MHC class I histocompatibility antigen HLA-A31 alpha chain (allele A*31012) precursor - human >sp P1618	gb AAA59599.1	6811	3	428	85	85	HWMBJ73	pSport1
2535	HWLVE15R	M1 subunit of ribonucleotide reductase [Homo sapiens] >emb CAA42180.1 large subunit ribonucleotide reductase [Homo sapiens] >pir S16680 S16680 ribonucleoside-diphosphate reductase (EC 1.17.4.1) chain M1 - human >sp P23921 RIR1_HUMAN RIBONUCLEOSIDE-DIPHOS	emb CAA42118.1	6812	3	392	96	96	HWLVE15	pSport1
2536	HCRMD64RA	MDA-7 [Homo sapiens] >sp Q13007 MDA7_HUMAN MDA-7 PROTEIN PRECURSOR (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 7). Length = 206	gb AAA91780.1	6813	3	185	96	96	HCRMD64	pSport1
2537	HCRNO44R	(AL117452) hypothetical protein [Homo sapiens] >emb CAB55934.1 (AL117452) hypothetical protein [Homo sapiens] >pir T17244 T17244 hypothetical protein DKFZp586G1517.1 - human (fragment) >sp CAB55934 CAB55934 Hypothetical 99.4 kd protein (fragment). >emb C	emb CAB55934.1	6814	299	514	78	78	HCRNO44	pSport1
2538	HNBTK71R	membrane protein [Homo sapiens] >emb CAA42708.1 MRP-1 (motility related protein) [Homo sapiens] >gb AA80320.1 CD9 antigen [Homo sapiens] >gb AAC60586.1 CD9 antigen [human, leukocytes, Peptide, 228 aa] [Homo sapiens] >pir A46123 A40402 CD9 antigen - hu	gb AA59982.1	6815	2	628	91	91	HNBTK71	pSport1

2539	HCROL22R	membrane protein with histidine rich charge clusters [Homo sapiens] >gb AAD12305.1 (AF117221) KE4 protein [Homo sapiens] >sp Q92504 Q92504 MEMBRANE PROTEIN WITH HISTIDINE RICH CHARGE CLUSTERS. Length = 429	dbj BAA11528.1	6816	3	371	45	47	HCROL22	pSport1
2540	HWLV152R	metalloproteinase inhibitor precursor [Homo sapiens] >gb AAA61186.1 metalloproteinase-2 inhibitor precursor [Homo sapiens] >gb AAB19474.1 tissue inhibitor of metalloproteinase 2, TIMP-2 {EC 3.4.24.-} [human, Peptide, 220 aa] [Homo sapiens] >pir A37128 A	gb AAA59581.1	6817	3	413	100	100	HWLV152	pSport1
2541	HSAMD89R	non-muscle alpha tropomyosin [Rattus norvegicus] >sp Q63582 Q63582 NON-MUSCLE ALPHA TROPOMYOSIN. Length = 284	gb AAA21805.1	6818	3	476	73	75	HSAMD89	pSport1
2542	HCQDI65R	mitochondrial ATP synthase subunit 9 precursor [Homo sapiens] >pir I38612 I38612 H ⁺ -transporting ATP synthase (EC 3.6.1.34) lipid-binding protein P3 precursor, mitochondrial - human >sp P48201 AT93_HUMAN ATP SYNTHASE LIPID-BINDING PROTEIN P3 PRECURSOR (EC	gb AAA78807.1	6819	112	222	96	96	HCQDI65	Lambda ZAP II
2543	HCROE42R	(AF184344) DNA polymerase accessory subunit precursor [Homo sapiens] >sp AAD56542 AAD56542 DNA polymerase accessory subunit precursor. Length = 485	gb AAD56542.1 AF1843	6820	3	551	80	82	HCROE42	pSport1
2544	HCROJ80R	mitochondrial intermediate peptidase precursor [Homo sapiens] >sp Q99797 PMIP_HUMAN MITOCHONDRIAL INTERMEDIATE PEPTIDASE PRECURSOR (EC 3.4.24.59) (MIP). Length = 713	gb AAC51231.1	6821	149	475	68	68	HCROJ80	pSport1

2545	HCWHT65R	mitochondrial intermediate peptidase precursor [Homo sapiens] >sp Q99797 PMP_HUMAN MITOCHONDRIAL INTERMEDIATE PEPTIDASE PRECURSOR (EC 3.4.24.59) (MIP). Length = 713	gb AAC51231.1	6822	1	432	70	74	HCWHT65	ZAP Express
2546	HCRMX32R			6823	1	300			HCRMX32	pSport1
2547	HCROE77R	MTHSP75 [Homo sapiens] >sp P38646 GR75_HUMAN MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED PROTEIN) (GRP 75) (PEPTIDE-BINDING PROTEIN 74) (PBP74) (MORTALIN) (MOT). Length = 679	gb AAA67526.1	6824	3	329	93	93	HCROE77	pSport1
2548	HCRMX69R	multifunctional protein CAD [Homo sapiens] >sp P27708 PYR1_HUMAN CAD PROTEIN [INCLUDES: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5); ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2); DIHYDROOROTASE (EC 3.5.2.3)]. >gb AAA51907.1 CAD [Homo sap	dbj BAA11423.1	6825	1	144	93	93	HCRMX69	pSport1
2549	HCQDH45R	myosin I heavy chain isoform [Gallus gallus] >sp Q02440 MYSD_CHICK DILUTE MYOSIN HEAVY CHAIN, ISOFORM I (MYOSIN HEAVY CHAIN P190) (MYOSIN-V). Length = 1829	emb CAA4767.3.1	6826	106	312	86	88	HCQDH45	Lambda ZAP II
2550	HOCTA19R	myosin II nonmuscle [Rana catesbeiana] >sp Q91304 Q91304 MYOSIN II NONMUSCLE (FRAGMENT). Length = 261	gb AAA65087.1	6827	217	504	80	92	HOCTA19	pSport1
2551	HWLRA67R	myosin regulatory light chain [Homo sapiens] >pir S11493 MOHULP myosin regulatory light chain, placental - human >sp P19105 MLRM_HUMAN MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC (MYOSIN RLC). {SUB 2-171} Length = 171	emb CAA3820.1.1	6828	1	117	68	78	HWLRA67	pSport1

2552	HWLOM88R	(AF132021) myosin X [Homo sapiens] >gb AAF17363.1 AF184153_1 (AF184153) myosin X [Homo sapiens] {SUB 347-495} Length = 1540	gb AAF36524.1 AF1320	6829	2	409	69	70	HWLOM88	pSport1
2553	H2CBI14R	myosin heavy chain 12 [Homo sapiens] >sp CAA69036 CAA69036 Myosin heavy chain 12. Length = 1828	emb CAA69036.1	6830	2	208	60	76	H2CBI14	pBluescript SK-
2554	HCRNI08R	N-acetylglucosaminyltransferase V [Homo sapiens] >gb AAD22449.1 AF113921_1 (AF113921) alpha-1,3(6)-mannosylglycoprotein beta-1,6-N-acetylglucosaminyltransferase [Homo sapiens] >pir JC2074 JC2074 alpha-1,3(6)-mannosylglycoprotein beta-1, 6-N-acetylglucosa	dbj BAA04570.1	6831	1	537	88	88	HCRNI08	pSport1
2555	HFPBS29R	NAD+-isocitrate dehydrogenase, gamma subunit [Macaca fascicularis] >pir S39065 S39065 isocitrate dehydrogenase (NAD+) (EC 1.1.1.41) gamma chain precursor - crab-eating macaque (fragment) >sp P41564 IDHG_MACFA ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT GAMMA,	emb CAA5222.4	6832	1	183	97	100	HFPBS29	Uni-ZAP XR
2556	HCQDL50R			6833	128	226			HCQDL50	Lambda ZAP II
2557	HCQCB43R	NADH dehydrogenase subunit 2 [Homo sapiens] >dbj BAA07291.1 NADH dehydrogenase subunit 2 [Homo sapiens] >sp Q34769 Q34769 NADH DEHYDROGENASE SUBUNIT 2. Length = 347	dbj BAA07291.1	6834	27	113	40	43	HCQCB43	Lambda ZAP II
2558	HCQDA51R	NADH dehydrogenase subunit 2 [Homo sapiens] >dbj BAA07291.1 NADH dehydrogenase subunit 2 [Homo sapiens] >sp Q34769 Q34769 NADH DEHYDROGENASE SUBUNIT 2. Length = 347	dbj BAA07291.1	6835	260	322	41	43	HCQDA51	Lambda ZAP II

2559	HCQDB27R	NADH dehydrogenase subunit 2 [Homo sapiens] >dbj BAA07291.1 NADH dehydrogenase subunit 2 [Homo sapiens] >sp Q34769 Q34769 NADH DEHYDROGENASE SUBUNIT 2. Length = 347	dbj BAA07291 .1	6836	23	109	58	63	HCQDB27	Lambda ZAP II
2560	HCQDS85R	NADH dehydrogenase subunit 2 [Homo sapiens] >dbj BAA07291.1 NADH dehydrogenase subunit 2 [Homo sapiens] >sp Q34769 Q34769 NADH DEHYDROGENASE SUBUNIT 2. Length = 347	dbj BAA07291 .1	6837	284	451	43	49	HCQDS85	Lambda ZAP II
2561	HCQCR82R	NADH dehydrogenase subunit 3 [Homo sapiens] >dbj BAA77672.1 NADH dehydrogenase subunit 3 [Homo sapiens] >sp BAA77672 BAA77672 NADH dehydrogenase subunit 3. >gb AAB63453.1 (AF004342) NADH dehydrogenase III [Homo sapiens] {SUB 10-115} >dbj BAA76519.1 (AB	dbj BAA77672 .1	6838	48	206	90	100	HCQCR82	Lambda ZAP II
2562	HCQDV94R	NADH dehydrogenase subunit 4 [Homo sapiens] >dbj BAA77673.1 NADH dehydrogenase subunit 4 [Homo sapiens] >sp BAA77673 BAA77673 NADH dehydrogenase subunit 4. Length = 459	dbj BAA77673 .1	6839	174	323	72	75	HCQDV94	Lambda ZAP II
2563	HCQCT16R			6840	2	49			HCQCT16	Lambda ZAP II
2564	HCQDA65R	neutrophil gelatinase associated lipocalin [Homo sapiens] >sp P80188 NGAL_HUMAN NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (25 KD ALPHA-2-MICROGLOBULIN-RELATED SUBUNIT OF MMP-9) (LIPOCALIN-2) (ONCOGENE 24P3). >gb AAD14168.1 S75256_1	emb CAA5812 7.1	6841	2	457	89	89	HCQDA65	Lambda ZAP II

2565	HWLWH33R	neutrophil gelatinase associated lipocalin [Homo sapiens] >sp P80188 NGAL_HUMAN NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (25 KD ALPHA-2-MICROGLOBULIN-RELATED SUBUNIT OF MMP-9) (LIPOCALIN-2) (ONCOGENE 24P3). >gb AAD14168.1 S75256_1 (AF043542) nucleoside diphosphate kinase [Gallus gallus] >sp O57535 O57535 NUCLEOSIDE DIPHOSPHATE KINASE. Length = 153	emb CAA5812.7.1	6842	200	547	90	91	HWLWH33	pSport1
2566	HCBYBJ83R	(AF043542) nucleoside diphosphate kinase [Gallus gallus] >sp O57535 O57535 NUCLEOSIDE DIPHOSPHATE KINASE. Length = 153	gb AAB99856.1	6843	285	494	81	86	HCBYBJ83	pBluescript SK-
2567	HWLRE17R	nuclear autoantigen [Homo sapiens] >pir A37244 A37244 nuclear autoantigen Sp-100 - human Length = 480	gb AAA35537.1	6844	2	415	73	73	HWLRE17	pSport1
2568	H2LAC53R	nucleophosmin [Homo sapiens] >gb AAA36385.1 nucleolar protein B23 [Homo sapiens] >gb AAA58386.1 nucleolar phosphoprotein B23 [Homo sapiens] >gb AAB94739.1 nucleophosmin phosphoprotein [Homo sapiens] >pir A33423 A32915 nucleophosmin - human >sp P06748 N	gb AAA36380.1	6845	1	399	86	87	H2LAC53	pBluescript SK-
2569	HWL0M10R	nucleolin [Homo sapiens] >pir A35804 A35804 nucleolin - human >sp P19338 NUCL_HUMAN NUCLEOLIN (PROTEIN C23). {SUB 2-707} Length = 707	gb AAA59954.1	6846	1	438	96	97	HWL0M10	pSport1
2570	HWLQO29R	ORF [Pan troglodytes] >sp Q28808 INI2_PANTR INTERFERON-INDUCED PROTEIN 6-16 PRECURSOR (IFI-6-16). Length = 130	dbj BAA01980.1	6847	3	332	76	76	HWLQO29	pSport1
2571	H2LBA48R	ORF YNL040w [Saccharomyces cerevisiae] >pir S62962 S62962 hypothetical protein YNL040w - yeast (Saccharomyces cerevisiae) >sp P53960 YNE0_YEAST HYPOTHETICAL 51.0 KD PROTEIN IN YIP3-TFC5 INTERGENIC REGION. Length = 456	emb CAA9590.7.1	6848	172	432	41	63	H2LBA48	pBluescript SK-

2572	HCRPZ16R	(AL033502) hypothetical protein [Candida albicans] >sp O94058 O94058 HYPOTHETICAL 85.6 KD PROTEIN. Length = 747	emb CAA2200 9.1	6849	294	659	38	64	HCRPZ16	pSport1
2573	HKCSA80R	ORF1 [Escherichia coli] Length = 334	gb AAA72122. 1	6850	245	3	66	69	HKCSA80	pBluescript
2574	HCQBD02R	ORFII [Homo sapiens] >sp Q14754 Q14754 ORFII. Length = 712	emb CAA3648 0.1	6851	2	145	54	72	HCQBD02	Lambda ZAP II
2575	HCRPH64R	ornithine decarboxylase antizyme [Homo sapiens] Length = 228	dbj BAA13497 1	6852	2	193	97	97	HCRPH64	pSport1
2576	HDTBZ03R	OS9 [Homo sapiens] Length = 474	gb AAC39523. 1	6853	2	319	83	83	HDTBZ03	pCMV/Sport 2.0
2577	HLYED39R			6854	216	347			HLYED39	pSport1
2578	HCQCB85R	peptidylprolyl isomerase [Homo sapiens] >emb CAA68264.1 cyclophilin (AA 1-165) [Homo sapiens] >gb AAB81959.1 (AF023859) cyclophilin A [Papio hamadryas] >gb AAB81960.1 (AF023860) cyclophilin A [Cercopithecus aethiops] >gb AAB81961.1 (AF023861) cyclophi	emb CAA3703 9.1	6855	1	246	97	98	HCQCB85	Lambda ZAP II
2579	HCRME24R	perforin [Homo sapiens] >gb AAA60167.1 perforin [Homo sapiens] >pir A45816 A37181 perforin 1 precursor - human >sp P14222 PERF_HUMAN PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP) (CYTOLYSIN). Length = 555	gb AAA60065. 1	6856	35	130	53	56	HCRME24	pSport1
2580	HWLQK64R	PEX5p [Mus musculus] >sp O09012 PEX5_MOUSE PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR (PEROXISOME RECEPTOR 1) (PEROXISOMAL C-TERMINAL TARGETING SIGNAL IMPORT RECEPTOR) (PTS1-BP) (PEROXIN-5) (PTS1 RECEPTOR) (PXRIP) (PTSIR). Length = 639	emb CAB0969 4.1	6857	445	239	63	73	HWLQK64	pSport1

2581	HCRNF48R	phosphate carrier protein [Homo sapiens] >emb CAB56612.1 phosphate carrier [Homo sapiens] >pir B53737 B53737 phosphate carrier protein, form B - human >sp CAB56612 CAB56612 Phosphate carrier. Length = 361	emb CAA4264 1.1	6858	3	383	78	78	HCRNF48	pSport1
2582	HCQDL14R	phosphofructokinase [Oryctolagus cuniculus] >pir A26550 KIRBF 6-phosphofructokinase (EC 2.7.1.11), muscle - rabbit >sp P00511 K6PF_RABIT 6-PHOSPHOFRUCTOKINASE, MUSCLE TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE I	gb AAA31441. 1	6859	1	339	77	83	HCQDL14	Lambda ZAP II
2583	HWLQA11R	phosphorylation regulatory protein HP-10 - human Length = 492	pir A61382 A6 1382	6860	48	257	69	72	HWLQA11	pSport1
2584	HCYBH73R	plakophilin 2a [Homo sapiens] >sp Q99960 Q99960 PLAKOPHILIN 2A. Length = 837	emb CAA6626 5.1	6861	3	269	75	78	HCYBH73	pBluescript SK-
2585	HCQCJ88R	fusion protein [Homo sapiens] >gb AAD13865.1 1680464_1 promyelocytic leukemia protein [Homo sapiens] {SUB 220-333} Length = 744	gb AAA59972. 1	6862	3	272	88	88	HCQCJ88	Lambda ZAP II
2586	HWLXJ34R	PRAJA1 [Mus musculus] >sp O55176 O55176 PRAJA1. Length = 424	gb AAC00205. 1	6863	3	416	83	86	HWLXJ34	pSport1
2587	HOCTB09R	C9 complement protein [Homo sapiens] Length = 557	gb AAA51889. 1	6864	1	477	92	94	HOCTB09	pSport1
2588	HCRQN67R	precursor polypeptide (AA -23 to 1120) [Homo sapiens] >gb AAD15273.1 T200 glycoprotein [Homo sapiens] >sp Q16614 Q16614 T200 LEUKOCYTE COMMON ANTIGEN (CD45, LC-A) PRECURSOR (EC 3.1.3.48) (CD45, LC-A). Length = 1143	emb CAA6826 9.1	6865	3	260	100	100	HCRQN67	pSport1
2589	HCYBH30R	(AF113123) carbonyl reductase [Homo sapiens] >sp AAF14864 AAF14864 Carbonyl reductase. Length = 244	gb AAF14864. 1 AF1131	6866	292	450	79	82	HCYBH30	pBluescript SK-

2590	HCRNO04R	preprocathepsin B [Homo sapiens] >pir A26498 KHHUB cathepsin B (EC 3.4.22.1) precursor - human >sp P07858 CATB_HUMAN CATHEPSIN B PRECURSOR (EC 3.4.22.1) (CATHEPSIN B1) (APP SECRETASE). Length = 339	gb AAA52129.1	6867	3	104	96	96	HCRNO04	pSportl
2591	HWLRC47R			6868	3	236			HWLRC47	pSportl
2592	HCROE26R	prostacyclin-stimulating factor, PGI2-stimulating factor, PSF [human, cultured diploid fibroblast cells, Peptide, 282 aa] [Homo sapiens] >pir S50031 S50031 prostacyclin-stimulating factor - human >sp Q16270 Q16270 PROSTACYCLIN- STIMULATING FACTOR. Length =	gb AB32370.1	6869	3	260	86	86	HCROE26	pSportl
2593	HOHBE57R	protein kinase [Homo sapiens] >sp Q92631 Q92631 PROTEIN KINASE (FRAGMENT). Length = 240	emb CAA7048.8.1	6870	59	535	76	84	HOHBE57	pCMVSPORT 2.0
2594	HCROK02R	protein phosphatase 2A alpha catalytic subunit (AA 1- 309) [Bos taurus] >emb CAA51381.1 protein phosphatase-2A [Bos taurus] >gb AAA30981.1 protein phosphatase 2A alpha subunit [Sus scrofa] >emb CAA29471.1 phosphatase (AA 1-309) [Oryctolagus cuniculus] >g	emb CAA3678.9.1	6871	2	310	98	98	HCROK02	pSportl
2595	HWMBB94R	protein tyrosine phosphatase [Homo sapiens] >gb AAA66496.1 protein phosphatase [Homo sapiens] >sp Q16667 CDN3_HUMAN CYCLIN- DEPENDENT KINASE INHIBITOR 3 (EC 3.1.3.48) (EC 3.1.3.16) (CDK2- ASSOCIATED DUAL SPECIFICITY PHOSPHATASE) (KINASE ASSOCIATED PHOSPHA	gb AAA60222.1	6872	81	272	98	100	HWMBB94	pSportl

2596	HUVHA17R	focal adhesion kinase [Mus musculus] >pir A46166 A46166 protein-tyrosine kinase (EC 2.7.1.112) - mouse >sp P34152 FAK1_MOUSE FOCAL ADHESION KINASE 1 (EC 2.7.1.112) (FADK 1) (PP125FAK). Length = 1052	gb AAA37592.1	6873	174	443	91	95	HUVHA17	Uni-ZAP XR
2597	HLTIJ91R			6874	3	230			HLTIJ91	Uni-ZAP XR
2598	HCRMC40R	put. ORF [Homo sapiens] >pir A31026 A31026 probable membrane receptor protein - human >sp P08910 HPS1_HUMAN PROTEIN PHPS1-2. Length = 425	emb CAA3097.6.1	6875	2	160	100	100	HCRMC40	pSport1
2599	HKCSL44R	Q1Z 7F5 [Homo sapiens] >gb AAA36378.1 may code for Wilm's tumor-related protein [Homo sapiens] >gb AAA63253.1 Wilm's tumor-related protein [Homo sapiens] >gb AAB27665.1 QM [human, nontumorigenic Wilms' microcell hybrid cells, Peptide, 214 aa] [Homo	gb AAA36021.1	6876	37	288	66	69	HKCSL44	pBluescript
2600	HCQAR83R	sperm membrane protein BS-63 [Homo sapiens] >sp AAB41848 AAB41848 Sperm membrane protein BS-63. >sp Q99666 Q99666 BS-63. {SUB 1197- 1765} Length = 1765	gb AAB41848.2	6877	11	184	93	95	HCQAR83	Lambda ZAP II
2601	HWLQD31R	rapamycin- and FK506-binding protein [Homo sapiens] >pir JC1365 JC1365 FK506/rapamycin- binding protein FKBP13 precursor - human Length = 142	gb AAA36563.1	6878	2	250	97	97	HWLQD31	pSport1
2602	HOUDN78R	Rab5c protein [Canis familiaris] >pir S65933 S65933 GTP-binding protein Rab5c - dog >sp P51147 RB5C_CANFA RAS-RELATED PROTEIN RAB-5C. Length = 216	emb CAA8162.6.1	6879	2	307	48	52	HOUDN78	Uni-ZAP XR
2603	HOSBE19R	ras-related GTP-binding protein [Homo sapiens] Length = 184	dbj BAA11211.1	6880	161	367	70	74	HOSBE19	Uni-ZAP XR
2604	HCROB08R			6881	42	170			HCROB08	pSport1

2605	HWLQG37R	ribosomal protein [Homo sapiens] >emb CAA40328.1 ribosomal protein L38 [Rattus rattus] >pir S15658 R5RT38 ribosomal protein L38 - rat >pir S38385 S38385 ribosomal protein L38 - human >sp P23411 RL38_HUMAN 60S RIBOSOMAL PROTEIN L38. {SUB 2-70} >dbj BAA258	emb CAA8148.8.1	6882	205	387	60	60	HWLQG37	pSportl
2606	HSAMB82R	ribosomal protein L11 [Homo sapiens] >emb CAA44072.1 ribosomal protein L11 [Rattus rattus] >pir S17351 R5RT11 ribosomal protein L11 precursor - rat >sp P39026 RL11_HUMAN 60S RIBOSOMAL PROTEIN L11. {SUB 2-178} >dbj BAA25831.1 (AB007171) ribosomal protein	gb AAC15856.1	6883	3	311	89	89	HSAMB82	pSportl
2607	HWLWE05R	ribosomal protein L21 [Homo sapiens] >gb AAA85655.1 ribosomal protein L21 [Homo sapiens] >pir S55913 S55913 ribosomal protein L21, cytosolic - human >sp P46778 RL21_HUMAN 60S RIBOSOMAL PROTEIN L21. {SUB 2-160} >dbj BAA25835.1 (AB007176) ribosomal protei	emb CAA6158.2.1	6884	18	323	76	76	HWLWE05	pSportl
2608	HWLRB68R	ribosomal protein L23a [Homo sapiens] >gb AAA35681.1 homology to rat ribosomal protein L23 [Homo sapiens] {SUB 10-156} Length = 156	gb AAA03341.1	6885	1	465	100	100	HWLRB68	pSportl
2609	HWLMB86R	ribosomal protein L27 [Homo sapiens] >gb AAC15857.1 ribosomal protein L27 [Homo sapiens] >emb CAA30313.1 ribosomal protein L27 (AA 1 - 136) [Rattus norvegicus] >gb AAF25951.1 AF214527_1 (AF214527) ribosomal protein L27 [Mus musculus] >emb CAA40181.1 ri	gb AAA19815.1	6886	39	149	85	85	HWLMB86	pSportl

2610	HWLQB60R	ribosomal protein L28 [Mus musculus] >pir 48738 48738 ribosomal protein L28 - mouse >sp P41105 RL28_MOUSE 60S RIBOSOMAL PROTEIN L28. {SUB 2-137} Length = 137	emb CAA5284 8.1	6887	2	430	100	100	HWLQB60	pSport1
2611	HAIDT43R			6888	3	140			HAIDT43	Uni-ZAP XR
2612	H2LAU86R	ribosomal protein L34 [Homo sapiens] >pir 68524 68524 ribosomal protein L34 - human >sp P49207 RL34_HUMAN 60S RIBOSOMAL PROTEIN L34. {SUB 2-117} Length = 117	gb AAC41916. 1	6889	1	477	98	99	H2LAU86	pBluescript SK-
2613	HCQDU05R	(AF013215) ribosomal protein S2 [Bos taurus] >sp O18789 RS2_BOVIN 40S RIBOSOMAL PROTEIN S2 (FRAGMENT). Length = 286	gb AAB65437. 1	6890	3	197	96	96	HCQDU05	Lambda ZAP II
2614	HCRPM16R	ribosomal protein S26 [Homo sapiens] >dbj BAA25824.1 (AB007161) ribosomal protein S26 [Homo sapiens] {SUB 62-106} >emb CAA55818.1 ribosomal protein S26 [Homo sapiens] {SUB 1-20} >dbj BAA25823.1 (AB007160) ribosomal protein S26 [Homo sapiens] {SUB 38-60}	emb CAA4934 5.1	6891	3	362	100	100	HCRPM16	pSport1
2615	HWLQA31R	ribosomal protein S29 [Bos taurus] >gb AA85661.1 ribosomal protein S29 [Homo sapiens] >gb AAB27426.1 homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >emb CAA41778.1 ribosomal protein S29 [Rattus norvegicus] >gb AAB27429.1 S29	gb AAB06757. 1	6892	1	240	87	90	HWLQA31	pSport1

2616	HFVKA92R	ribosomal protein S6 [Homo sapiens] >emb CAA47719.1 ribosomal protein S6 [Homo sapiens] >gb AAA42079.1 ribosomal protein S6 [Rattus norvegicus] >emb CAA68430.1 ribosomal protein S6 [Mus musculus] >emb CAA90936.1 rpS6 [Mus musculus] >pir JC1394 R3HU6 r	gb AAA60289.1	6893	3	257	83	87	HFVKA92	pBluescript
2617	HKLSA82R	Rieske Fe-S protein [Homo sapiens] >sp P47985 UCRI_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR (EC 1.10.2.2) (RIESKE IRON-SULFUR PROTEIN) (RISP). Length = 274	gb AAC41754.1	6894	3	296	67	70	HKLSA82	pBluescript
2618	HKLSA88R	replication protein A complex 34 kd subunit homolog Rpa4 [Homo sapiens] >sp AAB08488 AAB08488 Replication protein A complex 34 kd subunit homolog Rpa4. Length = 261	gb AAB08488.2	6895	127	246	100	100	HKLSA88	pBluescript
2619	HWLNK27R	S-lac lectin [Homo sapiens] >gb AAA59513.1 S-lac lectin [Homo sapiens] >emb CAB42834.1 (AL022315) dJ117715.3 (Lectin, Galactose-binding, soluble, 2 (Galactin 2, S-Lac Lectin 2, HL14)) [Homo sapiens] >pir A38140 A38140 galectin 2 - human >sp P05162 LEG2_	gb AAA59512.1	6896	34	345	84	85	HWLNK27	pSport1
2620	HCRNT24R	S100P calcium-binding protein [Homo sapiens] >pir S24146 S24146 S-100 protein P - human >sp P25815 S10E_HUMAN S-100P PROTEIN. Length = 95	emb CAA4656.6.1	6897	27	299	81	81	HCRNT24	pSport1
2621	HCQAW95R	similar to product encoded by GenBank Accession number S62516 [Rattus norvegicus] >sp Q62742 Q62742 SA (FRAGMENT). Length = 106	gb AAA95995.1	6898	1	474	85	94	HCQAW95	Lambda ZAP II
2622	HWLMP89R	sarcolemmal associated protein-2 [Oryctolagus cuniculus] >sp Q28622 Q28622 SARCOLEMMA ASSOCIATED PROTEIN-2. Length = 402	gb AAA65596.1	6899	2	328	82	84	HWLMP89	pSport1

2623	HWLVA90R	SB beta-chain (1 is 2nd base in codon) [Homo sapiens] >sp Q14465 Q14465 SB BETA-CHAIN (CLONE PII-BETA-7) (FRAGMENT). >gb AAA36311.1 MHC HLA-SB beta chain [Homo sapiens] {SUB 48-234} >gb AAA59746.1 MHC DP-beta, allele DPB7 [Homo sapiens] {SUB 1-87} Length	emb CAA25210.1	6900	3	278	86	94	HWLVA90	pSport1
2624	HKCSI14R	secretory protein [Homo sapiens] >gb AAA83628.1 intestinal trefoil factor [Homo sapiens] >pir A48284 A48284 intestinal trefoil factor 3 precursor - human >sp Q07654 ITF_HUMAN INTESTINAL TREFOIL FACTOR PRECURSOR (HP1.B). Length = 80	gb AAA59981.1	6901	3	95	96	96	HKCSI14	pBluescript
2625	HFCE53R			6902	1	165			HFCE53	Uni-ZAP XR
2626	HCQCQ84R	serine protease [Homo sapiens] >sp O15393 TMS2_HUMAN TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-). Length = 492	gb AAC51784.1	6903	3	404	94	94	HCQCQ84	Lambda ZAP II
2627	HWLMV10R	serine/threonine protein kinase [Homo sapiens] >pir S32831 S32831 serine/threonine-specific protein kinase PCTAIRE-3 (EC 2.7.1.-) - human (fragment) >sp Q07002 KPT3_HUMAN SERINE/THREONINE PROTEIN KINASE PCTAIRE-3 (EC 2.7.1.-) (FRAGMENT). Length = 380	emb CAA47005.1	6904	3	155	78	78	HWLMV10	pSport1
2628	HWMB92R	integrin binding protein kinase [Mus musculus] >sp O55222 O55222 INTEGRIN LINKED KINASE (INTEGRIN BINDING PROTEIN KINASE). Length = 452	gb AAB94646.1	6905	2	268	96	96	HWMB92	pSport1

2629	HBJMM52R	seryl-tRNA synthetase [Homo sapiens] >pir G01026 G01026 serine--tRNA ligase (EC 6.1.1.11) - human >sp P49591 SYS_HUMAN SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (SERRS). >pir S00490 S00490 RNA-binding protein, 62K - rabbit (fragment) {SUB	emb CAA6263 5.1	6906	1	333	73	74	HBJMM52	Uni-ZAP XR
2630	HCROZ52R			6907	2	115			HCROZ52	pSportl
2631	HWLQQ35R	similar to human DNA-binding protein 5. [Homo sapiens] >sp Q14673 Q14673 KIAA0164 PROTEIN. .1 Length = 920	dbj BAA11481 .1	6908	3	413	75	76	HWLQQ35	pSportl
2632	HHMMF20R			6909	3	101			HHMMF20	pSportl
2633	HHEUW25R	similar to mouse Int-6 [Homo sapiens] >gb AAB8873.1 Int-6 [Homo sapiens] >gb AAC51760.1 eIF3-p48 [Homo sapiens] >gb AAC51919.1 mammary tumor-associated protein INT6 [Homo sapiens] >sp Q64252 F36_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT	gb AAB58251. 1	6910	1	336	98	98	HHEUW25	pCMVSPORT 3.0
2634	HCRNZ02R	sodium channel 2 [Homo sapiens] >sp P78349 P78349 SODIUM CHANNEL 2. Length = 528	gb AAB48981. 1	6911	3	344	89	91	HCRNZ02	pSportl
2635	HCQDT79R	Son of sevenless 1 [Rattus norvegicus] >sp Q9Z111 Q9Z111 SON OF SEVENLESS 1 (FRAGMENT). Length = 204	dbj BAA74949 .1	6912	119	361	84	92	HCQDT79	Lambda ZAP II
2636	HCQDL92R			6913	3	152			HCQDL92	Lambda ZAP II
2637	HWLVG33R	splicing factor [Homo sapiens] >emb CAA53512.1 gClq-R [Homo sapiens] >pir J0762 J0762 pre-mRNA splicing factor SF2 P32 chain precursor - human >sp Q07021 MA32_HUMAN COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN, MITOCHONDRIAL PRECURSOR (GLYCOP	gb AAA16315. 1	6914	3	377	67	68	HWLVG33	pSportl

2638	HCROO13R	(AF164515) Cps7G [Streptococcus suis] >sp AAF18954 AAF18954 Cps7G. Length = 404	gb AAF18954.1 AF1645	6915	2	373	51	72	HCROO13	pSport1
2639	HCQDW65R	(AK001659) unnamed protein product [Homo sapiens] Length = 359	dbj BAA91818.1	6916	40	408	92	93	HCQDW65	Lambda ZAP II
2640	HCQCV70R	(AB012910) anti-HBsAg immunoglobulin Fab kappa chain [Homo sapiens] Length = 214	dbj BAA33580.1	6917	1	162	81	91	HCQCV70	Lambda ZAP II
2641	HCQDN27R	TAFII31 [Homo sapiens] >gb AAA91318.1 TBP-associated factor TAFII31 [Homo sapiens] >gb AAC50153.1 TAFII32 precursor [Homo sapiens] >pir 39141 39141 transcription factor TFIID 32K chain TAFII32 - human >sp Q16594 T2D7_HUMAN TRANSCRIPTION INITIATION FAC	gb AAA84389.1	6918	143	448	91	93	HCQDN27	Lambda ZAP II
2642	HCQC192R	ribosomal protein L3 [Homo sapiens] >emb CAA18450.1 (AL022326) dJ333H23.1 (60S Ribosomal Protein L3) [Homo sapiens] >pir S34195 S34195 ribosomal protein L3, cytosolic - human >sp P39023 RL3_HUMAN 60S RIBOSOMAL PROTEIN L3 (HIV-1 TAR RNA BINDING PROTEIN B)	emb CAA5183.9.1	6919	2	220	90	91	HCQC192	Lambda ZAP II
2643	HCRMP36RA	tenascin [Homo sapiens] Length = 2199	emb CAA3962.8.1	6920	3	353	95	98	HCRMP36	pSport1
2644	HCROV67R	tenascin [Gallus gallus] >pir S27939 S27939 tensin - chicken Length = 1733	gb AAA49087.1	6921	5	397	55	62	HCROV67	pSport1
2645	HCROT79R	tesmin [Homo sapiens] >sp Q9Y4I5 Q9Y4I5 TESMIN. Length = 299	gb AAD24668.1 U86074	6922	2	160	100	100	HCROT79	pSport1
2646	H2CAA07R	(AJ012449) NS1-binding protein [Homo sapiens] >sp Q9Y480 Q9Y480 NS1-BINDING PROTEIN. Length = 619	emb CAA1002.9.1	6923	1	360	35	57	H2CAA07	pBluescript SK-
2647	H2LAD20R	The KIAA0146 gene product is novel. [Homo sapiens] >sp Q14159 Q14159 KIAA0146 PROTEIN (FRAGMENT). Length = 918	dbj BAA09767.1	6924	130	258	57	67	H2LAD20	pBluescript SK-

2648	HWLQZ32R	threonyl-tRNA synthetase [Homo sapiens] >pir A38867 YSHUT threonine--tRNA ligase (EC 6.1.1.3) - human >sp P26639 SYTC_HUMAN THREONYL-tRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE-- TRNA LIGASE) (THRS). Length = 712	gb AAB04939.1	6925	28	405	61	61	HWLQZ32	pSport1
2649	HKAOU89R	tissue factor precursor [Homo sapiens] Length = 295	gb AAA61151.1	6926	29	280	70	70	HKAOU89	pCMVSPORT 2.0
2650	HWLUO92R	tissue-specific secretory protein [synthetic construct] >emb CAA47928.1 orf [Homo sapiens] >gb AAA67077.1 epididymal secretory protein precursor [Pan troglodytes] >emb CAA55013.1 epididymal secretory protein 14.6 [Macaca fascicularis] >pir I53929 I5392	emb CAA0143.1	6927	2	112	97	97	HWLUO92	pSport1
2651	HCROW19R	HNF-1 peptides [Rattus norvegicus] Length = 464	emb CAA3738.7.1	6928	1	147	90	90	HCROW19	pSport1
2652	HCRQK79R	transcription factor Sp-1 [Homo sapiens] >pir A29635 A29635 transcription factor Sp1 - human (fragment) >sp P08047 SP1_HUMAN TRANSCRIPTION FACTOR SP1 (FRAGMENT). Length = 696	gb AAA61154.1	6929	1	258	82	82	HCRQK79	pSport1
2653	HCQAD53R			6930	257	96			HCQAD53	Lambda ZAP II
2654	HKCUD58R	trypsinogen IV b-form [Homo sapiens] >sp Q15665 Q15665 TRYPSINOGEN IV B-FORM. Length = 259	emb CAA5048.4.1	6931	45	323	80	81	HKCUD58	pBluescript
2655	HCRNR93R	TSC-22 [Homo sapiens] >emb CAA10951.1 (AJ222700) TSC-22 [Homo sapiens] >gb AAC50566.1 TSC-22 protein [Homo sapiens] >pir JC4813 JC4813 TGF beta-stimulated clone-22 protein - human >sp Q15714 TS22_HUMAN PUTATIVE REGULATORY PROTEIN TSC-22 (TGFB STIMULATED	dbj BAA07598.1	6932	2	334	82	82	HCRNR93	pSport1

2656	HWLQH13R	protein tyrosine phosphatase (EC 3.1.3.48) [Homo sapiens] >pir A36065 A36065 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type alpha precursor - human Length = 802	gb AAA36528.1	6933	2	487	100	100	HWLQH13	pSport1
2657	H2CBQ60R	ubiquitin conjugating enzyme [Homo sapiens] >emb CAA05359.1 (AJ002385) ubiquitin-conjugating enzyme, UBC9 [Homo sapiens] >emb CAA65287.1 ubiquitin conjugating enzyme [Homo sapiens] >gb AAA86662.1 ubiquitin-conjugating enzyme [Homo sapiens] >gb AAB02181	dbj BAA08091.1	6934	211	495	98	98	H2CBQ60	pBluescript SK-
2658	H2LAW43R	ubiquitin-conjugating enzyme [Mus musculus] >pir T31067 T31067 BIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse >sp O88738 O88738 UBIQUITIN-CONJUGATING ENZYME. Length = 4845	emb CAA7672.0.1	6935	3	584	88	93	H2LAW43	pBluescript SK-
2659	HWLVJ22R	(AB032025) ubiquitin [Canis familiaris] >dbj BAA89414.1 (AB036698) ubiquitin [Felis catus] >gb AAB52914.1 ubiquitin/ribosomal fusion protein [Sus scrofa] >emb CAA40313.1 ubiquitin-52 amino acid fusion protein [Homo sapiens] >emb CAA40312.1 ubiquitin-5	dbj BAA83996.1	6936	2	259	100	100	HWLVJ22	pSport1
2660	HWLRQ77R	UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase [Homo sapiens] >pir I37405 I37405 polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - human >sp Q10471 Q10471 POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACET	emb CAA5938.1.1	6937	3	596	98	99	HWLRQ77	pSport1
2661	H2CAA28R			6938	2	256			H2CAA28	pBluescript SK-
2662	H2CAA36R			6939	2	109			H2CAA36	pBluescript SK-
2663	H2CBF10R			6940	209	352			H2CBF10	pBluescript SK-

2664	H2CBG84R				6941	157	315				H2CBG84	pBluescript SK-
2665	H2CBJ35R				6942	1	366				H2CBJ35	pBluescript SK-
2666	H2CBJ62R				6943	94	252				H2CBJ62	pBluescript SK-
2667	H2CBK71R				6944	275	466				H2CBK71	pBluescript SK-
2668	H2CBN87R				6945	176	310				H2CBN87	pBluescript SK-
2669	H2CBP73R				6946	28	282				H2CBP73	pBluescript SK-
2670	H2CBS94R				6947	2	172				H2CBS94	pBluescript SK-
2671	H2CBV19R				6948	189	413				H2CBV19	pBluescript SK-
2672	H2CBV81R				6949	3	185				H2CBV81	pBluescript SK-
2673	H2CBW73RB	(AF080171) zinc finger protein ZNF232 [Homo sapiens] >sp AAD46135 AAD46135 Zinc finger protein ZNF232. Length = 417		gb AAD46135.1	6950	84	365	100	100		H2CBW73	pBluescript SK-
2674	H2LAD79R				6951	13	231				H2LAD79	pBluescript SK-
2675	H2LAJ28RB				6952	23	370				H2LAJ28	pBluescript SK-
2676	H2LAZ29R				6953	134	409				H2LAZ29	pBluescript SK-
2677	H2LAZ92R				6954	71	355				H2LAZ92	pBluescript SK-
2678	H2LBA33R				6955	108	326				H2LBA33	pBluescript SK-
2679	H2LBB20R	(AB032952) KIAA1126 protein [Homo sapiens] >sp BAA86440 BAA86440 KIAA1126 protein (fragment). Length = 618		dbj BAA86440.1	6956	2	343	100	100		H2LBB20	pBluescript SK-
2680	HAAAJ56R				6957	1	78				HAAAJ56	pSport1

2681	HADTN09R				6958	4	87			HADTN09	pBluescript
2682	HAUBK53R				6959	1	219			HAUBK53	Uni-ZAP XR
2683	HBAHC91R				6960	1	147			HBAHC91	pSport1
2684	HBMCP86R				6961	62	280			HBMCP86	pBluescript
2685	HCEOM04R				6962	142	393			HCEOM04	Uni-ZAP XR
2686	HCFOE14R				6963	111	320			HCFOE14	pSport1
2687	HCHOX67R				6964	66	287			HCHOX67	pSport1
2688	HCQAB27R				6965	127	240			HCQAB27	Lambda ZAP II
2689	HCQAB42R				6966	1	93			HCQAB42	Lambda ZAP II
2690	HCQAB43R				6967	186	422			HCQAB43	Lambda ZAP II
2691	HCQAB44R				6968	130	474			HCQAB44	Lambda ZAP II
2692	HCQAB53R				6969	97	285			HCQAB53	Lambda ZAP II
2693	HCQAC03R				6970	49	345			HCQAC03	Lambda ZAP II
2694	HCQAC24R				6971	228	437			HCQAC24	Lambda ZAP II
2695	HCQAC80R				6972	3	179			HCQAC80	Lambda ZAP II
2696	HCQAD19R				6973	21	197			HCQAD19	Lambda ZAP II
2697	HCQAD25R				6974	1	138			HCQAD25	Lambda ZAP II
2698	HCQAD31R				6975	3	158			HCQAD31	Lambda ZAP II
2699	HCQAD62R				6976	68	319			HCQAD62	Lambda ZAP II
2700	HCQAD71R				6977	291	485			HCQAD71	Lambda ZAP II

2701	HCQAE24R				6978	312	491			HCQAE24	Lambda ZAP II
2702	HCQAE30R				6979	304	498			HCQAE30	Lambda ZAP II
2703	HCQAE32R				6980	234	437			HCQAE32	Lambda ZAP II
2704	HCQAE39R				6981	3	260			HCQAE39	Lambda ZAP II
2705	HCQAF13R				6982	125	373			HCQAF13	Lambda ZAP II
2706	HCQAF78R				6983	17	394			HCQAF78	Lambda ZAP II
2707	HCQAF94R				6984	326	499			HCQAF94	Lambda ZAP II
2708	HCQAG17R				6985	26	178			HCQAG17	Lambda ZAP II
2709	HCQAG32R				6986	243	494			HCQAG32	Lambda ZAP II
2710	HCQAG34R				6987	3	398			HCQAG34	Lambda ZAP II
2711	HCQAG93R				6988	2	193			HCQAG93	Lambda ZAP II
2712	HCQAH27R				6989	11	100			HCQAH27	Lambda ZAP II
2713	HCQAH33R				6990	204	494			HCQAH33	Lambda ZAP II
2714	HCQAH54R				6991	3	131			HCQAH54	Lambda ZAP II
2715	HCQAH63R				6992	324	494			HCQAH63	Lambda ZAP II
2716	HCQAH89R				6993	190	489			HCQAH89	Lambda ZAP II
2717	HCQAI15R				6994	1	207			HCQAI15	Lambda ZAP II
2718	HCQAJ29R				6995	99	287			HCQAJ29	Lambda ZAP II

2719	HCQAJ44R	(AF161451) HSPC333 [Homo sapiens] >sp AAF29011 AAF29011 HSPC333 (fragment). Length = 147	gb AAF29011.1 AF1614	6996	3	320	55	63	HCQAJ44	Lambda ZAP II
2720	HCQAJ49R			6997	45	263			HCQAJ49	Lambda ZAP II
2721	HCQAK16R	(AF147790) transmembrane mucin 12 [Homo sapiens] >sp AAD55678 AAD55678 Transmembrane mucin 12 (fragment). Length = 585	gb AAD55678.1 AF1477	6998	1	345	84	86	HCQAK16	Lambda ZAP II
2722	HCQAK17R			6999	2	241			HCQAK17	Lambda ZAP II
2723	HCQAK38R			7000	70	300			HCQAK38	Lambda ZAP II
2724	HCQAL71R			7001	201	299			HCQAL71	Lambda ZAP II
2725	HCQAL81R			7002	139	300			HCQAL81	Lambda ZAP II
2726	HCQAM32R			7003	3	203			HCQAM32	Lambda ZAP II
2727	HCQAM57R			7004	170	334			HCQAM57	Lambda ZAP II
2728	HCQAM70R			7005	175	384			HCQAM70	Lambda ZAP II
2729	HCQAM78R			7006	62	247			HCQAM78	Lambda ZAP II
2730	HCQAN20R			7007	181	306			HCQAN20	Lambda ZAP II
2731	HCQAN43R			7008	134	358			HCQAN43	Lambda ZAP II
2732	HCQAN44R			7009	166	342			HCQAN44	Lambda ZAP II
2733	HCQAN53R			7010	1	258			HCQAN53	Lambda ZAP II
2734	HCQAN74R			7011	1	345			HCQAN74	Lambda ZAP II

2735	HCQAN95R				7012	208	501			HCQAN95	Lambda ZAP II
2736	HCQAQ35R				7013	3	74			HCQAQ35	Lambda ZAP II
2737	HCQAQ94R				7014	2	82			HCQAQ94	Lambda ZAP II
2738	HCQAR19R				7015	1	54			HCQAR19	Lambda ZAP II
2739	HCQAR63R				7016	271	468			HCQAR63	Lambda ZAP II
2740	HCQAR70R				7017	258	395			HCQAR70	Lambda ZAP II
2741	HCQAR86R				7018	307	405			HCQAR86	Lambda ZAP II
2742	HCQAS25R				7019	1	84			HCQAS25	Lambda ZAP II
2743	HCQAS32R				7020	1	93			HCQAS32	Lambda ZAP II
2744	HCQAS58R				7021	1	75			HCQAS58	Lambda ZAP II
2745	HCQAS60R				7022	3	224			HCQAS60	Lambda ZAP II
2746	HCQAS89R				7023	230	361			HCQAS89	Lambda ZAP II
2747	HCQAT10R				7024	1	51			HCQAT10	Lambda ZAP II
2748	HCQAT12R				7025	56	157			HCQAT12	Lambda ZAP II
2749	HCQAT52R				7026	128	280			HCQAT52	Lambda ZAP II
2750	HCQAT57R				7027	97	258			HCQAT57	Lambda ZAP II
2751	HCQAT94R				7028	136	234			HCQAT94	Lambda ZAP II
2752	HCQAV18R				7029	2	235			HCQAV18	Lambda ZAP II

2753	HCQAV23R			7030	55	255				HCQAV23	Lambda ZAP II
2754	HCQAV58R			7031	3	77				HCQAV58	Lambda ZAP II
2755	HCQAV66R			7032	1	96				HCQAV66	Lambda ZAP II
2756	HCQAV73R			7033	2	148				HCQAV73	Lambda ZAP II
2757	HCQAW23R			7034	1	51				HCQAW23	Lambda ZAP II
2758	HCQAW26R			7035	2	70				HCQAW26	Lambda ZAP II
2759	HCQAW40R			7036	3	227				HCQAW40	Lambda ZAP II
2760	HCQAW67R			7037	3	266				HCQAW67	Lambda ZAP II
2761	HCQBA47R			7038	1	144				HCQBA47	Lambda ZAP II
2762	HCQBA89R			7039	85	381				HCQBA89	Lambda ZAP II
2763	HCQBD01R			7040	65	253				HCQBD01	Lambda ZAP II
2764	HCQBE07R			7041	1	51				HCQBE07	Lambda ZAP II
2765	HCQBE13R			7042	2	115				HCQBE13	Lambda ZAP II
2766	HCQBE19R			7043	82	288				HCQBE19	Lambda ZAP II
2767	HCQBE53R			7044	2	166				HCQBE53	Lambda ZAP II
2768	HCQBE55R			7045	266	403				HCQBE55	Lambda ZAP II
2769	HCQBH24R			7046	106	285				HCQBH24	Lambda ZAP II
2770	HCQBH79R			7047	46	261				HCQBH79	Lambda ZAP II

2771	HCQBL10R				7048	192	314		HCQBL10	Lambda ZAP II
2772	HCQBL61R				7049	174	353		HCQBL61	Lambda ZAP II
2773	HCQBM04R				7050	2	121		HCQBM04	Lambda ZAP II
2774	HCQBM11R				7051	108	302		HCQBM11	Lambda ZAP II
2775	HCQBM58R				7052	91	240		HCQBM58	Lambda ZAP II
2776	HCQBN06RA				7053	61	162		HCQBN06	Lambda ZAP II
2777	HCQBN15RA				7054	2	160		HCQBN15	Lambda ZAP II
2778	HCQBN27RA				7055	23	157		HCQBN27	Lambda ZAP II
2779	HCQBN52R				7056	3	62		HCQBN52	Lambda ZAP II
2780	HCQBN57RA				7057	2	310		HCQBN57	Lambda ZAP II
2781	HCQBN65R				7058	1	93		HCQBN65	Lambda ZAP II
2782	HCQBN81RA				7059	2	334		HCQBN81	Lambda ZAP II
2783	HCQCA12R				7060	1	111		HCQCA12	Lambda ZAP II
2784	HCQCA17R				7061	204	437		HCQCA17	Lambda ZAP II
2785	HCQCA21R				7062	1	72		HCQCA21	Lambda ZAP II
2786	HCQCA27R				7063	26	286		HCQCA27	Lambda ZAP II
2787	HCQCB64R				7064	243	494		HCQCB64	Lambda ZAP II
2788	HCQCB78R				7065	2	154		HCQCB78	Lambda ZAP II

2789	HCQCB91R				7066	1	99			HCQCB91	Lambda ZAP II
2790	HCQCC50R				7067	2	115			HCQCC50	Lambda ZAP II
2791	HCQCC51R				7068	2	115			HCQCC51	Lambda ZAP II
2792	HCQCC72R				7069	192	416			HCQCC72	Lambda ZAP II
2793	HCQCC88R				7070	35	196			HCQCC88	Lambda ZAP II
2794	HCQCC93R				7071	139	240			HCQCC93	Lambda ZAP II
2795	HCQCD10R				7072	84	437			HCQCD10	Lambda ZAP II
2796	HCQCD46R				7073	211	384			HCQCD46	Lambda ZAP II
2797	HCQCE19R				7074	43	447			HCQCE19	Lambda ZAP II
2798	HCQCE22R				7075	93	446			HCQCE22	Lambda ZAP II
2799	HCQCE28R				7076	1	123			HCQCE28	Lambda ZAP II
2800	HCQCE32R				7077	1	192			HCQCE32	Lambda ZAP II
2801	HCQCE42R				7078	2	103			HCQCE42	Lambda ZAP II
2802	HCQCE46R				7079	2	199			HCQCE46	Lambda ZAP II
2803	HCQCE59R				7080	1	231			HCQCE59	Lambda ZAP II
2804	HCQCE68R				7081	263	427			HCQCE68	Lambda ZAP II
2805	HCQCE72R				7082	1	453			HCQCE72	Lambda ZAP II
2806	HCQCE79R				7083	2	139			HCQCE79	Lambda ZAP II

2807	HCQCE80R				7084	2	76				HCQCE80	Lambda ZAP II
2808	HCQCE83R				7085	2	139				HCQCE83	Lambda ZAP II
2809	HCQCE92R				7086	1	75				HCQCE92	Lambda ZAP II
2810	HCQCE95R				7087	2	349				HCQCE95	Lambda ZAP II
2811	HCQCE96R				7088	48	437				HCQCE96	Lambda ZAP II
2812	HCQCF26R				7089	3	224				HCQCF26	Lambda ZAP II
2813	HCQCF39R				7090	2	52				HCQCF39	Lambda ZAP II
2814	HCQCF74R				7091	2	97				HCQCF74	Lambda ZAP II
2815	HCQCF77R				7092	261	506				HCQCF77	Lambda ZAP II
2816	HCQCF80R				7093	1	117				HCQCF80	Lambda ZAP II
2817	HCQCF82R				7094	57	269				HCQCF82	Lambda ZAP II
2818	HCQCF88R				7095	1	168				HCQCF88	Lambda ZAP II
2819	HCQCG14R				7096	1	111				HCQCG14	Lambda ZAP II
2820	HCQCG19R				7097	1	123				HCQCG19	Lambda ZAP II
2821	HCQCG42R				7098	1	105				HCQCG42	Lambda ZAP II
2822	HCQCG49R				7099	2	130				HCQCG49	Lambda ZAP II
2823	HCQCG56R				7100	1	99				HCQCG56	Lambda ZAP II
2824	HCQCG74R				7101	1	69				HCQCG74	Lambda ZAP II

2825	HCQCH01R			7102	2	82			HCQCH01	Lambda ZAP II
2826	HCQCH03R			7103	41	295			HCQCH03	Lambda ZAP II
2827	HCQCH16R			7104	26	235			HCQCH16	Lambda ZAP II
2828	HCQCH30R			7105	1	111			HCQCH30	Lambda ZAP II
2829	HCQCH32R			7106	1	282			HCQCH32	Lambda ZAP II
2830	HCQCH33R			7107	2	100			HCQCH33	Lambda ZAP II
2831	HCQCH47R			7108	3	239			HCQCH47	Lambda ZAP II
2832	HCQCH61R			7109	3	83			HCQCH61	Lambda ZAP II
2833	HCQCH69R			7110	1	129			HCQCH69	Lambda ZAP II
2834	HCQCH83R			7111	3	98			HCQCH83	Lambda ZAP II
2835	HCQCI18R			7112	103	309			HCQCI18	Lambda ZAP II
2836	HCQCI28R			7113	1	102			HCQCI28	Lambda ZAP II
2837	HCQCI42R			7114	1	231			HCQCI42	Lambda ZAP II
2838	HCQCI57R			7115	1	96			HCQCI57	Lambda ZAP II
2839	HCQCI63R			7116	76	213			HCQCI63	Lambda ZAP II
2840	HCQCI64R			7117	120	302			HCQCI64	Lambda ZAP II
2841	HCQCI69R			7118	1	96			HCQCI69	Lambda ZAP II
2842	HCQCI75R			7119	1	60			HCQCI75	Lambda ZAP II

2843	HCQCJ89R				7120	166	360			HCQCJ89	Lambda ZAP II
2844	HCQCJ11R				7121	3	176			HCQCJ11	Lambda ZAP II
2845	HCQCJ21R				7122	1	111			HCQCJ21	Lambda ZAP II
2846	HCQCJ25R				7123	60	173			HCQCJ25	Lambda ZAP II
2847	HCQCJ34R				7124	1	99			HCQCJ34	Lambda ZAP II
2848	HCQCJ38R				7125	41	313			HCQCJ38	Lambda ZAP II
2849	HCQCJ42R				7126	43	234			HCQCJ42	Lambda ZAP II
2850	HCQCJ45R				7127	7	75			HCQCJ45	Lambda ZAP II
2851	HCQCJ50R				7128	1	99			HCQCJ50	Lambda ZAP II
2852	HCQCJ51R				7129	3	116			HCQCJ51	Lambda ZAP II
2853	HCQCJ68R				7130	1	99			HCQCJ68	Lambda ZAP II
2854	HCQCJ76R				7131	1	48			HCQCJ76	Lambda ZAP II
2855	HCQCJ77R				7132	2	130			HCQCJ77	Lambda ZAP II
2856	HCQCJ85R				7133	1	129			HCQCJ85	Lambda ZAP II
2857	HCQCJ89R				7134	182	415			HCQCJ89	Lambda ZAP II
2858	HCQCJ94R				7135	46	207			HCQCJ94	Lambda ZAP II
2859	HCQCK03R				7136	2	103			HCQCK03	Lambda ZAP II
2860	HCQCK17R				7137	1	246			HCQCK17	Lambda ZAP II

2861	HCQCK25R			7138	1	159			HCQCK25	Lambda ZAP II
2862	HCQCK34R			7139	1	114			HCQCK34	Lambda ZAP II
2863	HCQCK39R			7140	3	140			HCQCK39	Lambda ZAP II
2864	HCQCK50R			7141	2	103			HCQCK50	Lambda ZAP II
2865	HCQCK54R			7142	1	99			HCQCK54	Lambda ZAP II
2866	HCQCK58R			7143	2	121			HCQCK58	Lambda ZAP II
2867	HCQCK59R			7144	119	280			HCQCK59	Lambda ZAP II
2868	HCQCK81R			7145	153	380			HCQCK81	Lambda ZAP II
2869	HCQCK90R			7146	22	201			HCQCK90	Lambda ZAP II
2870	HCQCL01R			7147	143	445			HCQCL01	Lambda ZAP II
2871	HCQCL05R			7148	91	252			HCQCL05	Lambda ZAP II
2872	HCQCL07R			7149	3	68			HCQCL07	Lambda ZAP II
2873	HCQCL11R			7150	1	102			HCQCL11	Lambda ZAP II
2874	HCQCL14R			7151	2	229			HCQCL14	Lambda ZAP II
2875	HCQCL19R			7152	3	104			HCQCL19	Lambda ZAP II
2876	HCQCL20R			7153	8	187			HCQCL20	Lambda ZAP II
2877	HCQCL22R			7154	142	279			HCQCL22	Lambda ZAP II
2878	HCQCL30R			7155	27	101			HCQCL30	Lambda ZAP II

2879	HCQCL35R				7156	1	102				HCQCL35	Lambda ZAP II
2880	HCQCL43R				7157	1	237				HCQCL43	Lambda ZAP II
2881	HCQCL46R				7158	1	69				HCQCL46	Lambda ZAP II
2882	HCQCL48R				7159	57	251				HCQCL48	Lambda ZAP II
2883	HCQCL51R				7160	2	100				HCQCL51	Lambda ZAP II
2884	HCQCL54R				7161	17	133				HCQCL54	Lambda ZAP II
2885	HCQCL55R				7162	2	100				HCQCL55	Lambda ZAP II
2886	HCQCL63R				7163	2	253				HCQCL63	Lambda ZAP II
2887	HCQCL64R				7164	1	144				HCQCL64	Lambda ZAP II
2888	HCQCL65R				7165	2	280				HCQCL65	Lambda ZAP II
2889	HCQCL66R				7166	1	231				HCQCL66	Lambda ZAP II
2890	HCQCL69R				7167	3	155				HCQCL69	Lambda ZAP II
2891	HCQCL73R				7168	110	214				HCQCL73	Lambda ZAP II
2892	HCQCL78R				7169	151	330				HCQCL78	Lambda ZAP II
2893	HCQCL79R				7170	34	177				HCQCL79	Lambda ZAP II
2894	HCQCL90R				7171	3	278				HCQCL90	Lambda ZAP II
2895	HCQCL92R				7172	6	134				HCQCL92	Lambda ZAP II
2896	HCQCM69R				7173	172	387				HCQCM69	Lambda ZAP II

2897	HCQCO30R			7174	2	193				HCQCO30	Lambda ZAP II
2898	HCQCO53R			7175	122	388				HCQCO53	Lambda ZAP II
2899	HCQCO57R			7176	82	273				HCQCO57	Lambda ZAP II
2900	HCQCO66R			7177	1	162				HCQCO66	Lambda ZAP II
2901	HCQCO79R			7178	29	151				HCQCO79	Lambda ZAP II
2902	HCQCO85R			7179	2	139				HCQCO85	Lambda ZAP II
2903	HCQCP08R			7180	3	338				HCQCP08	Lambda ZAP II
2904	HCQCP14R			7181	108	296				HCQCP14	Lambda ZAP II
2905	HCQCP15R			7182	2	55				HCQCP15	Lambda ZAP II
2906	HCQCP19R			7183	15	128				HCQCP19	Lambda ZAP II
2907	HCQCP23R			7184	1	105				HCQCP23	Lambda ZAP II
2908	HCQCP27R			7185	213	365				HCQCP27	Lambda ZAP II
2909	HCQCP30R			7186	102	200				HCQCP30	Lambda ZAP II
2910	HCQCP35R			7187	3	62				HCQCP35	Lambda ZAP II
2911	HCQCP42R			7188	1	48				HCQCP42	Lambda ZAP II
2912	HCQCP58R			7189	1	180				HCQCP58	Lambda ZAP II
2913	HCQCP75R			7190	1	72				HCQCP75	Lambda ZAP II
2914	HCQCP79R			7191	1	108				HCQCP79	Lambda ZAP II

2915	HCQCP86R			7192	1	99			HCQCP86	Lambda ZAP II
2916	HCQCP89R			7193	2	166			HCQCP89	Lambda ZAP II
2917	HCQCCQ09R			7194	300	575			HCQCCQ09	Lambda ZAP II
2918	HCQCCQ17R			7195	22	159			HCQCCQ17	Lambda ZAP II
2919	HCQCCQ48R			7196	1	111			HCQCCQ48	Lambda ZAP II
2920	HCQCR15R			7197	140	436			HCQCR15	Lambda ZAP II
2921	HCQCR44R			7198	173	400			HCQCR44	Lambda ZAP II
2922	HCQCR69R			7199	70	186			HCQCR69	Lambda ZAP II
2923	HCQCT38R			7200	71	184			HCQCT38	Lambda ZAP II
2924	HCQCT49R			7201	3	158			HCQCT49	Lambda ZAP II
2925	HCQCT84R			7202	1	198			HCQCT84	Lambda ZAP II
2926	HCQCT89R			7203	2	367			HCQCT89	Lambda ZAP II
2927	HCQCU08R			7204	3	122			HCQCU08	Lambda ZAP II
2928	HCQCU19R			7205	235	453			HCQCU19	Lambda ZAP II
2929	HCQCU37R			7206	2	97			HCQCU37	Lambda ZAP II
2930	HCQCU55R			7207	265	486			HCQCU55	Lambda ZAP II
2931	HCQCU57R			7208	274	456			HCQCU57	Lambda ZAP II
2932	HCQCU59R			7209	1	51			HCQCU59	Lambda ZAP II

2933	HCQCU67R				7210	1	168				HCQCU67	Lambda ZAP II
2934	HCQCU72R				7211	131	238				HCQCU72	Lambda ZAP II
2935	HCQCU73R				7212	1	99				HCQCU73	Lambda ZAP II
2936	HCQCV01R				7213	371	628				HCQCV01	Lambda ZAP II
2937	HCQCV21R				7214	1	99				HCQCV21	Lambda ZAP II
2938	HCQCV50R				7215	330	584				HCQCV50	Lambda ZAP II
2939	HCQCV68R				7216	425	625				HCQCV68	Lambda ZAP II
2940	HCQCV73R				7217	1	183				HCQCV73	Lambda ZAP II
2941	HCQCV91R				7218	84	227				HCQCV91	Lambda ZAP II
2942	HCQCX11R				7219	177	524				HCQCX11	Lambda ZAP II
2943	HCQCX18R				7220	100	264				HCQCX18	Lambda ZAP II
2944	HCQCX21R				7221	209	562				HCQCX21	Lambda ZAP II
2945	HCQCX22R				7222	2	364				HCQCX22	Lambda ZAP II
2946	HCQCX33R				7223	32	277				HCQCX33	Lambda ZAP II
2947	HCQCX57R				7224	166	399				HCQCX57	Lambda ZAP II
2948	HCQCX90R				7225	213	344				HCQCX90	Lambda ZAP II
2949	HCQDA09R				7226	346	636				HCQDA09	Lambda ZAP II
2950	HCQDA20R				7227	375	704				HCQDA20	Lambda ZAP II

2951	HCQDA28R				7228	68	349			HCQDA28	Lambda ZAP II
2952	HCQDA36R				7229	1	141			HCQDA36	Lambda ZAP II
2953	HCQDA52R				7230	1	102			HCQDA52	Lambda ZAP II
2954	HCQDA55R				7231	176	454			HCQDA55	Lambda ZAP II
2955	HCQDA66R				7232	1	252			HCQDA66	Lambda ZAP II
2956	HCQDA86R				7233	238	333			HCQDA86	Lambda ZAP II
2957	HCQDB17R				7234	2	268			HCQDB17	Lambda ZAP II
2958	HCQDB26R				7235	303	494			HCQDB26	Lambda ZAP II
2959	HCQDB29R				7236	2	148			HCQDB29	Lambda ZAP II
2960	HCQDB41R				7237	61	150			HCQDB41	Lambda ZAP II
2961	HCQDB48R				7238	282	461			HCQDB48	Lambda ZAP II
2962	HCQDB49R				7239	1	120			HCQDB49	Lambda ZAP II
2963	HCQDB52R				7240	2	373			HCQDB52	Lambda ZAP II
2964	HCQDB54R				7241	2	391			HCQDB54	Lambda ZAP II
2965	HCQDB55R				7242	126	293			HCQDB55	Lambda ZAP II
2966	HCQDB78R				7243	1	60			HCQDB78	Lambda ZAP II
2967	HCQDC02R				7244	3	185			HCQDC02	Lambda ZAP II
2968	HCQDC12R				7245	156	329			HCQDC12	Lambda ZAP II

2969	HCQDC13R			7246	45	209		HCQDC13	Lambda ZAP II
2970	HCQDC15R			7247	2	94		HCQDC15	Lambda ZAP II
2971	HCQDC28R			7248	45	155		HCQDC28	Lambda ZAP II
2972	HCQDC29R			7249	132	317		HCQDC29	Lambda ZAP II
2973	HCQDC33R			7250	17	175		HCQDC33	Lambda ZAP II
2974	HCQDC44R			7251	408	542		HCQDC44	Lambda ZAP II
2975	HCQDC63R			7252	273	509		HCQDC63	Lambda ZAP II
2976	HCQDC74R			7253	145	360		HCQDC74	Lambda ZAP II
2977	HCQDC88R			7254	303	515		HCQDC88	Lambda ZAP II
2978	HCQDD35R			7255	90	224		HCQDD35	Lambda ZAP II
2979	HCQDD65R			7256	270	617		HCQDD65	Lambda ZAP II
2980	HCQDD91R			7257	316	465		HCQDD91	Lambda ZAP II
2981	HCQDE04R			7258	24	98		HCQDE04	Lambda ZAP II
2982	HCQDE10R			7259	163	396		HCQDE10	Lambda ZAP II
2983	HCQDE20R			7260	1	99		HCQDE20	Lambda ZAP II
2984	HCQDE25R			7261	255	482		HCQDE25	Lambda ZAP II
2985	HCQDE31R			7262	1	99		HCQDE31	Lambda ZAP II
2986	HCQDE38R			7263	107	322		HCQDE38	Lambda ZAP II

2987	HCQDE45R				7264	185	340			HCQDE45	Lambda ZAP II
2988	HCQDE52R				7265	74	265			HCQDE52	Lambda ZAP II
2989	HCQDE58R				7266	1	114			HCQDE58	Lambda ZAP II
2990	HCQDE59R				7267	17	214			HCQDE59	Lambda ZAP II
2991	HCQDE61R				7268	1	198			HCQDE61	Lambda ZAP II
2992	HCQDE68R				7269	3	146			HCQDE68	Lambda ZAP II
2993	HCQDF22R				7270	2	61			HCQDF22	Lambda ZAP II
2994	HCQDF44R				7271	125	427			HCQDF44	Lambda ZAP II
2995	HCQDF51R				7272	50	127			HCQDF51	Lambda ZAP II
2996	HCQDF66R				7273	1	111			HCQDF66	Lambda ZAP II
2997	HCQDF69R				7274	2	184			HCQDF69	Lambda ZAP II
2998	HCQDF70R				7275	3	116			HCQDF70	Lambda ZAP II
2999	HCQDF79R				7276	1	129			HCQDF79	Lambda ZAP II
3000	HCQDF93R				7277	153	332			HCQDF93	Lambda ZAP II
3001	HCQDG40R				7278	79	279			HCQDG40	Lambda ZAP II
3002	HCQDG62R				7279	1	99			HCQDG62	Lambda ZAP II
3003	HCQDG71R				7280	21	92			HCQDG71	Lambda ZAP II
3004	HCQDG80R				7281	152	271			HCQDG80	Lambda ZAP II

3005	HCQDG86R				7282	1	108		HCQDG86	Lambda ZAP II
3006	HCQDH18R				7283	31	141		HCQDH18	Lambda ZAP II
3007	HCQDH41R				7284	1	57		HCQDH41	Lambda ZAP II
3008	HCQDH42R				7285	83	292		HCQDH42	Lambda ZAP II
3009	HCQDH50R				7286	150	443		HCQDH50	Lambda ZAP II
3010	HCQDH57R				7287	176	346		HCQDH57	Lambda ZAP II
3011	HCQDH60R				7288	2	124		HCQDH60	Lambda ZAP II
3012	HCQDH65R				7289	6	68		HCQDH65	Lambda ZAP II
3013	HCQDH66R				7290	1	147		HCQDH66	Lambda ZAP II
3014	HCQDH68R				7291	1	102		HCQDH68	Lambda ZAP II
3015	HCQDH78R				7292	1	102		HCQDH78	Lambda ZAP II
3016	HCQDH79R				7293	1	102		HCQDH79	Lambda ZAP II
3017	HCQDH95R				7294	2	109		HCQDH95	Lambda ZAP II
3018	HCQDI19R				7295	1	54		HCQDI19	Lambda ZAP II
3019	HCQDI42R				7296	2	229		HCQDI42	Lambda ZAP II
3020	HCQDI63R				7297	1	105		HCQDI63	Lambda ZAP II
3021	HCQDI67R				7298	290	541		HCQDI67	Lambda ZAP II
3022	HCQDI77R				7299	241	444		HCQDI77	Lambda ZAP II

3023	HCQDI78R			7300	3	140		HCQDI78	Lambda ZAP II
3024	HCQDI85R			7301	185	427		HCQDI85	Lambda ZAP II
3025	HCQDI95R			7302	117	461		HCQDI95	Lambda ZAP II
3026	HCQDI13R			7303	1	108		HCQDI13	Lambda ZAP II
3027	HCQDI19R			7304	299	544		HCQDI19	Lambda ZAP II
3028	HCQDI21R			7305	58	363		HCQDI21	Lambda ZAP II
3029	HCQDI22R			7306	1	102		HCQDI22	Lambda ZAP II
3030	HCQDI52R			7307	1	102		HCQDI52	Lambda ZAP II
3031	HCQDI68R			7308	238	543		HCQDI68	Lambda ZAP II
3032	HCQDI70R			7309	1	69		HCQDI70	Lambda ZAP II
3033	HCQDI83R			7310	1	111		HCQDI83	Lambda ZAP II
3034	HCQDI84R			7311	1	114		HCQDI84	Lambda ZAP II
3035	HCQDI91R			7312	3	182		HCQDI91	Lambda ZAP II
3036	HCQDI93R			7313	152	445		HCQDI93	Lambda ZAP II
3037	HCQDI95R			7314	93	473		HCQDI95	Lambda ZAP II
3038	HCQDK13R			7315	186	422		HCQDK13	Lambda ZAP II
3039	HCQDK19R			7316	259	393		HCQDK19	Lambda ZAP II
3040	HCQDK20R			7317	1	114		HCQDK20	Lambda ZAP II

3041	HCQDK34R				7318	3	59			HCQDK34	Lambda ZAP II
3042	HCQDK49R				7319	1	105			HCQDK49	Lambda ZAP II
3043	HCQDK50R				7320	1	153			HCQDK50	Lambda ZAP II
3044	HCQDK56R				7321	2	154			HCQDK56	Lambda ZAP II
3045	HCQDK58R				7322	14	127			HCQDK58	Lambda ZAP II
3046	HCQDK75R				7323	1	114			HCQDK75	Lambda ZAP II
3047	HCQDK89R				7324	154	360			HCQDK89	Lambda ZAP II
3048	HCQDL12R				7325	22	246			HCQDL12	Lambda ZAP II
3049	HCQDL24R				7326	3	200			HCQDL24	Lambda ZAP II
3050	HCQDL36R				7327	1	132			HCQDL36	Lambda ZAP II
3051	HCQDL43R				7328	1	114			HCQDL43	Lambda ZAP II
3052	HCQDL52R				7329	1	54			HCQDL52	Lambda ZAP II
3053	HCQDL54R				7330	2	292			HCQDL54	Lambda ZAP II
3054	HCQDL57R				7331	55	174			HCQDL57	Lambda ZAP II
3055	HCQDL93R				7332	1	99			HCQDL93	Lambda ZAP II
3056	HCQDL96R				7333	1	135			HCQDL96	Lambda ZAP II
3057	HCQDM01R				7334	3	107			HCQDM01	Lambda ZAP II
3058	HCQDM17R				7335	3	53			HCQDM17	Lambda ZAP II

3059	HCQDM49R				7336	3	146				HCQDM49	Lambda ZAP II
3060	HCQDM55R				7337	1	66				HCQDM55	Lambda ZAP II
3061	HCQDM58R				7338	1	114				HCQDM58	Lambda ZAP II
3062	HCQDN08R				7339	67	213				HCQDN08	Lambda ZAP II
3063	HCQDN32R				7340	3	56				HCQDN32	Lambda ZAP II
3064	HCQDN33R				7341	252	515				HCQDN33	Lambda ZAP II
3065	HCQDN78R				7342	1	105				HCQDN78	Lambda ZAP II
3066	HCQDO05R				7343	122	286				HCQDO05	Lambda ZAP II
3067	HCQDO07R				7344	40	171				HCQDO07	Lambda ZAP II
3068	HCQDO25R				7345	138	413				HCQDO25	Lambda ZAP II
3069	HCQDO44R				7346	69	296				HCQDO44	Lambda ZAP II
3070	HCQDO60R				7347	2	241				HCQDO60	Lambda ZAP II
3071	HCQDO75R				7348	1	63				HCQDO75	Lambda ZAP II
3072	HCQDO83R				7349	112	300				HCQDO83	Lambda ZAP II
3073	HCQDO88R				7350	82	186				HCQDO88	Lambda ZAP II
3074	HCQDP14R				7351	237	443				HCQDP14	Lambda ZAP II
3075	HCQDP18R				7352	61	240				HCQDP18	Lambda ZAP II
3076	HCQDP41R				7353	1	54				HCQDP41	Lambda ZAP II

3077	HCQDP50R				7354	1	102			HCQDP50	Lambda ZAP II
3078	HCQDP91R				7355	247	390			HCQDP91	Lambda ZAP II
3079	HCQDQ08R				7356	241	360			HCQDQ08	Lambda ZAP II
3080	HCQDQ09R				7357	269	427			HCQDQ09	Lambda ZAP II
3081	HCQDQ45R				7358	1	102			HCQDQ45	Lambda ZAP II
3082	HCQDQ80R				7359	62	283			HCQDQ80	Lambda ZAP II
3083	HCQDR04R				7360	286	516			HCQDR04	Lambda ZAP II
3084	HCQDR49R				7361	1	99			HCQDR49	Lambda ZAP II
3085	HCQDR54R				7362	86	292			HCQDR54	Lambda ZAP II
3086	HCQDR89R				7363	216	446			HCQDR89	Lambda ZAP II
3087	HCQDS01R				7364	1	300			HCQDS01	Lambda ZAP II
3088	HCQDS14R				7365	177	542			HCQDS14	Lambda ZAP II
3089	HCQDS29R				7366	3	152			HCQDS29	Lambda ZAP II
3090	HCQDS34R				7367	1	105			HCQDS34	Lambda ZAP II
3091	HCQDS40R				7368	130	360			HCQDS40	Lambda ZAP II
3092	HCQDS51R				7369	183	416			HCQDS51	Lambda ZAP II
3093	HCQDS53R				7370	348	548			HCQDS53	Lambda ZAP II
3094	HCQDS56R				7371	339	533			HCQDS56	Lambda ZAP II

3095	HCQDS61R				7372	1	300			HCQDS61	Lambda ZAP II
3096	HCQDS62R				7373	3	290			HCQDS62	Lambda ZAP II
3097	HCQDS63R				7374	388	564			HCQDS63	Lambda ZAP II
3098	HCQDS67R				7375	1	114			HCQDS67	Lambda ZAP II
3099	HCQDS83R				7376	432	590			HCQDS83	Lambda ZAP II
3100	HCQDS84R				7377	1	102			HCQDS84	Lambda ZAP II
3101	HCQDS89R				7378	1	78			HCQDS89	Lambda ZAP II
3102	HCQDT17R				7379	398	733			HCQDT17	Lambda ZAP II
3103	HCQDT48RA				7380	113	361			HCQDT48	Lambda ZAP II
3104	HCQDT63R				7381	2	61			HCQDT63	Lambda ZAP II
3105	HCQDT64R				7382	141	347			HCQDT64	Lambda ZAP II
3106	HCQDT93RA				7383	236	418			HCQDT93	Lambda ZAP II
3107	HCQDU24R				7384	31	102			HCQDU24	Lambda ZAP II
3108	HCQDU34R				7385	3	128			HCQDU34	Lambda ZAP II
3109	HCQDU59R				7386	57	194			HCQDU59	Lambda ZAP II
3110	HCQDU60R				7387	1	102			HCQDU60	Lambda ZAP II
3111	HCQDU65R				7388	2	115			HCQDU65	Lambda ZAP II
3112	HCQDU69R				7389	1	156			HCQDU69	Lambda ZAP II

3113	HCQDU94R			7390	2	76			HCQDU94	Lambda ZAP II
3114	HCQDV27R			7391	17	112			HCQDV27	Lambda ZAP II
3115	HCQDV41R			7392	1	528			HCQDV41	Lambda ZAP II
3116	HCQDV44R			7393	2	274			HCQDV44	Lambda ZAP II
3117	HCQDV49R			7394	87	419			HCQDV49	Lambda ZAP II
3118	HCQDV53R			7395	96	260			HCQDV53	Lambda ZAP II
3119	HCQDV62R			7396	43	99			HCQDV62	Lambda ZAP II
3120	HCQDV63R			7397	37	174			HCQDV63	Lambda ZAP II
3121	HCQDV64R			7398	1	102			HCQDV64	Lambda ZAP II
3122	HCQDV74R			7399	1	123			HCQDV74	Lambda ZAP II
3123	HCQDV76R			7400	1	105			HCQDV76	Lambda ZAP II
3124	HCQDV79R			7401	7	72			HCQDV79	Lambda ZAP II
3125	HCQDV83R			7402	26	238			HCQDV83	Lambda ZAP II
3126	HCQDW01R			7403	2	127			HCQDW01	Lambda ZAP II
3127	HCQDW02R			7404	3	98			HCQDW02	Lambda ZAP II
3128	HCQDW15R			7405	2	97			HCQDW15	Lambda ZAP II
3129	HCQDW30R			7406	2	100			HCQDW30	Lambda ZAP II
3130	HCQDW38R			7407	1	156			HCQDW38	Lambda ZAP II

3131	HCQDW69R				7408	22	135				HCQDW69	Lambda ZAP II
3132	HCQDW73R				7409	2	112				HCQDW73	Lambda ZAP II
3133	HCQDW77R				7410	74	409				HCQDW77	Lambda ZAP II
3134	HCQDW85R				7411	1	72				HCQDW85	Lambda ZAP II
3135	HCQDW88R				7412	30	98				HCQDW88	Lambda ZAP II
3136	HCRMA34R				7413	1	93				HCRMA34	pSportl
3137	HCRMA60R				7414	1	135				HCRMA60	pSportl
3138	HCRMA62R				7415	5	61				HCRMA62	pSportl
3139	HCRMA71R				7416	207	377				HCRMA71	pSportl
3140	HCRMB13R				7417	3	128				HCRMB13	pSportl
3141	HCRMB18R				7418	2	142				HCRMB18	pSportl
3142	HCRMB19R				7419	22	153				HCRMB19	pSportl
3143	HCRMB44R				7420	108	374				HCRMB44	pSportl
3144	HCRMB65R				7421	2	79				HCRMB65	pSportl
3145	HCRMB82R				7422	3	245				HCRMB82	pSportl
3146	HCRMB86R				7423	110	460				HCRMB86	pSportl
3147	HCRMC01R				7424	36	200				HCRMC01	pSportl
3148	HCRMC13R				7425	161	322				HCRMC13	pSportl
3149	HCRMC85R				7426	1	99				HCRMC85	pSportl
3150	HCRMD01RA				7427	2	100				HCRMD01	pSportl
3151	HCRMD24R				7428	1	234				HCRMD24	pSportl
3152	HCRMD33R				7429	148	405				HCRMD33	pSportl
3153	HCRMD57R				7430	184	435				HCRMD57	pSportl
3154	HCRMD77R				7431	3	185				HCRMD77	pSportl
3155	HCRME08R				7432	56	214				HCRME08	pSportl
3156	HCRME25R				7433	1	162				HCRME25	pSportl
3157	HCRME49R				7434	41	274				HCRME49	pSportl
3158	HCRMF03R				7435	1	111				HCRMF03	pSportl

3159	HCRMF07R			7436	1	201			HCRMF07	pSportl
3160	HCRMF23R			7437	3	98			HCRMF23	pSportl
3161	HCRMF24R			7438	75	305			HCRMF24	pSportl
3162	HCRMF33R			7439	2	106			HCRMF33	pSportl
3163	HCRMF38R			7440	50	151			HCRMF38	pSportl
3164	HCRMF47R			7441	261	473			HCRMF47	pSportl
3165	HCRMF67R			7442	2	151			HCRMF67	pSportl
3166	HCRMF72R			7443	1	195			HCRMF72	pSportl
3167	HCRMF82R			7444	16	234			HCRMF82	pSportl
3168	HCRMF84R			7445	1	213			HCRMF84	pSportl
3169	HCRMF91R			7446	2	106			HCRMF91	pSportl
3170	HCRMF93R			7447	91	375			HCRMF93	pSportl
3171	HCRMF94R			7448	1	402			HCRMF94	pSportl
3172	HCRMG20R			7449	139	255			HCRMG20	pSportl
3173	HCRMG43R			7450	1	201			HCRMG43	pSportl
3174	HCRMG80R			7451	2	466			HCRMG80	pSportl
3175	HCRMH08R			7452	1	87			HCRMH08	pSportl
3176	HCRMH75R			7453	4	84			HCRMH75	pSportl
3177	HCRMH83R			7454	17	196			HCRMH83	pSportl
3178	HCRMH94R			7455	1	99			HCRMH94	pSportl
3179	HCRMI04R			7456	197	346			HCRMI04	pSportl
3180	HCRMI33R			7457	1	144			HCRMI33	pSportl
3181	HCRMI40R			7458	229	354			HCRMI40	pSportl
3182	HCRMI47R			7459	3	62			HCRMI47	pSportl
3183	HCRMI60R			7460	2	337			HCRMI60	pSportl
3184	HCRMJ03R			7461	1	60			HCRMJ03	pSportl
3185	HCRMJ21R			7462	194	508			HCRMJ21	pSportl
3186	HCRMJ54R			7463	1	90			HCRMJ54	pSportl
3187	HCRMJ80R			7464	2	118			HCRMJ80	pSportl
3188	HCRMJ81R	(AB023584) reduced expression in cancer [Homo sapiens] >sp BAA88923 BAA88923 Rec protein. Length = 367	dbj BAA88923.1	7465	207	473	100	100	HCRMJ81	pSportl
3189	HCRMJ84R			7466	2	58			HCRMJ84	pSportl

3190	HCRMK11R				7467	3	299			HCRMK11	pSport1
3191	HCRMK94R				7468	30	92			HCRMK94	pSport1
3192	HCRMN04R				7469	16	201			HCRMN04	pSport1
3193	HCRMO53R				7470	1	99			HCRMO53	pSport1
3194	HCRMO55R				7471	3	140			HCRMO55	pSport1
3195	HCRMP32RA				7472	160	390			HCRMP32	pSport1
3196	HCRM07R				7473	2	67			HCRM07	pSport1
3197	HCRM28R				7474	2	274			HCRM28	pSport1
3198	HCRM50R				7475	1	144			HCRM50	pSport1
3199	HCRM51R				7476	2	100			HCRM51	pSport1
3200	HCRMS48R				7477	159	332			HCRMS48	pSport1
3201	HCRMS54R				7478	1	99			HCRMS54	pSport1
3202	HCRMS55R				7479	13	72			HCRMS55	pSport1
3203	HCRMT03R				7480	2	82			HCRMT03	pSport1
3204	HCRMT32R				7481	1	69			HCRMT32	pSport1
3205	HCRMU10R				7482	237	476			HCRMU10	pSport1
3206	HCRMU21R				7483	217	378			HCRMU21	pSport1
3207	HCRMU34R				7484	130	321			HCRMU34	pSport1
3208	HCRMU36R				7485	9	131			HCRMU36	pSport1
3209	HCRMU63R				7486	2	64			HCRMU63	pSport1
3210	HCRMU67R				7487	1	60			HCRMU67	pSport1
3211	HCRMU76R				7488	41	79			HCRMU76	pSport1
3212	HCRMU78R				7489	1	66			HCRMU78	pSport1
3213	HCRMU85R				7490	3	245			HCRMU85	pSport1
3214	HCRMV06R				7491	2	82			HCRMV06	pSport1
3215	HCRMV52R				7492	19	90			HCRMV52	pSport1
3216	HCRMV67R				7493	2	247			HCRMV67	pSport1
3217	HCRMV78R				7494	12	146			HCRMV78	pSport1
3218	HCRMV95R				7495	1	54			HCRMV95	pSport1
3219	HCRMW15R				7496	2	205			HCRMW15	pSport1
3220	HCRMW62R				7497	2	283			HCRMW62	pSport1
3221	HCRMW90R				7498	2	142			HCRMW90	pSport1
3222	HCRMX02R				7499	1	180			HCRMX02	pSport1

3223	HCRMX11R			7500	374	502			HCRMX11	pSportl
3224	HCRMY28R			7501	1	105			HCRMY28	pSportl
3225	HCRMY29R			7502	2	109			HCRMY29	pSportl
3226	HCRMY39R			7503	2	157			HCRMY39	pSportl
3227	HCRMZ13R			7504	1	69			HCRMZ13	pSportl
3228	HCRMZ36R			7505	104	451			HCRMZ36	pSportl
3229	HCRMZ53R			7506	2	97			HCRMZ53	pSportl
3230	HCRMZ71R	(AL022313) dJ1119A7.5 (novel protein (isoform 2)) [Homo sapiens] >sp CAB62989 CAB62989 DJ1119A7.5 (novel protein (isoform 2)) (fragment). Length = 100	emb CAB6298 9.1	7507	114	440	85	89	HCRMZ71	pSportl
3231	HCRMZ92R			7508	312	482			HCRMZ92	pSportl
3232	HCRNA39R			7509	3	56			HCRNA39	pSportl
3233	HCRNA44R			7510	40	168			HCRNA44	pSportl
3234	HCRNA64R			7511	13	108			HCRNA64	pSportl
3235	HCRNA88R			7512	1	51			HCRNA88	pSportl
3236	HCRNB36R			7513	1	387			HCRNB36	pSportl
3237	HCRNB47R			7514	2	130			HCRNB47	pSportl
3238	HCRNB56R			7515	2	97			HCRNB56	pSportl
3239	HCRNB61R			7516	3	116			HCRNB61	pSportl
3240	HCRNB69R			7517	1	114			HCRNB69	pSportl
3241	HCRNB77R			7518	10	87			HCRNB77	pSportl
3242	HCRNB85R			7519	1	105			HCRNB85	pSportl
3243	HCRNC23R			7520	130	444			HCRNC23	pSportl
3244	HCRND21R			7521	195	395			HCRND21	pSportl
3245	HCRND28R			7522	1	141			HCRND28	pSportl
3246	HCRND30R			7523	1	105			HCRND30	pSportl
3247	HCRND45R			7524	217	369			HCRND45	pSportl
3248	HCRNE04R			7525	443	682			HCRNE04	pSportl
3249	HCRNE11R			7526	1	207			HCRNE11	pSportl
3250	HCRNE15R			7527	442	696			HCRNE15	pSportl
3251	HCRNE17R			7528	2	130			HCRNE17	pSportl
3252	HCRNE18R			7529	1	132			HCRNE18	pSportl

3253	HCRNE34R			7530	1	54			HCRNE34	pSportl
3254	HCRNE50R			7531	39	146			HCRNE50	pSportl
3255	HCRNE60R			7532	1	279			HCRNE60	pSportl
3256	HCRNF01R			7533	194	349			HCRNF01	pSportl
3257	HCRNF66R			7534	334	453			HCRNF66	pSportl
3258	HCRNF90R			7535	1	108			HCRNF90	pSportl
3259	HCRNG33R			7536	7	168			HCRNG33	pSportl
3260	HCRNG44R			7537	61	195			HCRNG44	pSportl
3261	HCRNH02R			7538	175	402			HCRNH02	pSportl
3262	HCRNH78R			7539	2	103			HCRNH78	pSportl
3263	HCRNI71R			7540	214	483			HCRNI71	pSportl
3264	HCRNJ25R	(AF231038) SP555 protein [Drosophila melanogaster] Length = 293	gb AAF34807.1 AF2310	7541	59	406	40	54	HCRNJ25	pSportl
3265	HCRNK13R			7542	3	116			HCRNK13	pSportl
3266	HCRNK40R			7543	195	464			HCRNK40	pSportl
3267	HCRNK94R			7544	200	493			HCRNK94	pSportl
3268	HCRNL17R			7545	6	50			HCRNL17	pSportl
3269	HCRNL38R			7546	2	202			HCRNL38	pSportl
3270	HCRNL52R			7547	100	198			HCRNL52	pSportl
3271	HCRNL55R			7548	1	57			HCRNL55	pSportl
3272	HCRNL60R			7549	3	311			HCRNL60	pSportl
3273	HCRNL69R			7550	2	85			HCRNL69	pSportl
3274	HCRNL86R			7551	1	72			HCRNL86	pSportl
3275	HCRNM46R			7552	3	122			HCRNM46	pSportl
3276	HCRNM50R			7553	45	188			HCRNM50	pSportl
3277	HCRNN08R			7554	1	51			HCRNN08	pSportl
3278	HCRNN11R			7555	1	141			HCRNN11	pSportl
3279	HCRNN79R			7556	1	57			HCRNN79	pSportl
3280	HCRNO40R			7557	1	204			HCRNO40	pSportl
3281	HCRNO41R			7558	295	471			HCRNO41	pSportl
3282	HCRNO49R			7559	274	546			HCRNO49	pSportl
3283	HCRNP05R			7560	1	159			HCRNP05	pSportl
3284	HCRNP07R			7561	64	183			HCRNP07	pSportl

3285	HCRNP22R			7562	2	172			HCRNP22	pSportl
3286	HCRNP34R			7563	1	315			HCRNP34	pSportl
3287	HCRNP45R			7564	2	130			HCRNP45	pSportl
3288	HCRNP65R			7565	390	524			HCRNP65	pSportl
3289	HCRNP76R			7566	1	114			HCRNP76	pSportl
3290	HCRNQ59R			7567	3	56			HCRNQ59	pSportl
3291	HCRNR03R			7568	84	353			HCRNR03	pSportl
3292	HCRNR84R			7569	1	198			HCRNR84	pSportl
3293	HCRNU20R			7570	1	225			HCRNU20	pSportl
3294	HCRNV70R			7571	132	338			HCRNV70	pSportl
3295	HCRNV94R			7572	2	298			HCRNV94	pSportl
3296	HCRNW29R			7573	87	263			HCRNW29	pSportl
3297	HCRNW34R			7574	2	91			HCRNW34	pSportl
3298	HCRNW36R			7575	42	182			HCRNW36	pSportl
3299	HCRNW40R			7576	56	304			HCRNW40	pSportl
3300	HCRNX03R			7577	3	134			HCRNX03	pSportl
3301	HCRNX05R			7578	2	103			HCRNX05	pSportl
3302	HCRNY53R			7579	224	409			HCRNY53	pSportl
3303	HCRNY85R			7580	59	217			HCRNY85	pSportl
3304	HCRNZ22R			7581	181	492			HCRNZ22	pSportl
3305	HCRNZ37R			7582	1	186			HCRNZ37	pSportl
3306	HCRNB24R			7583	1	240			HCRNB24	pSportl
3307	HCRNB35R			7584	1	261			HCRNB35	pSportl
3308	HCRNB68R			7585	119	358			HCRNB68	pSportl
3309	HCRNB83R			7586	1	69			HCRNB83	pSportl
3310	HCRNB85R			7587	193	504			HCRNB85	pSportl
3311	HCRNB36R			7588	23	217			HCRNB36	pSportl
3312	HCRNE09R			7589	14	172			HCRNE09	pSportl
3313	HCRNE19R			7590	30	218			HCRNE19	pSportl
3314	HCRNE67R	(AB028984) KIAA1061 protein [Homo sapiens] >sp BAA83013 BAA83013 KIAA1061 protein (fragment). Length = 693	dbj BAA83013 .1	7591	1	522	79	80	HCRNE67	pSportl
3315	HCRNE81R			7592	1	66			HCRNE81	pSportl

3316	HCROE89R			7593	227	406		HCROE89	pSportl
3317	HCROF29R			7594	12	62		HCROF29	pSportl
3318	HCROF67R			7595	149	463		HCROF67	pSportl
3319	HCROF73R			7596	1	105		HCROF73	pSportl
3320	HCROG40R			7597	43	132		HCROG40	pSportl
3321	HCROG51R			7598	2	394		HCROG51	pSportl
3322	HCROG58R			7599	334	561		HCROG58	pSportl
3323	HCROG62R			7600	116	301		HCROG62	pSportl
3324	HCROG80R			7601	112	408		HCROG80	pSportl
3325	HCROH29R			7602	164	505		HCROH29	pSportl
3326	HCROH55R			7603	1	117		HCROH55	pSportl
3327	HCROH61R			7604	2	88		HCROH61	pSportl
3328	HCROH86R			7605	1	66		HCROH86	pSportl
3329	HCROI10R			7606	75	266		HCROI10	pSportl
3330	HCROI79R			7607	1	168		HCROI79	pSportl
3331	HCROI81R			7608	3	278		HCROI81	pSportl
3332	HCROI83R			7609	203	376		HCROI83	pSportl
3333	HCROI21R			7610	15	59		HCROI21	pSportl
3334	HCROI35R			7611	216	452		HCROI35	pSportl
3335	HCROI40R			7612	72	155		HCROI40	pSportl
3336	HCROI88R			7613	1	246		HCROI88	pSportl
3337	HCROK12R			7614	3	62		HCROK12	pSportl
3338	HCROK28R			7615	29	250		HCROK28	pSportl
3339	HCROK29R			7616	103	267		HCROK29	pSportl
3340	HCROK32R			7617	2	157		HCROK32	pSportl
3341	HCROK33R			7618	1	150		HCROK33	pSportl
3342	HCROK42R			7619	2	151		HCROK42	pSportl
3343	HCROK47R			7620	45	215		HCROK47	pSportl
3344	HCROK70R			7621	3	131		HCROK70	pSportl
3345	HCROK84R			7622	1	102		HCROK84	pSportl
3346	HCROK95R			7623	2	115		HCROK95	pSportl
3347	HCROL14R			7624	113	244		HCROL14	pSportl
3348	HCROL47R			7625	1	99		HCROL47	pSportl

3349	HCR0L55R				7626	2	70		HCR0L55	pSport1
3350	HCR0L69R				7627	76	372		HCR0L69	pSport1
3351	HCR0M07R				7628	1	216		HCR0M07	pSport1
3352	HCR0M39R				7629	3	59		HCR0M39	pSport1
3353	HCR0M50R				7630	1	39		HCR0M50	pSport1
3354	HCR0M53R				7631	2	226		HCR0M53	pSport1
3355	HCR0M56R				7632	90	311		HCR0M56	pSport1
3356	HCR0M63R				7633	44	256		HCR0M63	pSport1
3357	HCR0M80R				7634	24	218		HCR0M80	pSport1
3358	HCR0M82R				7635	2	100		HCR0M82	pSport1
3359	HCR0N01R				7636	2	88		HCR0N01	pSport1
3360	HCR0N04R				7637	3	260		HCR0N04	pSport1
3361	HCR0N39R				7638	1	108		HCR0N39	pSport1
3362	HCR0N42R				7639	1	147		HCR0N42	pSport1
3363	HCR0N65R				7640	2	64		HCR0N65	pSport1
3364	HCR0N70R				7641	2	88		HCR0N70	pSport1
3365	HCR0O20R				7642	60	221		HCR0O20	pSport1
3366	HCR0O46R				7643	199	447		HCR0O46	pSport1
3367	HCR0P24R				7644	1	51		HCR0P24	pSport1
3368	HCR0P51R				7645	26	58		HCR0P51	pSport1
3369	HCR0P55R				7646	1	99		HCR0P55	pSport1
3370	HCR0P63R				7647	2	82		HCR0P63	pSport1
3371	HCR0P69R				7648	1	90		HCR0P69	pSport1
3372	HCR0P88R				7649	11	64		HCR0P88	pSport1
3373	HCR0Q04R				7650	2	85		HCR0Q04	pSport1
3374	HCR0Q13R				7651	3	122		HCR0Q13	pSport1
3375	HCR0Q79R				7652	2	100		HCR0Q79	pSport1
3376	HCR0Q92R				7653	164	325		HCR0Q92	pSport1
3377	HCR0R38R				7654	1	66		HCR0R38	pSport1
3378	HCR0R69R				7655	1	282		HCR0R69	pSport1
3379	HCR0R76R				7656	18	89		HCR0R76	pSport1
3380	HCR0R80R				7657	1	60		HCR0R80	pSport1
3381	HCR0S08R				7658	69	200		HCR0S08	pSport1

3382	HCROS22R			7659	14	64			HCROS22	pSportl
3383	HCROS2R			7660	2	109			HCROS2	pSportl
3384	HCROT14R			7661	1	99			HCROT14	pSportl
3385	HCROT15R			7662	60	218			HCROT15	pSportl
3386	HCROT19R			7663	60	227			HCROT19	pSportl
3387	HCROT23R			7664	90	245			HCROT23	pSportl
3388	HCROT75R			7665	1	75			HCROT75	pSportl
3389	HCROT84R			7666	3	236			HCROT84	pSportl
3390	HCROT94R			7667	7	63			HCROT94	pSportl
3391	HCROV04R			7668	125	433			HCROV04	pSportl
3392	HCROV08R			7669	32	229			HCROV08	pSportl
3393	HCROV64R			7670	1	375			HCROV64	pSportl
3394	HCROV82R			7671	1	42			HCROV82	pSportl
3395	HCROW39R			7672	1	63			HCROW39	pSportl
3396	HCROW68R			7673	1	66			HCROW68	pSportl
3397	HCROW69R			7674	138	392			HCROW69	pSportl
3398	HCROX16R			7675	1	105			HCROX16	pSportl
3399	HCROX18R			7676	1	75			HCROX18	pSportl
3400	HCROX32R			7677	1	108			HCROX32	pSportl
3401	HCROX38R			7678	1	105			HCROX38	pSportl
3402	HCROX52R			7679	2	100			HCROX52	pSportl
3403	HCROX92R			7680	1	111			HCROX92	pSportl
3404	HCROZ19R			7681	184	363			HCROZ19	pSportl
3405	HCROZ34R			7682	2	232			HCROZ34	pSportl
3406	HCROZ45R			7683	3	413			HCROZ45	pSportl
3407	HCROZ68R			7684	1	129			HCROZ68	pSportl
3408	HCROZ73R			7685	1	90			HCROZ73	pSportl
3409	HCROZ75R			7686	1	102			HCROZ75	pSportl
3410	HCROZ76R			7687	224	397			HCROZ76	pSportl
3411	HCSPA09R			7688	233	463			HCSPA09	pSportl
3412	HCSPA19R			7689	1	318			HCSPA19	pSportl
3413	HCSPA21R			7690	38	187			HCSPA21	pSportl
3414	HCSPA61R			7691	3	59			HCSPA61	pSportl

3415	HCRPA91R				7692	2	79			HCRPA91	pSportl
3416	HCRPB73R				7693	15	59			HCRPB73	pSportl
3417	HCRPC14R				7694	1	63			HCRPC14	pSportl
3418	HCRPC30R				7695	3	125			HCRPC30	pSportl
3419	HCRPC42R				7696	15	113			HCRPC42	pSportl
3420	HCRPC55R				7697	51	338			HCRPC55	pSportl
3421	HCRPC56R				7698	161	340			HCRPC56	pSportl
3422	HCRPC58R				7699	2	121			HCRPC58	pSportl
3423	HCRPC65R				7700	279	458			HCRPC65	pSportl
3424	HCRPC80R				7701	1	99			HCRPC80	pSportl
3425	HCRPC90R				7702	83	247			HCRPC90	pSportl
3426	HCRPD57R				7703	2	82			HCRPD57	pSportl
3427	HCRPD85R				7704	1	162			HCRPD85	pSportl
3428	HCRPE32R				7705	1	174			HCRPE32	pSportl
3429	HCRPE74R				7706	25	276			HCRPE74	pSportl
3430	HCRPF41R				7707	1	51			HCRPF41	pSportl
3431	HCRPF62R				7708	42	209			HCRPF62	pSportl
3432	HCRPF90R				7709	223	423			HCRPF90	pSportl
3433	HCRPF92R				7710	246	392			HCRPF92	pSportl
3434	HCRPG02R				7711	3	116			HCRPG02	pSportl
3435	HCRPG03R				7712	3	152			HCRPG03	pSportl
3436	HCRPG11R				7713	1	69			HCRPG11	pSportl
3437	HCRPG16R				7714	2	211			HCRPG16	pSportl
3438	HCRPG28R				7715	95	229			HCRPG28	pSportl
3439	HCRPG37R				7716	1	402			HCRPG37	pSportl
3440	HCRPG49R				7717	42	164			HCRPG49	pSportl
3441	HCRPG93R				7718	2	85			HCRPG93	pSportl
3442	HCRPH31R				7719	15	173			HCRPH31	pSportl
3443	HCRPH50RA				7720	7	117			HCRPH50	pSportl
3444	HCRPH58RA				7721	76	315			HCRPH58	pSportl
3445	HCRPH93R				7722	2	79			HCRPH93	pSportl
3446	HCRPI35RA				7723	2	217			HCRPI35	pSportl
3447	HCRPI58RA				7724	1	102			HCRPI58	pSportl

3448	HCRPI60RA			7725	54	221			HCRPI60	pSportl
3449	HCRPI94RA			7726	7	90			HCRPI94	pSportl
3450	HCRPI68RA			7727	1	126			HCRPI68	pSportl
3451	HCRPK17R			7728	202	354			HCRPK17	pSportl
3452	HCRPK70R			7729	2	157			HCRPK70	pSportl
3453	HCRPL10R			7730	2	76			HCRPL10	pSportl
3454	HCRPL29R			7731	2	91			HCRPL29	pSportl
3455	HCRPL35R			7732	56	145			HCRPL35	pSportl
3456	HCRPL63R			7733	82	282			HCRPL63	pSportl
3457	HCRPL79R			7734	3	56			HCRPL79	pSportl
3458	HCRPL80R			7735	59	235			HCRPL80	pSportl
3459	HCRPL85R			7736	3	83			HCRPL85	pSportl
3460	HCRPM51R			7737	26	460			HCRPM51	pSportl
3461	HCRPM52R			7738	2	67			HCRPM52	pSportl
3462	HCRPM85R			7739	1	63			HCRPM85	pSportl
3463	HCRPN29R			7740	2	61			HCRPN29	pSportl
3464	HCRPN38R			7741	2	295			HCRPN38	pSportl
3465	HCRPN49R			7742	1	249			HCRPN49	pSportl
3466	HCRPN73R			7743	3	71			HCRPN73	pSportl
3467	HCRPN86R			7744	3	143			HCRPN86	pSportl
3468	HCRPN88R			7745	3	50			HCRPN88	pSportl
3469	HCRPO31R			7746	60	350			HCRPO31	pSportl
3470	HCRPO32R			7747	2	58			HCRPO32	pSportl
3471	HCRPO69R			7748	3	146			HCRPO69	pSportl
3472	HCRPP07R			7749	9	185			HCRPP07	pSportl
3473	HCRPP20R			7750	3	59			HCRPP20	pSportl
3474	HCRPP73R			7751	1	54			HCRPP73	pSportl
3475	HCRPQ23R			7752	2	91			HCRPQ23	pSportl
3476	HCRPQ52R			7753	1	63			HCRPQ52	pSportl
3477	HCRPQ72R	(AB033071) KIAA1245 protein [Homo sapiens] >sp BAA86559 BAA86559 KIAA1245 protein (fragment). Length = 892	dbj BAA86559 .1	7754	99	305	88	90	HCRPQ72	pSportl
3478	HCRPQ79R			7755	7	57			HCRPQ79	pSportl

3479	HCRPR23R				7756	3	107			HCRPR23	pSport1
3480	HCRPR62R				7757	2	196			HCRPR62	pSport1
3481	HCRPR70R				7758	18	161			HCRPR70	pSport1
3482	HCRPR91R				7759	17	160			HCRPR91	pSport1
3483	HCRPR95R				7760	1	66			HCRPR95	pSport1
3484	HCRPS10R				7761	62	136			HCRPS10	pSport1
3485	HCRPS24R				7762	2	67			HCRPS24	pSport1
3486	HCRPS50R				7763	67	228			HCRPS50	pSport1
3487	HCRPT04R				7764	1	144			HCRPT04	pSport1
3488	HCRPT34R				7765	279	383			HCRPT34	pSport1
3489	HCRPT78R				7766	2	133			HCRPT78	pSport1
3490	HCRPT82R				7767	191	352			HCRPT82	pSport1
3491	HCRPT85R				7768	1	57			HCRPT85	pSport1
3492	HCRPU09R				7769	65	271			HCRPU09	pSport1
3493	HCRPU76R				7770	202	312			HCRPU76	pSport1
3494	HCRPV27R				7771	3	74			HCRPV27	pSport1
3495	HCRPV39R				7772	1	174			HCRPV39	pSport1
3496	HCRPV62R				7773	340	534			HCRPV62	pSport1
3497	HCRPV86R				7774	2	172			HCRPV86	pSport1
3498	HCRPV91R	(AK000857) unnamed protein product [Homo sapiens] Length = 180	dbj BAA91400.1		7775	2	406	100	100	HCRPV91	pSport1
3499	HCRPW68R				7776	3	86			HCRPW68	pSport1
3500	HCRPW72R				7777	2	52			HCRPW72	pSport1
3501	HCRPX21R				7778	23	103			HCRPX21	pSport1
3502	HCRPX71R				7779	3	161			HCRPX71	pSport1
3503	HCRPY01R				7780	223	429			HCRPY01	pSport1
3504	HCRPY59R				7781	2	58			HCRPY59	pSport1
3505	HCRPY91R				7782	6	218			HCRPY91	pSport1
3506	HCRPZ13R				7783	2	163			HCRPZ13	pSport1
3507	HCRPZ39R				7784	1	96			HCRPZ39	pSport1
3508	HCRQB75R				7785	33	257			HCRQB75	pSport1
3509	HCRQC36R				7786	28	294			HCRQC36	pSport1
3510	HCRQC38R				7787	271	519			HCRQC38	pSport1

3511	HCRQD29R				7788	118	303				HCRQD29	pSport1
3512	HCRQD41R				7789	1	102				HCRQD41	pSport1
3513	HCRQD47R				7790	2	418				HCRQD47	pSport1
3514	HCRQD62R				7791	3	122				HCRQD62	pSport1
3515	HCRQD75R				7792	1	66				HCRQD75	pSport1
3516	HCRQF95R				7793	1	207				HCRQF95	pSport1
3517	HCRQG25R	unnamed protein product [unidentified] Length = 180 emb CAB6919 5.1			7794	213	395	71	81		HCRQG25	pSport1
3518	HCRQG72R				7795	44	229				HCRQG72	pSport1
3519	HCRQI03R				7796	3	164				HCRQI03	pSport1
3520	HCRQI32R				7797	1	153				HCRQI32	pSport1
3521	HCRQI34R				7798	310	573				HCRQI34	pSport1
3522	HCRQI65R				7799	1	54				HCRQI65	pSport1
3523	HCRQI91R				7800	425	583				HCRQI91	pSport1
3524	HCRQI04R				7801	10	54				HCRQI04	pSport1
3525	HCRQI08R				7802	1	90				HCRQI08	pSport1
3526	HCRQI19R				7803	3	137				HCRQI19	pSport1
3527	HCRQI26R				7804	2	91				HCRQI26	pSport1
3528	HCRQI54R				7805	1	48				HCRQI54	pSport1
3529	HCRQJ70R				7806	123	374				HCRQJ70	pSport1
3530	HCRQK15R				7807	1	54				HCRQK15	pSport1
3531	HCRQL13R				7808	307	462				HCRQL13	pSport1
3532	HCRQL65R				7809	267	458				HCRQL65	pSport1
3533	HCRQM37R				7810	1	498				HCRQM37	pSport1
3534	HCRQM45R				7811	37	162				HCRQM45	pSport1
3535	HCRQM58R				7812	2	118				HCRQM58	pSport1
3536	HCRQM59R				7813	173	403				HCRQM59	pSport1
3537	HCRQM68R				7814	120	293				HCRQM68	pSport1
3538	HCRQN36R				7815	210	323				HCRQN36	pSport1
3539	HCRQN42R				7816	3	134				HCRQN42	pSport1
3540	HCUDT18R				7817	2	235				HCUDT18	ZAP Express

3541	HCYBA36R				7818	1	189			HCYBA36	pBluescript SK-
3542	HCYBC11R				7819	46	123			HCYBC11	pBluescript SK-
3543	HCYBD19R				7820	54	245			HCYBD19	pBluescript SK-
3544	HCYBE06R				7821	75	227			HCYBE06	pBluescript SK-
3545	HCYBE34R	(AF146568) MIL1 protein [Homo sapiens] >sp AAAF03602 AAAF03602 MIL1 protein. Length = 386	gb AAAF03602.1		7822	2	370	98	98	HCYBE34	pBluescript SK-
3546	HCYBF65R				7823	3	245			HCYBF65	pBluescript SK-
3547	HCYBH59R				7824	145	240			HCYBH59	pBluescript SK-
3548	HCYBH81R				7825	288	437			HCYBH81	pBluescript SK-
3549	HCYBH89R				7826	357	530			HCYBH89	pBluescript SK-
3550	HCYBH93R				7827	275	469			HCYBH93	pBluescript SK-
3551	HCYBK65R				7828	62	232			HCYBK65	pBluescript SK-
3552	HDLAX76R				7829	91	264			HDLAX76	pCMV'Sport 2.0
3553	HDPPE11R	(AF184617) proprotein convertase aPC6C isoform [Branchiostoma californiense] >sp AAAF26302 AAAF26302 Proprotein convertase aPC6C isoform. Length = 1323	gb AAAF26302.1 AAAF1846		7830	2	355	86	88	HDPPE11	pCMV'Sport 3.0
3554	HDPPU63R				7831	1	57			HDPPU63	pCMV'Sport 3.0
3555	HDQDZ61R				7832	2	154			HDQDZ61	pCMV'Sport 3.0
3556	HDQFV12R				7833	294	482			HDQFV12	pCMV'Sport 3.0

3557	HDQGH10R				7834	1	60		HDQGH10	pCMVSPORT 3.0
3558	HDTDS96R				7835	240	431		HDTDS96	pCMVSPORT 2.0
3559	HDTMG03R				7836	263	409		HDTMG03	pCMVSPORT 2.0
3560	HE2JZ65R				7837	245	409		HE2JZ65	Uni-ZAP XR
3561	HE2RS12R				7838	3	101		HE2RS12	Uni-ZAP XR
3562	HE2TA21R				7839	51	305		HE2TA21	Uni-ZAP XR
3563	HE8AE77R				7840	202	309		HE8AE77	Uni-ZAP XR
3564	HEOAB66RA				7841	3	158		HEOAB66	pBluescript
3565	HEONL43R				7842	2	76		HEONL43	pSport1
3566	HEOSS64R				7843	283	399		HEOSS64	pSport1
3567	HFIXZ28R				7844	72	317		HFIXZ28	pSport1
3568	HFKHA60R				7845	3	440		HFKHA60	Uni-ZAP XR
3569	HFPJM42R				7846	2	67		HFPJM42	Uni-ZAP XR
3570	HFRBW76R				7847	170	325		HFRBW76	Uni-ZAP XR
3571	HFVIF71R				7848	59	232		HFVIF71	pBluescript
3572	HGBBA17R				7849	96	308		HGBBA17	Uni-ZAP XR
3573	HGLAW93R				7850	28	150		HGLAW93	Uni-ZAP XR
3574	HHEAA94R				7851	4	141		HHEAA94	pCMVSPORT 3.0
3575	HHEBR58R				7852	2	133		HHEBR58	pCMVSPORT 3.0
3576	HHEQA63R				7853	260	544		HHEQA63	pCMVSPORT 3.0

3577	HHEWA82R				7854	43	183		HHEWA82	pCMVSport 3.0
3578	HHFMJ42R				7855	1	87		HHFMJ42	Uni-ZAP XR
3579	HHMMA39R				7856	1	270		HHMMA39	pSportl
3580	HHMMA54R				7857	1	123		HHMMA54	pSportl
3581	HHMMA69R				7858	1	96		HHMMA69	pSportl
3582	HHMMB02R				7859	3	344		HHMMB02	pSportl
3583	HHMMB03R				7860	2	166		HHMMB03	pSportl
3584	HHMMB13R				7861	30	221		HHMMB13	pSportl
3585	HHMMC03R				7862	1	63		HHMMC03	pSportl
3586	HHMMC40R				7863	5	157		HHMMC40	pSportl
3587	HHMMC69R				7864	297	470		HHMMC69	pSportl
3588	HHMMD04R				7865	1	84		HHMMD04	pSportl
3589	HHMMD09R				7866	1	177		HHMMD09	pSportl
3590	HHMMD42R				7867	1	99		HHMMD42	pSportl
3591	HHMMD57R				7868	1	51		HHMMD57	pSportl
3592	HHMME06R				7869	1	99		HHMME06	pSportl
3593	HHMME20R				7870	3	290		HHMME20	pSportl
3594	HHMME64R				7871	2	109		HHMME64	pSportl
3595	HHMMF06R				7872	2	61		HHMMF06	pSportl
3596	HHMMF15R				7873	2	97		HHMMF15	pSportl
3597	HHMMF16R				7874	1	108		HHMMF16	pSportl
3598	HHMMF32R				7875	1	99		HHMMF32	pSportl
3599	HHMMF43R				7876	1	63		HHMMF43	pSportl
3600	HHMMF48R				7877	7	252		HHMMF48	pSportl
3601	HHMMF55R				7878	1	102		HHMMF55	pSportl
3602	HHMMF62R				7879	2	229		HHMMF62	pSportl
3603	HISDB01RA				7880	3	314		HISDB01	pSportl
3604	HJMBH59R				7881	288	446		HJMBH59	pCMVSport 3.0
3605	HKABL65R				7882	1	186		HKABL65	pCMVSport 2.0

3606	HKCAA84R			7883	80	253		HKCAA84	Uni-ZAP XR
3607	HKCSA76R			7884	60	287		HKCSA76	pBluescript
3608	HKCSB18R			7885	282	476		HKCSB18	pBluescript
3609	HKCSB45R			7886	1	240		HKCSB45	pBluescript
3610	HKCSB47R			7887	2	289		HKCSB47	pBluescript
3611	HKCSC92R			7888	11	223		HKCSC92	pBluescript
3612	HKCSF11R			7889	25	357		HKCSF11	pBluescript
3613	HKCSH46R			7890	2	478		HKCSH46	pBluescript
3614	HKCSI81R			7891	3	86		HKCSI81	pBluescript
3615	HKCSJ63R			7892	57	479		HKCSJ63	pBluescript
3616	HKCSL33R			7893	103	225		HKCSL33	pBluescript
3617	HKCSO21R			7894	1	390		HKCSO21	pBluescript
3618	HKCSP88R			7895	191	487		HKCSP88	pBluescript
3619	HKCSP90R			7896	170	358		HKCSP90	pBluescript
3620	HKCTB29R			7897	151	336		HKCTB29	pBluescript
3621	HKCTB80R			7898	47	271		HKCTB80	pBluescript
3622	HKCTD01R			7899	55	354		HKCTD01	pBluescript
3623	HKCTD27R			7900	81	500		HKCTD27	pBluescript
3624	HKLAA31R			7901	159	413		HKLAA31	Lambda ZAP II
3625	HKLAB37R			7902	302	439		HKLAB37	Lambda ZAP II
3626	HKLAB56R			7903	245	487		HKLAB56	Lambda ZAP II
3627	HKLRA55R			7904	214	492		HKLRA55	pBluescript
3628	HKLRA63R			7905	72	344		HKLRA63	pBluescript
3629	HKLRB06R			7906	207	497		HKLRB06	pBluescript
3630	HKLRB21R			7907	64	246		HKLRB21	pBluescript
3631	HKLRB75R			7908	2	58		HKLRB75	pBluescript
3632	HKLSA15R			7909	24	239		HKLSA15	pBluescript
3633	HKLSA23R			7910	3	212		HKLSA23	pBluescript
3634	HKLSA28R			7911	305	427		HKLSA28	pBluescript

3635	HKLSB04R				7912	20	262			HKLSB04	pBluescript
3636	HKLSB05R				7913	1	378			HKLSB05	pBluescript
3637	HKLSB41R				7914	110	388			HKLSB41	pBluescript
3638	HKLSB76R				7915	3	227			HKLSB76	pBluescript
3639	HKLSB93R				7916	177	503			HKLSB93	pBluescript
3640	HKLSC29R				7917	77	337			HKLSC29	pBluescript
3641	HKLSC42R				7918	218	334			HKLSC42	pBluescript
3642	HKLSD10R				7919	96	245			HKLSD10	pBluescript
3643	HKLSD26R				7920	215	400			HKLSD26	pBluescript
3644	HKLSD61R				7921	111	323			HKLSD61	pBluescript
3645	HKLSD79R				7922	169	318			HKLSD79	pBluescript
3646	HKLSD93R				7923	89	298			HKLSD93	pBluescript
3647	HLDC57R				7924	2	436			HLDC57	pCMVSPORT 3.0
3648	HLQFP01R				7925	18	104			HLQFP01	Lambda ZAP II
3649	HL YBW70R				7926	249	413			HL YBW70	pSport1
3650	HMWDE95R				7927	2	316			HMWDE95	Uni-ZAP XR
3651	HNBTH48R				7928	41	190			HNBTH48	pSport1
3652	HNBTM76R				7929	122	259			HNBTM76	pSport1
3653	HNOAT40R				7930	96	317			HNOAT40	pSport1
3654	HNTCO26R				7931	46	453			HNTCO26	pCMVSPORT 3.0
3655	HNTDI71R				7932	44	493			HNTDI71	pCMVSPORT 3.0
3656	HOCTA23R				7933	37	387			HOCTA23	pSport1
3657	HOCTA91R				7934	1	339			HOCTA91	pSport1
3658	HOCTB04R				7935	45	194			HOCTB04	pSport1
3659	HOCTB19R				7936	70	216			HOCTB19	pSport1
3660	HOCTB32R				7937	130	318			HOCTB32	pSport1
3661	HOCTB56R				7938	1	459			HOCTB56	pSport1
3662	HOCTB95R				7939	1	63			HOCTB95	pSport1

3663	HOCTC25R			7940	2	100			HOCTC25	pSportl
3664	HOCTC38R			7941	2	361			HOCTC38	pSportl
3665	HOCTC55R			7942	2	385			HOCTC55	pSportl
3666	HOCTC61R			7943	1	138			HOCTC61	pSportl
3667	HOCTC73R			7944	190	366			HOCTC73	pSportl
3668	HOCTD31R			7945	1	102			HOCTD31	pSportl
3669	HOCTD35R			7946	172	264			HOCTD35	pSportl
3670	HOCTD64R			7947	3	83			HOCTD64	pSportl
3671	HOCTD88R			7948	2	73			HOCTD88	pSportl
3672	HOCTD95R			7949	1	102			HOCTD95	pSportl
3673	HOCTE12R			7950	242	397			HOCTE12	pSportl
3674	HOCTE91R			7951	1	51			HOCTE91	pSportl
3675	HOCTF24R			7952	2	61			HOCTF24	pSportl
3676	HOCTF43R			7953	21	278			HOCTF43	pSportl
3677	HOCTF84R			7954	1	213			HOCTF84	pSportl
3678	HODFV69R			7955	64	210			HODFV69	Uni-ZAP XR
3679	HOEKT71R			7956	47	184			HOEKT71	Uni-ZAP XR
3680	HOEKU65R			7957	3	95			HOEKU65	Uni-ZAP XR
3681	HOGEE21R			7958	3	383			HOGEE21	pCMV Sport 2.0
3682	HOHAS78R			7959	83	481			HOHAS78	pCMV Sport 2.0
3683	HOHEE72R			7960	136	309			HOHEE72	pCMV Sport 2.0
3684	HOSNW54R	(AL137661) hypothetical protein [Homo sapiens] >emb CAB70863.1 (AL137661) hypothetical protein [Homo sapiens] >sp CAB70863 CAB70863 Hypothetical 73.8 kd protein. Length = 661	emb CAB70863.1	7961	20	439	70	70	HOSNW54	Uni-ZAP XR
3685	HOVDH84R			7962	1	165			HOVDH84	pSportl

3686	HPCRD42R	(AF151075) HSPC241 [Homo sapiens] Length = 128 1 AF1510	7963	139	456	82	83	HPCRD42	Other
3687	HPDOA19R		7964	70	306			HPDOA19	pSportl
3688	HPFCN76R		7965	90	467			HPFCN76	Uni-ZAP XR
3689	HPJBZ88R	(AL122042) hypothetical protein [Homo sapiens] >pir T34520 T34520 hypothetical protein DKFZp564J157.1 - human (fragment) >sp CAB59179 CAB59179 Hypothetical 17.9 kd protein (fragment). >emb CAB59179.2 (AL122042) hypothetical protein [Homo sapiens] {SUB 22	7966	30	383	94	94	HPJBZ88	Uni-ZAP XR
3690	HRACX76R		7967	2	136			HRACX76	pCMV Sport 3.0
3691	HSIFC66R		7968	85	258			HSIFC66	Uni-ZAP XR
3692	HSOBF88R		7969	212	394			HSOBF88	Uni-ZAP XR
3693	HSODE15R		7970	355	444			HSODE15	Uni-ZAP XR
3694	HSVBO17R		7971	1	363			HSVBO17	Uni-ZAP XR
3695	HT4CI88R		7972	1	501			HT4CI88	Uni-ZAP XR
3696	HTGEL09R		7973	135	278			HTGEL09	Uni-ZAP XR
3697	HTXRF56R		7974	2	256			HTXRF56	Uni-ZAP XR
3698	HTYND19RA		7975	3	320			HTYND19	pSportl
3699	HTYSJ08Ra		7976	3	236			HTYSJ08	pBluescript
3700	HWACX88R		7977	3	191			HWACX88	pCMV Sport 3.0
3701	HWLMA16R		7978	110	253			HWLMA16	pSportl
3702	HWLMA24R		7979	2	190			HWLMA24	pSportl
3703	HWLMA58R		7980	242	475			HWLMA58	pSportl

3704	HWLMA60R				7981	198	347			HWLMA60	pSportl
3705	HWLMA75R				7982	273	458			HWLMA75	pSportl
3706	HWLMA91R				7983	161	469			HWLMA91	pSportl
3707	HWLMB42R				7984	68	262			HWLMB42	pSportl
3708	HWLMC65R				7985	88	204			HWLMC65	pSportl
3709	HWLMC79R				7986	181	348			HWLMC79	pSportl
3710	HWLMD83R				7987	3	437			HWLMD83	pSportl
3711	HWLME13R				7988	85	195			HWLME13	pSportl
3712	HWLME59R				7989	129	227			HWLME59	pSportl
3713	HWLME69R				7990	2	157			HWLME69	pSportl
3714	HWLME71R				7991	166	387			HWLME71	pSportl
3715	HWLME84R				7992	1	84			HWLME84	pSportl
3716	HWLMF91R				7993	11	94			HWLMF91	pSportl
3717	HWLMG12R				7994	1	111			HWLMG12	pSportl
3718	HWLMG15R				7995	1	153			HWLMG15	pSportl
3719	HWLMG30R				7996	1	246			HWLMG30	pSportl
3720	HWLMG39R				7997	2	106			HWLMG39	pSportl
3721	HWLMG54R				7998	38	235			HWLMG54	pSportl
3722	HWLMG56R				7999	2	136			HWLMG56	pSportl
3723	HWLMG57R				8000	1	249			HWLMG57	pSportl
3724	HWLMG63R				8001	1	99			HWLMG63	pSportl
3725	HWLMG84R				8002	2	394			HWLMG84	pSportl
3726	HWLMG95R				8003	73	216			HWLMG95	pSportl
3727	HWLMH11R				8004	216	344			HWLMH11	pSportl
3728	HWLMH24R				8005	35	103			HWLMH24	pSportl
3729	HWLMH50R				8006	110	220			HWLMH50	pSportl
3730	HWLMI05R				8007	2	61			HWLMI05	pSportl
3731	HWLMI76R				8008	2	52			HWLMI76	pSportl
3732	HWLMJ70R				8009	107	247			HWLMJ70	pSportl
3733	HWLMJ80R				8010	1	246			HWLMJ80	pSportl
3734	HWLMK20R				8011	57	176			HWLMK20	pSportl
3735	HWLMK25R				8012	1	99			HWLMK25	pSportl
3736	HWLMK31R				8013	3	278			HWLMK31	pSportl

3737	HWLMK62R			8014	8	187			HWLMK62	pSportl
3738	HWLMM68R			8015	10	198			HWLMM68	pSportl
3739	HWLMM93R			8016	1	48			HWLMM93	pSportl
3740	HWLMN01R			8017	2	112			HWLMN01	pSportl
3741	HWLMN51R			8018	18	119			HWLMN51	pSportl
3742	HWLMP20R			8019	2	202			HWLMP20	pSportl
3743	HWLMP58R			8020	2	190			HWLMP58	pSportl
3744	HWLMP60R			8021	1	48			HWLMP60	pSportl
3745	HWLMP71R			8022	1	63			HWLMP71	pSportl
3746	HWLMQ01R			8023	104	283			HWLMQ01	pSportl
3747	HWLMQ73R			8024	38	190			HWLMQ73	pSportl
3748	HWLMR23R			8025	2	67			HWLMR23	pSportl
3749	HWLMR69R			8026	3	347			HWLMR69	pSportl
3750	HWLMS31R			8027	2	103			HWLMS31	pSportl
3751	HWLMT42R			8028	2	103			HWLMT42	pSportl
3752	HWLMT57R			8029	1	111			HWLMT57	pSportl
3753	HWLMT64R			8030	3	110			HWLMT64	pSportl
3754	HWLMU07R			8031	48	143			HWLMU07	pSportl
3755	HWLMU13R			8032	4	123			HWLMU13	pSportl
3756	HWLMU26R			8033	377	583			HWLMU26	pSportl
3757	HWLMU41R			8034	3	203			HWLMU41	pSportl
3758	HWLMV34R			8035	2	94			HWLMV34	pSportl
3759	HWLMV60R			8036	137	343			HWLMV60	pSportl
3760	HWLMV66R			8037	1	99			HWLMV66	pSportl
3761	HWLMV70R			8038	204	344			HWLMV70	pSportl
3762	HWLMW93R			8039	3	275			HWLMW93	pSportl
3763	HWLMX13R			8040	103	285			HWLMX13	pSportl
3764	HWLMX67R			8041	158	349			HWLMX67	pSportl
3765	HWLMY52R			8042	2	121			HWLMY52	pSportl
3766	HWLMZ84R			8043	2	208			HWLMZ84	pSportl
3767	HWLND18R			8044	7	150			HWLND18	pSportl
3768	HWLND58R			8045	1	105			HWLND58	pSportl
3769	HWLND71R			8046	3	158			HWLND71	pSportl

3770	HWLNF67R				8047	357	524			HWLNF67	pSport1
3771	HWLNF68R				8048	2	73			HWLNF68	pSport1
3772	HWLNG81R				8049	1	54			HWLNG81	pSport1
3773	HWLNH76R				8050	1	150			HWLNH76	pSport1
3774	HWLNI43R				8051	1	99			HWLNI43	pSport1
3775	HWLNI93R				8052	25	111			HWLNI93	pSport1
3776	HWLNJ40R				8053	24	122			HWLNJ40	pSport1
3777	HWLNK59R				8054	1	75			HWLNK59	pSport1
3778	HWLNL41R				8055	2	382			HWLNL41	pSport1
3779	HWLNL71R				8056	1	66			HWLNL71	pSport1
3780	HWLNO22R				8057	35	190			HWLNO22	pSport1
3781	HWLNP11R				8058	1	51			HWLNP11	pSport1
3782	HWLNP22R				8059	2	226			HWLNP22	pSport1
3783	HWLNP43R				8060	53	250			HWLNP43	pSport1
3784	HWLNP65R				8061	322	477			HWLNP65	pSport1
3785	HWLNR24R				8062	1	225			HWLNR24	pSport1
3786	HWLNR26R				8063	84	176			HWLNR26	pSport1
3787	HWLNR27R				8064	3	50			HWLNR27	pSport1
3788	HWLNR48R				8065	25	108			HWLNR48	pSport1
3789	HWLNR57R				8066	25	153			HWLNR57	pSport1
3790	HWLNR81R				8067	136	195			HWLNR81	pSport1
3791	HWLNR83R				8068	3	161			HWLNR83	pSport1
3792	HWLNR92R				8069	1	51			HWLNR92	pSport1
3793	HWLNS19R				8070	44	109			HWLNS19	pSport1
3794	HWLNS37R				8071	2	88			HWLNS37	pSport1
3795	HWLNT23R				8072	2	82			HWLNT23	pSport1
3796	HWLNT40R				8073	1	177			HWLNT40	pSport1
3797	HWLNT48R				8074	2	94			HWLNT48	pSport1
3798	HWLNV90R				8075	2	238			HWLNV90	pSport1
3799	HWLNV92R				8076	2	88			HWLNV92	pSport1
3800	HWLNX01R				8077	70	249			HWLNX01	pSport1
3801	HWLNX64R				8078	1	54			HWLNX64	pSport1
3802	HWLNY25R				8079	2	238			HWLNY25	pSport1

3803	HWLNY40R				8080	2	100			HWLNY40	pSportl
3804	HWLNY67R				8081	3	125			HWLNY67	pSportl
3805	HWLNZ75R				8082	45	152			HWLNZ75	pSportl
3806	HWLOA09R				8083	3	293			HWLOA09	pSportl
3807	HWLOA83R				8084	109	276			HWLOA83	pSportl
3808	HWLOB93R				8085	2	73			HWLOB93	pSportl
3809	HWLOC19R	unnamed protein product [unidentified] Length = 180 5.1	emb CAB6919		8086	156	326	83	86	HWLOC19	pSportl
3810	HWLOC65R				8087	3	218			HWLOC65	pSportl
3811	HWLOE46R				8088	3	125			HWLOE46	pSportl
3812	HWLOF10R				8089	119	253			HWLOF10	pSportl
3813	HWLOF46R				8090	17	163			HWLOF46	pSportl
3814	HWLOF52R				8091	1	105			HWLOF52	pSportl
3815	HWLOF79R				8092	1	123			HWLOF79	pSportl
3816	HWLOG15R				8093	246	482			HWLOG15	pSportl
3817	HWLOG17R				8094	1	150			HWLOG17	pSportl
3818	HWLOG59R				8095	46	252			HWLOG59	pSportl
3819	HWLOI04R				8096	2	118			HWLOI04	pSportl
3820	HWLOI17R				8097	136	414			HWLOI17	pSportl
3821	HWLOI25R				8098	71	145			HWLOI25	pSportl
3822	HWLOI27R				8099	9	74			HWLOI27	pSportl
3823	HWLOI67R				8100	1	363			HWLOI67	pSportl
3824	HWLOJ13R				8101	12	167			HWLOJ13	pSportl
3825	HWLOJ19R				8102	210	431			HWLOJ19	pSportl
3826	HWLOJ28R				8103	1	126			HWLOJ28	pSportl
3827	HWLOJ51R				8104	6	167			HWLOJ51	pSportl
3828	HWLOK12R				8105	2	238			HWLOK12	pSportl
3829	HWLOK36R				8106	1	54			HWLOK36	pSportl
3830	HWLOK45R				8107	154	309			HWLOK45	pSportl
3831	HWLOK73R				8108	392	637			HWLOK73	pSportl
3832	HWLOK90R				8109	163	336			HWLOK90	pSportl
3833	HWLOL50R				8110	238	435			HWLOL50	pSportl
3834	HWLOM71R				8111	2	115			HWLOM71	pSportl

3835	HWLON66R			8112	1	69			HWLON66	pSportl
3836	HWLON71R			8113	1	66			HWLON71	pSportl
3837	HWLOO16R			8114	1	51			HWLOO16	pSportl
3838	HWLOQ52R			8115	102	215			HWLOQ52	pSportl
3839	HWLOR01R			8116	1	180			HWLOR01	pSportl
3840	HWLOR15R			8117	10	252			HWLOR15	pSportl
3841	HWLOR65R			8118	171	497			HWLOR65	pSportl
3842	HWLOS10R			8119	3	98			HWLOS10	pSportl
3843	HWLOS39R			8120	1	63			HWLOS39	pSportl
3844	HWLOS70R			8121	1	63			HWLOS70	pSportl
3845	HWLOT17R			8122	3	74			HWLOT17	pSportl
3846	HWLOT29R			8123	1	186			HWLOT29	pSportl
3847	HWLOT54R			8124	1	66			HWLOT54	pSportl
3848	HWLOU39R			8125	1	234			HWLOU39	pSportl
3849	HWLOU73R			8126	18	68			HWLOU73	pSportl
3850	HWLOU85R			8127	1	60			HWLOU85	pSportl
3851	HWLOV47R			8128	1	63			HWLOV47	pSportl
3852	HWLOV75R			8129	49	156			HWLOV75	pSportl
3853	HWLOV76R			8130	46	129			HWLOV76	pSportl
3854	HWLOV78R			8131	54	152			HWLOV78	pSportl
3855	HWLOX29R			8132	101	301			HWLOX29	pSportl
3856	HWLOX45R			8133	10	90			HWLOX45	pSportl
3857	HWLOY59R			8134	338	496			HWLOY59	pSportl
3858	HWLOY73R			8135	3	317			HWLOY73	pSportl
3859	HWLOZ31R			8136	1	60			HWLOZ31	pSportl
3860	HWLOZ87R			8137	29	268			HWLOZ87	pSportl
3861	HWLQA09R			8138	1	243			HWLQA09	pSportl
3862	HWLQA16R			8139	2	316			HWLQA16	pSportl
3863	HWLQA28R			8140	2	181			HWLQA28	pSportl
3864	HWLQA32R			8141	61	258			HWLQA32	pSportl
3865	HWLQA77R			8142	110	214			HWLQA77	pSportl
3866	HWLQB49R			8143	53	124			HWLQB49	pSportl
3867	HWLQC82R			8144	150	314			HWLQC82	pSportl

3868	HWLQD15R			8145	2	307			HWLQD15	pSportl
3869	HWLQD16R			8146	3	356			HWLQD16	pSportl
3870	HWLQD30R			8147	125	550			HWLQD30	pSportl
3871	HWLQD40R			8148	1	228			HWLQD40	pSportl
3872	HWLQD42R			8149	141	548			HWLQD42	pSportl
3873	HWLQD43R			8150	3	449			HWLQD43	pSportl
3874	HWLQD46R			8151	62	274			HWLQD46	pSportl
3875	HWLQD89R			8152	52	549			HWLQD89	pSportl
3876	HWLQD92R			8153	1	99			HWLQD92	pSportl
3877	HWLQD94R			8154	182	505			HWLQD94	pSportl
3878	HWLQE28R			8155	1	63			HWLQE28	pSportl
3879	HWLQE47R			8156	139	243			HWLQE47	pSportl
3880	HWLQE74R			8157	1	66			HWLQE74	pSportl
3881	HWLQE83R			8158	1	144			HWLQE83	pSportl
3882	HWLQE91R			8159	3	98			HWLQE91	pSportl
3883	HWLQF21R			8160	2	97			HWLQF21	pSportl
3884	HWLQF47R			8161	1	99			HWLQF47	pSportl
3885	HWLQF64R			8162	1	102			HWLQF64	pSportl
3886	HWLQF73R			8163	2	187			HWLQF73	pSportl
3887	HWLQH32R			8164	250	408			HWLQH32	pSportl
3888	HWLQH58R			8165	153	368			HWLQH58	pSportl
3889	HWLQH95R			8166	1	102			HWLQH95	pSportl
3890	HWLQI87R			8167	2	73			HWLQI87	pSportl
3891	HWLQK59R			8168	93	338			HWLQK59	pSportl
3892	HWLQM69R			8169	12	68			HWLQM69	pSportl
3893	HWLQM91R			8170	44	130			HWLQM91	pSportl
3894	HWLQN26R			8171	104	247			HWLQN26	pSportl
3895	HWLQN30R			8172	3	173			HWLQN30	pSportl
3896	HWLQN44R			8173	2	67			HWLQN44	pSportl
3897	HWLQP15R			8174	1	219			HWLQP15	pSportl
3898	HWLQP18R			8175	2	124			HWLQP18	pSportl
3899	HWLQP26R			8176	1	51			HWLQP26	pSportl
3900	HWLQQ83R			8177	122	334			HWLQQ83	pSportl

3901	HWLQR90R			8178	3	374			HWLQR90	pSportl
3902	HWLQR94R			8179	105	209			HWLQR94	pSportl
3903	HWLQT04R			8180	1	51			HWLQT04	pSportl
3904	HWLQT41R			8181	1	93			HWLQT41	pSportl
3905	HWLQT52R			8182	19	474			HWLQT52	pSportl
3906	HWLQT70R			8183	1	69			HWLQT70	pSportl
3907	HWLQU41R			8184	1	75			HWLQU41	pSportl
3908	HWLQU50R			8185	26	175			HWLQU50	pSportl
3909	HWLQU60R			8186	2	103			HWLQU60	pSportl
3910	HWLQW60R			8187	1	87			HWLQW60	pSportl
3911	HWLQW86R			8188	258	422			HWLQW86	pSportl
3912	HWLQX77R			8189	9	71			HWLQX77	pSportl
3913	HWLQY73R			8190	1	105			HWLQY73	pSportl
3914	HWLRB15R			8191	142	699			HWLRB15	pSportl
3915	HWLRC07R			8192	1	69			HWLRC07	pSportl
3916	HWLRC56R			8193	1	87			HWLRC56	pSportl
3917	HWLRE01R			8194	85	312			HWLRE01	pSportl
3918	HWLRE49R			8195	235	381			HWLRE49	pSportl
3919	HWLRF43R			8196	164	355			HWLRF43	pSportl
3920	HWLRF74R			8197	54	239			HWLRF74	pSportl
3921	HWLRH34R			8198	3	80			HWLRH34	pSportl
3922	HWLRH55R			8199	1	138			HWLRH55	pSportl
3923	HWLRH68R			8200	3	263			HWLRH68	pSportl
3924	HWLRL65R			8201	1	264			HWLRL65	pSportl
3925	HWLRM35R			8202	53	115			HWLRM35	pSportl
3926	HWLRM93R			8203	1	102			HWLRM93	pSportl
3927	HWLRN30R			8204	1	99			HWLRN30	pSportl
3928	HWLRN32R			8205	1	99			HWLRN32	pSportl
3929	HWLRO35R			8206	111	314			HWLRO35	pSportl
3930	HWLRO92R			8207	3	155			HWLRO92	pSportl
3931	HWLRP18R			8208	6	113			HWLRP18	pSportl
3932	HWLRP48R			8209	1	99			HWLRP48	pSportl
3933	HWLRP84R			8210	1	99			HWLRP84	pSportl

3934	HWLRQ43R			8211	1	99			HWLRQ43	pSport1
3935	HWLRR85R			8212	1	51			HWLRR85	pSport1
3936	HWLRS49R			8213	3	86			HWLRS49	pSport1
3937	HWLRS85R			8214	14	79			HWLRS85	pSport1
3938	HWLRT45R			8215	3	65			HWLRT45	pSport1
3939	HWLRT46R			8216	30	116			HWLRT46	pSport1
3940	HWLRT77R			8217	89	187			HWLRT77	pSport1
3941	HWLRV63R			8218	3	398			HWLRV63	pSport1
3942	HWLUF10R			8219	1	129			HWLUF10	pSport1
3943	HWLUF62R			8220	126	281			HWLUF62	pSport1
3944	HWLUG36R			8221	2	52			HWLUG36	pSport1
3945	HWLUG53R			8222	109	255			HWLUG53	pSport1
3946	HWLUG72R			8223	2	145			HWLUG72	pSport1
3947	HWLUH57R			8224	3	68			HWLUH57	pSport1
3948	HWLUH72R			8225	2	334			HWLUH72	pSport1
3949	HWLUH79R			8226	54	179			HWLUH79	pSport1
3950	HWLU144R			8227	39	95			HWLU144	pSport1
3951	HWLU155R			8228	1	312			HWLU155	pSport1
3952	HWLU183R			8229	24	155			HWLU183	pSport1
3953	HWLU104R			8230	20	130			HWLU104	pSport1
3954	HWLU119R			8231	1	390			HWLU119	pSport1
3955	HWLU146R			8232	3	137			HWLU146	pSport1
3956	HWLUL02R			8233	37	186			HWLUL02	pSport1
3957	HWLUL39R			8234	1	114			HWLUL39	pSport1
3958	HWLUL44R			8235	1	126			HWLUL44	pSport1
3959	HWLUL47R			8236	56	202			HWLUL47	pSport1
3960	HWLUL65R			8237	30	134			HWLUL65	pSport1
3961	HWLUN02R			8238	2	55			HWLUN02	pSport1
3962	HWLUN03R			8239	1	150			HWLUN03	pSport1
3963	HWLUN23R			8240	1	216			HWLUN23	pSport1
3964	HWLUN46R			8241	3	122			HWLUN46	pSport1
3965	HWLUN55R			8242	73	138			HWLUN55	pSport1
3966	HWLUN76R			8243	1	117			HWLUN76	pSport1

3967	HWLUN77R			8244	31	102			HWLUN77	pSportl
3968	HWLUN78R			8245	59	196			HWLUN78	pSportl
3969	HWLUN94R			8246	1	54			HWLUN94	pSportl
3970	HWLUO12R			8247	1	48			HWLUO12	pSportl
3971	HWLUP38R			8248	12	92			HWLUP38	pSportl
3972	HWLUP63R			8249	102	221			HWLUP63	pSportl
3973	HWLUQ35R			8250	2	151			HWLUQ35	pSportl
3974	HWLUQ51R			8251	2	154			HWLUQ51	pSportl
3975	HWLUQ54R			8252	3	98			HWLUQ54	pSportl
3976	HWLUQ79R			8253	1	66			HWLUQ79	pSportl
3977	HWLUQ87R			8254	149	289			HWLUQ87	pSportl
3978	HWLUQ94R			8255	2	178			HWLUQ94	pSportl
3979	HWLUR41R			8256	33	155			HWLUR41	pSportl
3980	HWLUT21R			8257	1	57			HWLUT21	pSportl
3981	HWLUT89R			8258	1	81			HWLUT89	pSportl
3982	HWLUT94R			8259	43	144			HWLUT94	pSportl
3983	HWLUU23R			8260	2	133			HWLUU23	pSportl
3984	HWLUU88R			8261	40	192			HWLUU88	pSportl
3985	HWLUV35R			8262	68	235			HWLUV35	pSportl
3986	HWLUV39R			8263	1	54			HWLUV39	pSportl
3987	HWLUV67R			8264	1	72			HWLUV67	pSportl
3988	HWLUX01R			8265	10	108			HWLUX01	pSportl
3989	HWLUX69R			8266	2	103			HWLUX69	pSportl
3990	HWLUX81R			8267	2	85			HWLUX81	pSportl
3991	HWLUX84R			8268	1	66			HWLUX84	pSportl
3992	HWLUZ07R			8269	2	127			HWLUZ07	pSportl
3993	HWLVA61R			8270	1	144			HWLVA61	pSportl
3994	HWLVA72R			8271	251	382			HWLVA72	pSportl
3995	HWLVA88R			8272	4	111			HWLVA88	pSportl
3996	HWLVB32R			8273	89	229			HWLVB32	pSportl
3997	HWLVB85R			8274	3	68			HWLVB85	pSportl
3998	HWLVD26R			8275	31	309			HWLVD26	pSportl
3999	HWLVD49R			8276	3	113			HWLVD49	pSportl

4000	HWLVD67R			8277	2	82			HWLVD67	pSportl
4001	HWLVD74R			8278	3	89			HWLVD74	pSportl
4002	HWLVE21R			8279	73	297			HWLVE21	pSportl
4003	HWLVF10R			8280	170	325			HWLVF10	pSportl
4004	HWLVF28R			8281	25	180			HWLVF28	pSportl
4005	HWLVF34R			8282	258	443			HWLVF34	pSportl
4006	HWLVH04R			8283	3	158			HWLVH04	pSportl
4007	HWLVH16R			8284	3	122			HWLVH16	pSportl
4008	HWLVH17R			8285	1	141			HWLVH17	pSportl
4009	HWLVH67R			8286	1	132			HWLVH67	pSportl
4010	HWLV140R			8287	2	169			HWLV140	pSportl
4011	HWLV141R			8288	118	267			HWLV141	pSportl
4012	HWLV115R			8289	1	186			HWLV115	pSportl
4013	HWLV184R			8290	2	190			HWLV184	pSportl
4014	HWLVK46R			8291	2	226			HWLVK46	pSportl
4015	HWLVK62R			8292	3	65			HWLVK62	pSportl
4016	HWLVK88R			8293	1	90			HWLVK88	pSportl
4017	HWLVK91R			8294	3	101			HWLVK91	pSportl
4018	HWLV10R			8295	2	226			HWLV10	pSportl
4019	HWLV171R			8296	2	100			HWLV171	pSportl
4020	HWLV181R			8297	1	105			HWLV181	pSportl
4021	HWLV1M05R			8298	61	129			HWLV1M05	pSportl
4022	HWLV1M23R			8299	1	57			HWLV1M23	pSportl
4023	HWLV1M49R			8300	3	134			HWLV1M49	pSportl
4024	HWLV1N12R			8301	112	231			HWLV1N12	pSportl
4025	HWLV1N73R			8302	3	101			HWLV1N73	pSportl
4026	HWLV1N79R			8303	2	109			HWLV1N79	pSportl
4027	HWLV1R30R			8304	126	227			HWLV1R30	pSportl
4028	HWLV1R40R			8305	2	70			HWLV1R40	pSportl
4029	HWLV1R92R			8306	162	407			HWLV1R92	pSportl
4030	HWLV1S21R			8307	1	69			HWLV1S21	pSportl
4031	HWLV1S40R			8308	18	407			HWLV1S40	pSportl
4032	HWLV1T36R			8309	3	251			HWLV1T36	pSportl

4033	HWLVV06R			8310	3	92			HWLVV06	pSportl
4034	HWLVV31R			8311	14	259			HWLVV31	pSportl
4035	HWLVV64R			8312	3	242			HWLVV64	pSportl
4036	HWLVV87R			8313	11	163			HWLVV87	pSportl
4037	HWLVW22R			8314	1	174			HWLVW22	pSportl
4038	HWLVW49R			8315	123	293			HWLVW49	pSportl
4039	HWLVW56R			8316	3	86			HWLVW56	pSportl
4040	HWLVW89R			8317	20	58			HWLVW89	pSportl
4041	HWLVX39R			8318	3	104			HWLVX39	pSportl
4042	HWLVX75R			8319	146	412			HWLVX75	pSportl
4043	HWLVY14R			8320	3	110			HWLVY14	pSportl
4044	HWLVY55R			8321	2	55			HWLVY55	pSportl
4045	HWLVY65R			8322	209	373			HWLVY65	pSportl
4046	HWLVZ12R			8323	3	53			HWLVZ12	pSportl
4047	HWLWA14R			8324	146	361			HWLWA14	pSportl
4048	HWLWA82R			8325	82	366			HWLWA82	pSportl
4049	HWLWA91R			8326	1	123			HWLWA91	pSportl
4050	HWLWB01R			8327	50	211			HWLWB01	pSportl
4051	HWLWB05R			8328	62	160			HWLWB05	pSportl
4052	HWLWB42R			8329	2	142			HWLWB42	pSportl
4053	HWLWB60R			8330	1	105			HWLWB60	pSportl
4054	HWLWB71R			8331	94	300			HWLWB71	pSportl
4055	HWLWB73R			8332	1	156			HWLWB73	pSportl
4056	HWLWB77R	(AK000419) unnamed protein product [Homo sapiens] >gb AF36534.1 (AF154829) 5'(3')-deoxyribonucleotidase [Homo sapiens] {SUB 50-201} Length = 201	dbj BAA91151.1	8333	66	374	93	93	HWLWB77	pSportl
4057	HWLWD32R			8334	26	193			HWLWD32	pSportl
4058	HWLWD56R			8335	149	343			HWLWD56	pSportl
4059	HWLWD60R			8336	156	317			HWLWD60	pSportl
4060	HWLWD66R			8337	2	184			HWLWD66	pSportl
4061	HWLWE25R			8338	95	316			HWLWE25	pSportl
4062	HWLWE80R			8339	1	102			HWLWE80	pSportl

4063	HWLWE81R					8340	3	149				HWLWE81	pSportl
4064	HWLWG36R					8341	1	72				HWLWG36	pSportl
4065	HWLWH49R					8342	6	104				HWLWH49	pSportl
4066	HWLWH93R					8343	1	69				HWLWH93	pSportl
4067	HWLWI26R					8344	2	52				HWLWI26	pSportl
4068	HWLWI69R					8345	8	166				HWLWI69	pSportl
4069	HWLWJ36R					8346	172	348				HWLWJ36	pSportl
4070	HWLWJ37R					8347	1	114				HWLWJ37	pSportl
4071	HWLWK48R					8348	1	39				HWLWK48	pSportl
4072	HWLWM95R					8349	2	88				HWLWM95	pSportl
4073	HWLWN12R					8350	3	98				HWLWN12	pSportl
4074	HWLWN42R					8351	1	51				HWLWN42	pSportl
4075	HWLWN48R					8352	20	256				HWLWN48	pSportl
4076	HWLWO57R	(AK001650) unnamed protein product [Homo sapiens] Length = 216	dbj BAA91810.1			8353	3	131	73	78		HWLWO57	pSportl
4077	HWLWO64R					8354	2	223				HWLWO64	pSportl
4078	HWLWO78R					8355	1	150				HWLWO78	pSportl
4079	HWLWP03R					8356	76	165				HWLWP03	pSportl
4080	HWLWP08R					8357	3	98				HWLWP08	pSportl
4081	HWLWP13R					8358	2	136				HWLWP13	pSportl
4082	HWLWP15R					8359	1	276				HWLWP15	pSportl
4083	HWLWP50R					8360	226	414				HWLWP50	pSportl
4084	HWLWP87R					8361	26	301				HWLWP87	pSportl
4085	HWLWQ05R					8362	2	82				HWLWQ05	pSportl
4086	HWLWQ49R					8363	3	146				HWLWQ49	pSportl
4087	HWLWR11R					8364	80	175				HWLWR11	pSportl
4088	HWLWR26R					8365	196	315				HWLWR26	pSportl
4089	HWLWR30R					8366	2	247				HWLWR30	pSportl
4090	HWLWS17R					8367	1	51				HWLWS17	pSportl
4091	HWLWS19R					8368	3	266				HWLWS19	pSportl
4092	HWLWS28R					8369	3	179				HWLWS28	pSportl
4093	HWLWS43R					8370	2	97				HWLWS43	pSportl
4094	HWLWS64R					8371	1	144				HWLWS64	pSportl

4095	HWLWU10R				8372	121	240			HWLWU16	pSport1
4096	HWLWU27R				8373	92	253			HWLWU27	pSport1
4097	HWLWW46R				8374	1	222			HWLWW46	pSport1
4098	HWLWW78R				8375	1	234			HWLWW78	pSport1
4099	HWLWW79R				8376	24	65			HWLWW79	pSport1
4100	HWLWX07R				8377	19	168			HWLWX07	pSport1
4101	HWLWX66R				8378	2	64			HWLWX66	pSport1
4102	HWLWX68R				8379	1	51			HWLWX68	pSport1
4103	HWLXA13R				8380	1	171			HWLXA13	pSport1
4104	HWLXA23R				8381	2	226			HWLXA23	pSport1
4105	HWLXA45R				8382	2	145			HWLXA45	pSport1
4106	HWLXC34R				8383	36	188			HWLXC34	pSport1
4107	HWLXE61R				8384	223	477			HWLXE61	pSport1
4108	HWLXE79R				8385	1	63			HWLXE79	pSport1
4109	HWLXI51R				8386	1	54			HWLXI51	pSport1
4110	HWLXI76R				8387	86	322			HWLXI76	pSport1
4111	HWLXI59R				8388	2	139			HWLXI59	pSport1
4112	HWLXI79R				8389	135	296			HWLXI79	pSport1
4113	HWLXK62R				8390	377	529			HWLXK62	pSport1
4114	HWLXN33R				8391	2	67			HWLXN33	pSport1
4115	HWLXO57R				8392	2	211			HWLXO57	pSport1
4116	HWLXO71R				8393	30	101			HWLXO71	pSport1
4117	HWLXO81R				8394	3	206			HWLXO81	pSport1
4118	HWLXP33R				8395	1	69			HWLXP33	pSport1
4119	HWLXP45R				8396	2	196			HWLXP45	pSport1
4120	HWLXP60R				8397	2	109			HWLXP60	pSport1
4121	HWLXQ33R				8398	2	52			HWLXQ33	pSport1
4122	HWLXQ50R				8399	2	52			HWLXQ50	pSport1
4123	HWLXQ71R				8400	3	236			HWLXQ71	pSport1
4124	HWLXQ81R				8401	3	110			HWLXQ81	pSport1
4125	HWLXR27R				8402	44	226			HWLXR27	pSport1
4126	HWLXR49R				8403	2	142			HWLXR49	pSport1
4127	HWLXR74R				8404	10	240			HWLXR74	pSport1

4128	HWLXT31R			8405	138	284			HWLXT31	pSportl
4129	HWLXV15R			8406	1	150			HWLXV15	pSportl
4130	HWLXV27R			8407	1	129			HWLXV27	pSportl
4131	HWLXW17R			8408	2	115			HWLXW17	pSportl
4132	HWLXW20R			8409	32	130			HWLXW20	pSportl
4133	HWMBM46R			8410	114	212			HWMBM46	pSportl
4134	HWMBD22R			8411	32	433			HWMBD22	pSportl
4135	HWMBD49R			8412	2	61			HWMBD49	pSportl
4136	HWMBD71R			8413	3	131			HWMBD71	pSportl
4137	HWMBE31R	(AF169797) adaptor protein APPL [Homo sapiens] >sp AAAF04012 AAAF04012 Adaptor protein APPL. Length = 709	gb AAAF04012.1 AAAF1697	8414	1	408	60	72	HWMBE31	pSportl
4138	HWMBE36R			8415	90	221			HWMBE36	pSportl
4139	HWMBF87R			8416	209	388			HWMBF87	pSportl
4140	HWMBG63R			8417	1	54			HWMBG63	pSportl
4141	HWMBG89R			8418	2	142			HWMBG89	pSportl
4142	HWMBH14R			8419	1	93			HWMBH14	pSportl
4143	HWMBI08R			8420	1	315			HWMBI08	pSportl
4144	HWMBI41R			8421	176	313			HWMBI41	pSportl
4145	HWMBI51R			8422	1	150			HWMBI51	pSportl
4146	HWMBK47R			8423	131	313			HWMBK47	pSportl
4147	HWMBL07R			8424	6	206			HWMBL07	pSportl
4148	HWMBL29R			8425	196	396			HWMBL29	pSportl
4149	HWMBL57R			8426	121	330			HWMBL57	pSportl
4150	HWMBL82R			8427	17	496			HWMBL82	pSportl
4151	HWMBM40R			8428	87	218			HWMBM40	pSportl
4152	HWMBM51R			8429	2	70			HWMBM51	pSportl
4153	HWMBM67R			8430	81	221			HWMBM67	pSportl
4154	HWMBM83R			8431	141	299			HWMBM83	pSportl
4155	HWMBM87R			8432	2	136			HWMBM87	pSportl
4156	HWMBN13R			8433	2	163			HWMBN13	pSportl
4157	HWMBN35R			8434	185	355			HWMBN35	pSportl
4158	HWMBN52R			8435	104	274			HWMBN52	pSportl

4159	HWMBN94R				8436	29	133		HWMBN94	pSportl
4160	HWMBP01R				8437	1	84		HWMBP01	pSportl
4161	HWMBP39R				8438	81	308		HWMBP39	pSportl
4162	HWMBP60R				8439	3	125		HWMBP60	pSportl
4163	HWMBP67R				8440	3	143		HWMBP67	pSportl
4164	HWMBP84R				8441	2	229		HWMBP84	pSportl
4165	HWMBR18R				8442	2	133		HWMBR18	pSportl
4166	HWMBR40R				8443	2	130		HWMBR40	pSportl
4167	HWMBR50R				8444	1	117		HWMBR50	pSportl
4168	HWMBR64R				8445	1	156		HWMBR64	pSportl
4169	HWMBR68R				8446	1	150		HWMBR68	pSportl
4170	HWMBR75R				8447	2	124		HWMBR75	pSportl
4171	HWMBR77R				8448	2	103		HWMBR77	pSportl
	A									
4172	HWMBR79R				8449	1	192		HWMBR79	pSportl
4173	HWMBR06R				8450	1	150		HWMBR06	pSportl
4174	HWMBR28R				8451	2	184		HWMBR28	pSportl
4175	HWMBR57R				8452	3	131		HWMBR57	pSportl
4176	HWMBR87R				8453	19	180		HWMBR87	pSportl
4177	HWMBT23R				8454	43	294		HWMBT23	pSportl
4178	HWMBT71R				8455	52	165		HWMBT71	pSportl
4179	HWMBU43R				8456	91	297		HWMBU43	pSportl
4180	HWMBU67R				8457	1	123		HWMBU67	pSportl
4181	HWMBV48R				8458	49	339		HWMBV48	pSportl
4182	HWMBW45R				8459	3	140		HWMBW45	pSportl
4183	HWMBW54R				8460	26	214		HWMBW54	pSportl
4184	HWMBX10R				8461	23	76		HWMBX10	pSportl
4185	HWMBX94R				8462	3	65		HWMBX94	pSportl
4186	HWMBY09R				8463	24	122		HWMBY09	pSportl
4187	HWMBY34R				8464	65	172		HWMBY34	pSportl
4188	HWMBY51R				8465	1	138		HWMBY51	pSportl
4189	HWMBY90R				8466	2	67		HWMBY90	pSportl
4190	HWMBZ52R				8467	250	411		HWMBZ52	pSportl

4191	HWMBZ60R			8468	3	74			HWMBZ60	pSportl
4192	HWMBZ74R			8469	19	210			HWMBZ74	pSportl
4193	HWMBZ84R			8470	6	161			HWMBZ84	pSportl
4194	HWMCA93R			8471	41	238			HWMCA93	pSportl
4195	HWMCB01R			8472	1	108			HWMCB01	pSportl
4196	HWMCB93R			8473	3	233			HWMCB93	pSportl
4197	HWMCC11R			8474	169	375			HWMCC11	pSportl
4198	HWMCC55R			8475	3	59			HWMCC55	pSportl
4199	HWMCD17R			8476	95	232			HWMCD17	pSportl
4200	HWMCD64R			8477	1	36			HWMCD64	pSportl
4201	HWMCD66R			8478	3	158			HWMCD66	pSportl
4202	HWMCE21R			8479	2	49			HWMCE21	pSportl
4203	HWMCE24R			8480	394	615			HWMCE24	pSportl
4204	HWMCF24R			8481	3	92			HWMCF24	pSportl
4205	HWMCF45R			8482	2	127			HWMCF45	pSportl
4206	HWMCH02R			8483	11	220			HWMCH02	pSportl
4207	HWMCH47R			8484	3	203			HWMCH47	pSportl
4208	HWMCH76R			8485	3	140			HWMCH76	pSportl
4209	HWMCI03R			8486	3	254			HWMCI03	pSportl
4210	HWMCI05R			8487	2	115			HWMCI05	pSportl
4211	HWMCI07R			8488	1	213			HWMCI07	pSportl
4212	HWMCI13R			8489	2	103			HWMCI13	pSportl
4213	HWMCI14R			8490	3	161			HWMCI14	pSportl
4214	HWMCI15R			8491	2	124			HWMCI15	pSportl
4215	HWMCI16R			8492	29	124			HWMCI16	pSportl
4216	HWMCI19R			8493	40	225			HWMCI19	pSportl
4217	HWMCI25R			8494	1	126			HWMCI25	pSportl
4218	HWMCI27R			8495	15	224			HWMCI27	pSportl
4219	HWMCI29R			8496	3	137			HWMCI29	pSportl
4220	HWMCI30R			8497	2	211			HWMCI30	pSportl
4221	HWMCI32R			8498	17	217			HWMCI32	pSportl
4222	HWMCI39R			8499	5	133			HWMCI39	pSportl
4223	HWMCI40R			8500	20	112			HWMCI40	pSportl

4224	HWMCI41R			8501	2	199			HWMCI41	pSportl
4225	HWMCI42R			8502	1	102			HWMCI42	pSportl
4226	HWMCI43R			8503	6	134			HWMCI43	pSportl
4227	HWMCI44R			8504	6	143			HWMCI44	pSportl
4228	HWMCI50R			8505	2	211			HWMCI50	pSportl
4229	HWMCI53R			8506	41	145			HWMCI53	pSportl
4230	HWMCI55R			8507	2	169			HWMCI55	pSportl
4231	HWMCI56R			8508	22	114			HWMCI56	pSportl
4232	HWMCI62R			8509	2	253			HWMCI62	pSportl
4233	HWMCI80R			8510	1	102			HWMCI80	pSportl
4234	HWMCI85R			8511	110	202			HWMCI85	pSportl
4235	HWMCI87R			8512	2	193			HWMCI87	pSportl
4236	HWMCI88R			8513	2	100			HWMCI88	pSportl
4237	HWMCI92R			8514	78	305			HWMCI92	pSportl
4238	HWMCI42R			8515	1	120			HWMCI42	pSportl
4239	HWMCK88R			8516	13	204			HWMCK88	pSportl
4240	HWMCK92R			8517	3	242			HWMCK92	pSportl
4241	HWMCL13R			8518	2	130			HWMCL13	pSportl
4242	HWMCL18R			8519	2	145			HWMCL18	pSportl
4243	HWMCL44R			8520	1	300			HWMCL44	pSportl
4244	HWMCL55R			8521	150	317			HWMCL55	pSportl
4245	HWMCL61R			8522	43	162			HWMCL61	pSportl
4246	HWMCL65R			8523	3	98			HWMCL65	pSportl
4247	HWMCL68R			8524	2	106			HWMCL68	pSportl
4248	HWMCL74R			8525	1	162			HWMCL74	pSportl
4249	HWMCM18R			8526	3	194			HWMCM18	pSportl
4250	HWMCM19R			8527	45	185			HWMCM19	pSportl
4251	HWMCM32R			8528	72	179			HWMCM32	pSportl
4252	HWMCM39R			8529	52	132			HWMCM39	pSportl
4253	HWMCM61R			8530	1	114			HWMCM61	pSportl
4254	HWMCM67R			8531	3	104			HWMCM67	pSportl
4255	HWMCM75R			8532	1	141			HWMCM75	pSportl
4256	HWMCM77R			8533	3	134			HWMCM77	pSportl

4257	HWMCM80R			8534	3	170			HWMCM80	pSport1
4258	HWMCM85R			8535	2	100			HWMCM85	pSport1
4259	HWMCM89R			8536	3	104			HWMCM89	pSport1
4260	HWMCM92R			8537	8	52			HWMCM92	pSport1
4261	HWTBE01R			8538	2	244			HWTBE01	Uni-ZAP XR
4262	HCQDD08R			8539	111	1			HCQDD08	Lambda ZAP II
4263	H2CBK69R	unnamed protein product [Homo sapiens] >emb CAA88750.1 TX protease precursor [Homo sapiens] >gb AAA75171.1 cysteine protease [Homo sapiens] >gb AAA86890.1 Ich-2 [Homo sapiens] >gb AAC99850.1 Mlh1/TX isoform alpha [Homo sapiens] >pir A57511 A57511 inte	emb CAA0315 4.1	8540	257	535	98	98	H2CBK69	pBluescript SK-
4264	H2CBD14R	unnamed protein product [unidentified] >emb CAB41416.1 (AJ238246) sarcolectin [Homo sapiens] >sp Q9Y3R7 Q9Y3R7 SARCOLECTIN. >emb CAA03727.1 unnamed protein product [unidentified] {SUB 1-135} Length = 469	emb CAA0372 6.1	8541	180	539	88	89	H2CBD14	pBluescript SK-
4265	HCQCJ66R			8542	20	235			HCQCJ66	Lambda ZAP II
4266	HCYBO53R	IDN4-GGTR14 PROTEIN. >dbj BAA77334.1 (AB019493) IDN4-GGTR9 [Homo sapiens] {SUB 57-414} >emb CAA22908.1 (AL035303) hypothetical protein [Homo sapiens] {SUB 159-414} Length = 414	sp Q9Y6Y5 Q9Y6Y5	8543	3	107	100	100	HCYBO53	pBluescript SK-
4267	HWMCK51R	unnamed protein product [unidentified] Length = 396	emb CAA0339 6.1	8544	24	284	95	95	HWMCK51	pSport1

4268	HCQCA92R	URF 2 (NADH dehydrogenase subunit) [Homo sapiens] >gb AAC25441.1 (AF014882) NADH dehydrogenase subunit 2 [Homo sapiens] >gb AAC25443.1 (AF014884) NADH dehydrogenase subunit 2 [Homo sapiens] >gb AAC25444.1 (AF014885) NADH dehydrogenase subunit 2 [Homo sapiens]	emb CAA24027.1	8545	73	231	57	63	HCQCA92	Lambda ZAP II
4269	HCQDK77R			8546	157	432			HCQDK77	Lambda ZAP II
4270	HDTEO77R	NADH dehydrogenase subunit 3 [Pan troglodytes] >dbj BAA85273.1 NADH dehydrogenase subunit 3 [Pan troglodytes] >sp BAA85273 BAA85273 NADH dehydrogenase subunit 3. Length = 115	dbj BAA85273.1	8547	72	230	87	96	HDTEO77	pCMVSPORT 2.0
4271	HCRNC15R	(AF102177) tumor antigen SLP-8p [Homo sapiens] Length = 966	gb AAF37319.1 AF1021	8548	3	539	98	99	HCRNC15	pSport1
4272	HWLRD05R	(AF155103) NY-REN-25 antigen [Homo sapiens] >sp Q9Y5A3 Q9Y5A3 NY-REN-25 ANTIGEN (FRAGMENT). Length = 285	gb AAD42869.1 AF1551	8549	2	496	62	73	HWLRD05	pSport1
4273	HPWBS43R	Whole ORF continues from bp19 (right after "tag") to bp1596 ("tga"); similar to chinese hamster phosphatidylserine synthase. [Homo sapiens] >sp P48651 PSS1_HUMAN PHOSPHATIDYL SERINE SYNTHASE 1 (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KJAA0024). Length	dbj BAA03520.1	8550	2	130	76	78	HPWBS43	Uni-ZAP XR
4274	H2CBU94R	(AL031393) dJ733D15.1 (Zinc-finger protein) [Homo sapiens] Length = 496	emb CAA20564.1	8551	1	360	52	68	H2CBU94	pBluescript SK-
4275	H2LAT50R	(AF080171) zinc finger protein ZNF232 [Homo sapiens] >sp AAD46135 AAD46135 Zinc finger protein ZNF232. Length = 417	gb AAD46135.1	8552	73	537	100	100	H2LAT50	pBluescript SK-
4276	HCQCO58R	zinc finger protein [Homo sapiens] >sp Q15917 Q15917 ZINC FINGER PROTEIN (FRAGMENT). Length = 622	gb AAA36817.1	8553	30	158	32	44	HCQCO58	Lambda ZAP II
4277	HWMCC56R			8554	206	3			HWMCC56	pSport1

The first column of Table 1 shows the "SEQ ID NO:X" for each of the 4277 polynucleotide sequences of the invention. The second column provides a unique "Sequence/Contig ID" for each sequence.

5 The third column in Table 1, "Gene Name", provides a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database, such as GenBank (NCBI). Methods for determining such sequence similarity are described in Example 1, below. The great majority of the cDNA sequences reported in Table 1 are unrelated to any sequences previously described in the literature. The fourth column in Table
10 1, "Overlap," provides the database accession no. for the database sequence having similarity.

The preferred translated amino acid sequence, is identified in column five as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these
15 alternative open reading frames are specifically contemplated by the present invention. Polynucleotides encoding an amino acid sequence comprising these regions are also embodied, as are polynucleotides which hybridize to polynucleotides encoding these regions.

The sixth and seventh columns in Table 1 provide the location (nucleotide
20 position nos.), "Start" and "End," in the polynucleotide sequence "SEQ ID NO:X" that aligns with homologous database sequence. In one embodiment, the invention provides a polypeptide comprising an amino acid sequence encoded by the portion of SEQ ID NO:X delineated by "Start" and "End". Also provided are polynucleotides encoding such polypeptides.

25 The eighth and ninth columns provide the "%Id" (percent identity) and "% Si" (percent similarity) observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence. The eleventh and twelfth columns shown in Table 1 provide a unique Clone identifier (Clone ID:Z) and the Cloning vector contained in the cDNA Clone ID, respectively. At least a portion
30 of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to

encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the colon and/or colon cancer related antigen polypeptides encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a

suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. Table 2 shows the material
5 deposited with the ATCC, the Deposit Date and the ATCC Designation Number.

Table 2

ATCC Deposits	Deposit Date	ATCC Designation Number
LP01, LP02, LP03, LP04, LP05, LP06, LP07, LP08, LP09, LP10, LP11,	May-20-97	209059, 209060, 209061, 209062, 209063, 209064, 209065, 209066, 209067, 209068, 209069
LP12	Jan-12-98	209579
LP13	Jan-12-98	209578
LP14	Jul-16-98	203067
LP15	Jul-16-98	203068
LP16	Feb-1-99	203609
LP17	Feb-1-99	203610
LP20	Nov-17-98	203485
LP21	Jun-18-99	PTA-252
LP22	Jun-18-99	PTA-253
PA-005 Phage, PA-005 DNA	Oct-28-99	PTA-881 PTA-882

each is a mixture of cDNA clones derived from a variety of human tissue and cloned
10 in either a plasmid vector or a phage vector, as shown in Table 9. These deposits are referred to as "the deposits" herein. The tissues from which the clones were derived are listed in Table 9, and the vector in which the cDNA is contained is also indicated in Table 9 as well as Table 1. The deposited material includes the cDNA clones which were partially sequenced and listed in Table 1. Thus, the DNA sequence of
15 Table 1 is only a portion of the sequence included in the clone from which the sequence was derived. Thus, a clone which is isolatable from the ATCC Deposits by

use of a sequence listed in Table 1 may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Although the sequence listing lists only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to complete the sequence of the DNA included in a clone isolatable from the ATCC Deposits by use of a sequence (or portion thereof) listed in Table 1 by procedures hereinafter further described, and others apparent to those skilled in the art.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone, using information from the sequences disclosed herein or the libraries deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

Table 3 summarizes the expression profile of polynucleotides corresponding to the clones disclosed in Table 1. The first column provides a unique clone identifier, "Clone ID:Z", for a cDNA clone related to each contig sequence disclosed in Table 1. Column 2, "Library Codes" shows the expression profile of tissue and/or cell line libraries which express the polynucleotides of the invention. Each Library Code in column 2 represents a tissue/cell source identifier code corresponding to the Library Code and Library description provided in Table 5. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. One of skill in the art could routinely use this information to identify tissues which show a

predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue expression.

Table 4, column 1, provides a nucleotide sequence identifier, "SEQ ID NO:X," that matches a nucleotide SEQ ID NO:X disclosed in Table 1, column 5. Table 4, column 2, provides the chromosomal location, "Cytologic Band or Chromosome," of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). If the putative chromosomal location of the Query overlapped with the chromosomal location of a Morbid Map entry, the OMIM reference identification number of the morbid map entry is provided in Table 4, column 3, labelled "OMIM ID." A key to the OMIM reference identification numbers is provided in Table 6.

Table 5 provides a key to the Library Code disclosed in Table 3. Column 1 provides the Library Code disclosed in Table 3, column 2. Column 2 provides a description of the tissue or cell source from which the corresponding library was derived.

Table 6 provides a key to the OMIM reference identification numbers disclosed in Table 4, column 3. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). Column 2 provides diseases associated

with the cytologic band disclosed in Table 4, column 2, as determined using the Morbid Map database.

Table 3.

Clone ID NO: Z	Library Codes
HCENL15	H0052 H0083 H0263 H0620 L0740 L0759 L0777
HSKII86	H0031 H0056 H0090 H0159 H0250 H0264 H0268 H0341 H0422 H0423 H0518 H0521 H0528 H0575 S0032 S0046 S0132 S0134 S0280 S3014 T0041 T0042
HNHDV16	S0053
HE8BQ01	H0013 H0090 H0263 L0438 L0439 L0521 L0655 L0686 L0731 L0748 L0750 L0752 L0755 L0766 L0769 L0776 S0148 S0360
HBMCT70	H0040 H0090 H0421 L0740 L0766
HNTBM67	H0013 H0031 H0032 H0040 H0046 H0052 H0123 H0163 H0170 H0171 H0178 H0201 H0266 H0355 H0369 H0373 H0381 H0390 H0411 H0427 H0428 H0435 H0438 H0486 H0519 H0520 H0539 H0550 H0551 H0555 H0562 H0590 H0602 H0615 H0623 H0624 H0648 H0659 H0660 H0662 H0667 H0670 H0672 H0682 H0685 H0686 L0005 L0366 L0370 L0372 L0438 L0439 L0471 L0483 L0518 L0520 L0521 L0526 L0527 L0564 L0565 L0595 L0596 L0598 L0602 L0637 L0641 L0646 L0650 L0659 L0662 L0663 L0664 L0665 L0666 L0731 L0740 L0751 L0753 L0754 L0755 L0756 L0758 L0759 L0768 L0769 L0771 L0773 L0774 L0776 L0777 L0779 L0783 L0806 S0003 S0026 S0028 S0031 S0036 S0045 S0046 S0049 S0051 S0194 S0196 S0212 S0222 S0242 S0260 S0280 S0328 S0330 S0354 S0356 S0360 S0370 S0374 S0376 S0380 S0388 S0418 S0450 S6028 T0006 T0040 T0110
HDPKC15	H0521 S0134 S0300 S0360
HE2OC31	H0170 H0412 H0641 L0759 L0766 L0770 L0775 L0779 S0360
HLWAY38	H0522 H0543 H0553 H0581 L0731 L0740 L0755 L0766 L0771 L0774 L0777 L0792 L0800 L0803
HBMXT67	H0012 H0052 H0135 H0144 H0171 H0351 H0369 H0457 H0543 H0620 H0644 H0653 H0658 H0663 L0167 L0438 L0439 L0471 L0526 L0541 L0591 L0599 L0638 L0646 L0666 L0743 L0747 L0748 L0750 L0754 L0756 L0758 L0761 L0763 L0764 L0765 L0766 L0770 L0774 L0777 L0779 L0803 L0809 S0006 S0007 S0010 S0116 S0134 S0360
HCRND41	H0156 H0545 H0587 H0672 L0055 L0663 L0743 L0747 L0752 L0756 L0759 L0768 L0774 L0775 L0776 L0777 L0783 L0784 S0050 S0278 S0356 S0360 T0041
HWLQA43	H0031 S0150 S0358 S0360
HWLQI33	H0013 H0135 H0163 H0271 H0423 H0549 H0648 L0731 L0740 L0751 L0759 L0761 L0764 L0766 L0769 L0770 L0776 L0777 L0779 L0783 L0789 L0796 L0805 L0806 L0809 S0114 S0126 S0190 S0360 S6024
HSXDD55	L0438 L0439 L0608 L0758 S0036 S0356
HDQPP57	H0522 L0748
HCPAC07	H0340 H0590 H0596 H0641 L0520 L0639 L0745 L0809
HCRNF04	H0171 H0620 H0624 L0592 L0751 L0769 L0774 L0777 S0222 S0356
HMWHN4 3	H0144 H0341 L0471 L0752 L0766 L0779 S0126 T0110
HTTEL19	H0009 H0031 H0038 H0040 H0041 H0046 H0052 H0059 H0122 H0124 H0144 H0156 H0250 H0253 H0254 H0255 H0264 H0268 H0392 H0411 H0436 H0445 H0478 H0506 H0521 H0543 H0547 H0556 H0563 H0575 H0594 H0596 H0616 H0620 H0622 H0627 H0650 H0651 H0652 H0657 H0666 L0055 L0351 L0372 L0382 L0438 L0439 L0456 L0471 L0526 L0543 L0593 L0599 L0638 L0646 L0653 L0655 L0659 L0662 L0664 L0665 L0666 L0731 L0740 L0743 L0744 L0747 L0748 L0751 L0754 L0755 L0756 L0757 L0758 L0766 L0769 L0770 L0771 L0775 L0776 L0788 L0794 L0803 L0805 S0026 S0027 S0038 S0049 S0126 S0132 S0134 S0212 S0222 S0250 S0276 S0278 S0280 S0360 S0376 S0380 S0422 S0424 S0436 S0468 S6028 T0002 T0006 T0042

	T0067 T0110
HMCFS02	H0170 H0255 H0294 H0423 H0478 H0529 H0539 H0583 H0618 H0656 H0665 H0688 H0702 L0055 L0438 L0483 L0599 L0629 L0636 L0643 L0645 L0653 L0659 L0665 L0666 L0731 L0749 L0750 L0751 L0754 L0755 L0757 L0758 L0761 L0764 L0766 L0776 L0779 L0788 L0789 L0790 L0791 L0794 L0803 L0804 L0805 L0806 L0809 S0282 S0330 S0344 S0420 S0428
HDTBY31	H0004 H0014 H0015 H0032 H0039 H0040 H0052 H0156 H0251 H0266 H0268 H0318 H0328 H0356 H0361 H0369 H0373 H0375 H0413 H0427 H0428 H0445 H0486 H0488 H0506 H0519 H0520 H0546 H0551 H0553 H0555 H0575 H0586 H0587 H0590 H0591 H0594 H0597 H0598 H0601 H0615 H0622 H0623 H0624 H0631 H0642 H0643 H0644 H0651 H0662 H0665 H0667 L0163 L0438 L0439 L0471 L0517 L0519 L0527 L0565 L0581 L0598 L0638 L0654 L0659 L0731 L0740 L0745 L0747 L0748 L0749 L0751 L0754 L0757 L0758 L0769 L0773 L0776 L0777 L0779 L0804 S0003 S0004 S0013 S0027 S0028 S0031 S0037 S0040 S0045 S0046 S0126 S0146 S0174 S0192 S0196 S0208 S0210 S0212 S0214 S0250 S0342 S0356 S0360 S0376 S0390 S0402 S0418 S0438 S3014 T0067
HTXFI40	H0265 H0444 H0595 L0779 S0376
HADFW62	H0052 H0156 H0333 H0427 H0478 H0521 H0556 H0617 H0646 H0670 L0384 L0439 L0543 L0591 L0646 L0657 L0745 L0747 L0749 L0756 L0757 L0764 L0769 L0776 S0116 S0210
HARMP12	H0592
HDPCN86	H0309 H0521 S0028 S0356
HFIAX76	H0057 H0529 L0055 L0483 L0750 L0756 L0758 L0759 L0766 L0773 L0776 L0779 S0192 S0300 S0360 S0378 S0422 S0452
HAFBC92	H0445 L0740 L0751 T0049
HFIZG43	H0208 H0251 H0445 H0486 H0615 L0439 L0740 L0750 S0214 S0242 T0041
HMEBY61	H0267 T0049
HTJNI76	H0263 H0435 H0486 H0488 H0520 H0579 H0662 H0687 L0438 L0527 L0645 L0656 L0751 L0753 L0766 L0771 L0779 L0783 L0809 S0192 S0300 S0376
HWLFM26	H0085 H0232 H0234 H0597 L0372 L0645 L0789 S0354 S0358 S0374 S0378 S0380 S0408 S0442
HAQBZ89	H0295 S0218
HWLEH32	S0354
HWLEL81	S0010 S0354 S0356 S0358 S0374 S0432 S0442
HTLHR67	H0013 H0037 H0052 H0187 H0251 H0416 H0509 H0518 H0538 H0543 H0549 H0551 H0617 H0618 L0362 L0643 L0666 L0717 L0720 L0731 L0748 L0752 L0754 L0755 L0774 L0775 L0777 L0779 L0789 L0804 S0003 S0010 S0049 S0116 S0280 S0356 S0360 T0067
HTSGO78	H0039 H0040 H0087 H0131 H0194 H0592 S0001
HCBBA51	H0009 H0013 H0023 H0031 H0039 H0040 H0042 H0044 H0046 H0052 H0087 H0100 H0125 H0134 H0136 H0144 H0150 H0163 H0170 H0171 H0173 H0177 H0201 H0204 H0231 H0238 H0255 H0294 H0306 H0309 H0341 H0373 H0393 H0408 H0411 H0412 H0413 H0421 H0422 H0423 H0428 H0441 H0445 H0486 H0494 H0546 H0576 H0581 H0586 H0595 H0596 H0597 H0598 H0599 H0606 H0609 H0616 H0617 H0622 H0633 H0634 H0635 H0646 H0648 H0651 H0653 H0657 H0658 H0659 H0661 H0663 H0664 H0669 H0670 H0672 H0674 H0682 H0685 H0686 H0690 L0005 L0163 L0373 L0375 L0394 L0500 L0519 L0520 L0521 L0522 L0526 L0542 L0588 L0598 L0622 L0623 L0637 L0653 L0731 L0747 L0750 L0751 L0755 L0757 L0758 L0759 L0761 L0762 L0763 L0764 L0767 L0768 L0769 L0772 L0773 L0774 L0775 L0782 L0783 L0789 L0803 L0808 L0809 S0003 S0007 S0011 S0026 S0027 S0031 S0032 S0045 S0046 S0048 S0051 S0053 S0116 S0126 S0132 S0134 S0142 S0144 S0152 S0188 S0194 S0222 S0260 S0278 S0280 S0282 S0328 S0330 S0344 S0358 S0360 S0366 S0374 S0376 S0378 S0380 S0388 S0394 S0422 S0428 S6022 S6024 T0002 T0006 T0023 T0039 T0041 T0048 T0049 T0069 T0109

HNTCW73	H0038 H0040 H0052 H0125 H0144 H0194 H0252 H0288 H0359 H0494 H0519 H0547 H0551 H0657 L0483 S0026 S0027 S0028 S0045 S0046 S0152 S0206 S0342 S0346 T0103
HLYGG06	H0181 H0444 H0445 H0596 H0657 H0670 L0373 L0439 L0499 L0500 L0502 L0504 L0505 L0506 L0507 L0508 L0509 L0511 L0540 L0659 L0663 L0740 L0748 L0750 L0752 L0754 L0758 L0763 L0764 L0768 L0769 L0777 L0779 L0783
HAPOA59	H0013 H0038 H0040 H0050 H0056 H0057 H0059 H0144 H0169 H0264 H0266 H0318 H0341 H0428 H0509 H0519 H0529 H0539 H0544 H0556 H0560 H0572 H0574 H0575 H0591 H0615 H0616 H0619 H0646 H0648 H0649 H0663 L0096 L0375 L0378 L0438 L0439 L0471 L0520 L0558 L0588 L0589 L0592 L0593 L0595 L0601 L0637 L0655 L0659 L0664 L0666 L0731 L0740 L0747 L0748 L0749 L0752 L0753 L0754 L0756 L0757 L0758 L0759 L0764 L0766 L0768 L0769 L0770 L0771 L0774 L0775 L0776 L0779 L0780 L0783 L0789 L0794 L0803 L0804 L0805 L0809 S0014 S0036 S0040 S0132 S0144 S0152 S0250 S0328 S0356 S0392 S0418 S0420 S0422 S0616 S0624 S0628 T0041 T0067 T0109 T0110
HKLRB18	H0002 H0013 H0014 H0036 H0046 H0050 H0144 H0163 H0234 H0251 H0266 H0411 H0412 H0413 H0427 H0545 H0550 H0551 H0586 H0593 H0599 H0615 H0672 L0005 L0163 L0366 L0471 L0542 L0591 L0599 L0659 L0731 L0748 L0750 L0756 L0757 L0758 L0759 L0777 L0783 L0803 S0026 S0027 S0045 S0152 S0192 S0206 S0212 S0276 S0328 S0356 S0360 S0418 S3014 T0040
HKAJZ24	H0263 H0494 S0354 S0358 T0039
HJPAU37	H0083 H0097 H0253 H0494 H0556 H0560 H0580 H0593 H0657 L0754 L0766 L0777 S0356
HHGCU20	H0039 H0052 H0087 H0125 H0135 H0144 H0253 H0318 H0333 H0380 H0445 H0494 H0542 H0556 H0617 H0624 H0657 H0661 L0471 L0520 L0526 L0622 L0623 L0731 L0747 L0748 L0749 L0758 L0759 L0764 L0766 L0769 L0774 L0779 L0806 L0809 S0144 S0210 S0222 S0344 S0360 S0420 S3012 S6022 T0008 T0049 T0082 T0115
HHEDO80	H0014 H0015 H0156 H0263 H0318 H0411 H0412 H0436 H0445 H0455 H0497 H0521 H0529 H0542 H0543 H0574 H0575 H0581 H0596 H0599 H0657 H0659 L0005 L0021 L0455 L0517 L0589 L0590 L0591 L0639 L0664 L0731 L0740 L0741 L0747 L0752 L0755 L0759 L0766 L0769 L0773 L0775 L0776 L0777 L0780 L0794 L0809 S0003 S0132 S0342 S0360 S0374 S0378 S6024
HFIHX78	H0031 H0036 H0051 H0250 H0251 H0263 H0393 H0427 H0436 H0486 H0520 H0575 H0580 H0592 H0596 H0598 H0635 H0661 H0662 L0065 L0373 L0439 L0666 L0731 L0748 L0752 L0774 L0783 S0194 S0358 S0360 T0023 T0067
HTXOJ32	H0013 H0052 H0056 H0087 H0100 H0150 H0212 H0255 H0352 H0369 H0408 H0486 H0556 H0595 H0599 H0619 H0652 H0670 L0352 L0369 L0381 L0415 L0438 L0439 L0518 L0519 L0528 L0530 L0543 L0588 L0591 L0596 L0605 L0629 L0646 L0659 L0731 L0741 L0747 L0751 L0757 L0758 L0761 L0764 L0768 L0769 L0771 L0773 L0774 L0809 S0003 S0031 S0038 S0045 S0106 S0126 S0134 S0222 S0242 S0250 S0314 S0354 S0356 S0360 S0376 T0010 T0041
HE6FT69	H0100 L0601
HFIHN81	H0012 H0046 H0050 H0051 H0052 H0059 H0090 H0098 H0144 H0170 H0264 H0309 H0328 H0356 H0370 H0412 H0427 H0428 H0459 H0509 H0521 H0546 H0547 H0562 H0575 H0591 H0596 H0598 H0616 H0624 H0628 H0634 H0648 H0658 H0659 H0670 H0672 H0684 L0021 L0157 L0362 L0439 L0444 L0485 L0518 L0523 L0599 L0600 L0646 L0657 L0659 L0662 L0663 L0664 L0665 L0717 L0731 L0738 L0745 L0750 L0751 L0752 L0754 L0756 L0758 L0759 L0766 L0768 L0770 L0774 L0776 L0777 L0779 L0783 S0003 S0026 S0126 S0194 S0212 S0214 S0222 S0242 S0260 S0328 S0330 S0354 S0356 S0360 S0376 S0378 S0426 S0464 S0628 T0006 T0067
HWACZ95	H0012 H0144 H0370 H0393 H0485 H0521 H0574 H0581 H0615 H0620 H0635 L0381 L0591 L0608 L0648 L0743 L0766 L0774 S0356 S0376
HOELH62	H0040 H0069 H0083 H0090 H0100 H0123 H0144 H0187 H0266 H0333 H0341 H0370 H0402 H0411 H0413 H0441 H0510 H0525 H0530 H0543 H0544 H0545

	H0546 H0580 H0634 L0361 L0375 L0588 L0740 L0747 L0748 L0752 L0767 S0026 S0040 S0045 S0112 S0114 S0116 S0126 S0182 S0196 S0354 S0358 S0374 S0404 S0462 S3012
HCE3J64	H0052 H0333 L0439 L0636 L0637 L0742 L0759 S0376 S0388
HWHGE39	H0038 H0051 H0136 H0144 H0178 H0222 H0235 H0305 H0341 H0373 H0393 H0428 H0435 H0441 H0494 H0506 H0519 H0520 H0542 H0543 H0547 H0555 H0586 H0587 H0624 H0646 H0648 H0650 H0657 H0667 H0670 H0684 L0021 L0352 L0438 L0439 L0517 L0586 L0592 L0662 L0664 L0666 L0731 L0740 L0744 L0747 L0748 L0749 L0752 L0755 L0756 L0757 L0758 L0759 L0766 L0768 L0773 L0776 L0777 L0779 L0784 L0804 L0809 S0002 S0007 S0010 S0036 S0132 S0192 S0328 S0356 S0358 S0376 S0424 S0460 T0010 T0115
HNGIN84	H0014 H0036 H0039 H0085 H0183 H0204 H0231 H0506 H0509 H0590 H0596 H0597 H0622 L0021 L0040 L0364 L0365 L0372 L0373 L0374 L0509 L0596 L0599 L0646 L0659 L0662 L0761 L0764 L0765 L0772 L0775 L0789 S0052 S0354 S0356 S0358 S0360 S0374 S0376 S0378 S0380 S0408 S0440 S0442 T0008 T0023 T0109
HPJCI42	H0309 H0370 H0550 H0622 H0624 H0632 H0634 L0005 L0662 L0666 L0764 L0769 L0775 L0776 L0794 S0036 S0152
HWLOF51	H0013 H0040 H0318 S0376
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HCQDE22	H0596 L0749
HWLVU33	L0758 S0360
HKGBP52	H0040 H0331 H0538 L0005 L0351 L0439 L0731 L0740 L0748 L0749 L0754 L0757 L0758 L0775 L0776 L0800 S0356 S0360 S0426

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HCRMW6 2	H0263 H0313 H0428 H0445 H0486 H0539 H0667 L0471 L0594 L0758 L0766 L0777 S0026 S0194 S0356
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Table 4

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9	6q21-q22	120110 121014 156225 164200 601410 601666 601757 602772
17	11q22	105580 133780 602574
18	3p21.3	116806 120120 120436 138320 168468 182280 600163
26	Xp11.21	300047 301300 301830 305400 308300 309470 309500 309610 311050
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36	Xq13	300011 300032 301310 305100 305450 308380 309605 311800 311870 314580
40	22q11.23	123620 600850
42	11q22-q23	105580 107680 107720 133780 147791 159555 168000 186740 186830 188025 203750 208900 261640 600048 601382 602574
46	17q12-q21	109270 113705 144200 148065 148066 148067 148069 148080 154275 168610 171190 176705 180240 182138 185800 200350 221820 232200 249000 252920 253250 600119 600881 601363 601687 601844 601954
47	19q13.2	107741 113900 122720 126340 126391 160900 164731 173850 207750 248600 258501
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69	12p12.1	112410 150100 168470 190070 200990 602096
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92	2p22	120435 182601 278300 601071 601771 602134
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279	14q24.3	104311 109150 182600 245200 601208
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358	7q34-q35	118425 152427 180105 222800 274180 276000 600510
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749	4q28-q32	107250 134820 134830 134850 181600 189800 208400 231675 266300 600983
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1708	20p12	112261 176640 236700 601920
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1975	5q35.3	
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1983	15q	
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1986	17p13	138190 254210 271900 600179 600977 601202 601777
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2189	12	
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2197	12q24.3	160781 181405
2199	8q13.3	214400 600415 601653 602476
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2215	12q13-q15	107777 120140 123829 123940 126337 139350 147570 148040 148041 148043 148070 181430 231550 232800 252940 264700 600194 600231 600536 600698 600808 600956 601284 601769 601928 602116 602153
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2239	16p13.3	141750 141800 141850 156850 186580 191092 600140 600273 601313 601785
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2266	2p12	147200 178640 216900
2267	2p12	147200 178640 216900
2268	2p22-p21	120435 126600 135300 136435 152790 157170 182601 278300 601071 601771 602134
2270	22q13.33	
2271	22q13.31	250100 250800
2272	22q13.1	103050 124030 138981 182380 188826 190040
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2281	5p14-p13	108962 120940 217050 217070 245050 600837 600946
2283	17q21	109270 113705 144200 148065 148066 148067 148069 148080 154275 168610 171190 176705 185800 200350 221820 232200 249000 252920 253250 600119 601363 601844
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2306	17p13.3	113721 247200 600059 601545
2307	10	
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2454	9cen-q34	
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2497	2p12	147200 178640 216900
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2547	5q31.1	131400 147061 147575 153455 159000 181460 600807 601596 602089
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2614	12q	
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2617	19q12-q13.1	109560 164731 172400 180901 205900 221770 248600 600652 600757 600918 602716
2619	22q13.1	103050 124030 138981 182380 188826 190040
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2621	16p13.11	145505 186580 278760
2623	6p21.3	106300 108800 120290 120810 120820 142857 142858 150270 167250 170261 177900 179450 201910 217000 222100 233100 235200 248611 256550 600202 600261 601868 602280 602475
2626	21q22.3	120220 120240 123580 151385 171860 190685 236100 236200 240300 267750 600065 601072 601145
2627	1q31-q32	114208 119300 120620 120920 134370 134580 145001 145260 150292 150310 179820 191045 208250 226450 600105 600759 600995 601494 601652 601975
2628	11p15.5-p15.4	125852 126452 130650 141900 142000 142200 142250 142270 150000 176730 190020 191290 192500 194071 204500 257200 600856 601680 602631
2629	1	
2633	8q22-q23	148900 216550 259730
2634	12q12	600194 600231 601284 601769
2635	2p22-p21	120435 126600 135300 136435 152790 157170 182601 278300 601071 601771 602134
2636	7q21.1	129900 154276 171050 171060 602136 602447
2637	17p13.3	113721 247200 600059 601545
2640	2p12	147200 178640 216900
2641	5q11.2-q13.1	126060 143200 181510 214300 253200 268800 600354 600887
2642	22q13.1	103050 124030 138981 182380 188826 190040
2645	11q13.2-q13.3	133780 151400 602078
2648	5p13-cen	
2650	14	
2651	12q24.2	100650 142410 160781 181405
2652	12q13.1	126337 600808 601284 601769 602116
2655	13q14	109543 600631 601499
2656	20p13	192340 234200
2657	16p13.3	141750 141800 141850 156850 186580 191092 600140 600273 601313 601785
2659	19p13.1-p12	143890 151440 600173 600276 600310 601011 601604

		601768 601843
2660	1q41-q42	106150 145260 173870 276901 600332 600759 600996 601744 601975
2681	8p22	148370 238600 600143 601385 602629
2682	19p13.3-p13.2	108725 120700 133171 136836 143890 145981 147141 147670 151440 164953 188070 231670 600276 600957 601238 601843 601846 602216 602477
2742	6p21.3	106300 108800 120290 120810 120820 142857 142858 150270 167250 170261 177900 179450 201910 217000 222100 233100 235200 248611 256550 600202 600261 601868 602280 602475
2744	22q12.1	123620 188826 600850 601669
2786	19q13.2-q13.4	107741 113900 122720 126340 126391 130410 134790 138570 152780 160900 164731 173850 191044 207750 248600 258501 600040 600138 602225
2808	17p13-p12	100710 138190 231200 254210 262850 271900 600179 600977 601202 601777
2815	3q21-q23	106165 110100 117700 150210 169600 180380 190000 203500 232050 276902 600882 601199 601471 601682
2844	11p13	102772 106210 107271 114550 115500 136530 151390 179615 179616 180385 194070 245349
2849	5q14-q22	143200 159350 162150 175100
2858	6p21.1-p12	179605 180297 230450 248611 251000 263200 600211 600364 600701 601498 601690
2863	10q26.3	263700
2869	12	
2901	2p12-p13	147200 178640 203800 216900 602404
2922	X	
2930	7q34	180105 222800 274180
2936	6q14	136550 203310 269920 602772
2942	14q11.2	182600 186880 190195 222700 600243 602279
2979	12q13	107777 123940 139350 148040 148041 148043 148070 231550 600194 600231 600536 600808 600956 601284 601769 601928 602116 602153
3024	12p13	103950 120580 131440 139130 142680 176260 190450 200990 216950 600228 600414 600618 602096
3070	5q31.1	131400 147061 147575 153455 159000 181460 600807 601596 602089
3079	6q14	136550 203310 269920 602772
3080	6q14	136550 203310 269920 602772
3082	7	
3117	1p36	118210 120550 120570 120575 121800 130500 133200 155600 171760 185470 211420 230350 255800 601990 602023 602771
3130	9p21	108120 112250 247640 600160 600221 601606
3133	11q25	602782
3154	12q24.1	124200 147440 160781 181405 261600 601406 601620 601621
3177	Xp22.32	306250 308100 312865
3178	4q34-q35	158900 189800 229000 264900

3183	11q13	102200 106100 131100 133780 147050 153700 161015 164009 168461 180721 180840 191181 193235 209901 232600 259700 259770 600045 600319 600528 601884
3187	13q14	109543 600631 601499
3205	17p13.3	113721 247200 600059 601545
3226	5q14-q22	143200 159350 162150 175100
3236	11q13	102200 106100 131100 133780 147050 153700 161015 164009 168461 180721 180840 191181 193235 209901 232600 259700 259770 600045 600319 600528 601884
3243	17q21	109270 113705 144200 148065 148066 148067 148069 148080 154275 168610 171190 176705 185800 200350 221820 232200 249000 252920 253250 600119 601363 601844
3259	13q14	109543 600631 601499
3281	14q24-q31	104311 107970 109150 115650 182600 245200 275200 601208 602091
3287	19q13.3	113900 126340 126391 130410 134790 138570 160900 173850 258501 600040 602225
3299	12q13-q14	107777 120140 123829 123940 126337 139350 147570 148040 148041 148043 148070 181430 231550 232800 252940 264700 600194 600231 600536 600808 600956 601284 601769 601928 602116 602153
3306	2p25	274500 602134
3316	2	
3323	22q13.2-q13.31	188826 250100 250800
3329	21q22.1	147450 176261 253270 601399
3335	15q15.3	114240 224120 600839 602099
3351	12q12-q13	107777 123940 139350 148040 148041 148043 148070 231550 600194 600231 600536 600808 600956 601284 601769 601928 602116 602153
3357	9q11-q22	190100 200150 229300 229600 264300 600429 600542 600884 600974 600998 602014 602088
3382	16q22.1	103850 114835 116800 140100 192090 245900 276600 600223
3392	19q13.4	134790 191044 600040 600138
3411	5q13	126060 143200 181510 253200 268800 600354
3429	9q22.3	162400 227645 229700 278700 601309 602088
3434	6p21	180297 248611 251000 263200 600211 600701 601690
3439	15q15	177070 182500 218000 227220 243500 600839 601800
3442	20q12	600281
3445	12	
3451	2q31	100690 120180 120190 142989 156232 178600 266100 600258 600321
3455	16q22	103850 114835 121360 217800 218030
3460	11q12	106100 147050 259700 259770 600045 601884
3465	11q13-q14	102200 106100 131100 133780 147050 151400 153700 161015 164009 168461 180721 180840 191181 193235 203100 209901 232600 245000 259700 259770 266150 276903 600045 600319 600528 601650 601884 602078
3477	1q12-1q21.2	104770 107670 110700 135940 145001 146760 146790

		152445 159001 174000 179755 182860 191315 230800 266200 600897 601105 601412 601652 601863 602491
3492	16q22.1	103850 114835 116800 140100 192090 245900 276600 600223
3497	17q25	114290 138033 162100 170500 180860 264470
3503	1p31-p12	102770 120280 164790 166600 170995 180069 188540 191540 201450 201810 232400 248610 274270 600234 600309 601414 601676 601691 601718 602094 602522
3526	20	
3532	5q23-31	121050 126150 131400 138040 153455 159000 179095 181460 192974 600807 601596 601692 602089 602121 602460
3544	2p25.2-p25.1	
3549	12q24	113100 124200 147440 158590 160781 163950 251170 276710 600175 601517
3551	12q13	107777 123940 139350 148040 148041 148043 148070 231550 600194 600231 600536 600808 600956 601284 601769 601928 602116 602153
3555	1p31	180069 201450 248610 600309 601676 602522
3559	5q33-q34	109690 123101 131400 154500 164770 180071 181460 222600 234000 272750 600584 600807 601411 601596 602089
3560	3q13.1-q13.2	600467 600882
3561	19q12	
3564	21q22.3	120220 120240 123580 151385 171860 190685 236100 236200 240300 267750 600065 601072 601145
3566	16q12-q13	114835 132700 172490 600968 602218 602639
3567	16q24.3	155555 227650 253000 602783
3573	1q32	114208 119300 120620 120920 134370 134580 145260 150310 179820 191045 600105 600759 601494 601975
3574	10q21.1	129010 601386 601493
3576	19	
3600	19q13.3-q13.4	113900 126340 126391 130410 134790 138570 152780 160900 173850 191044 258501 600040 600138 602225
3607	12q13	107777 123940 139350 148040 148041 148043 148070 231550 600194 600231 600536 600808 600956 601284 601769 601928 602116 602153
3608	1p33-p34	120260 130500 133200 138140 168360 171760 176100 178300 230000 246450 255800
3611	2	
3623	17q25	114290 138033 162100 170500 180860 264470
3636	7q11	
3646	3p21.3	116806 120120 120436 138320 168468 182280 600163
3647	11q13	102200 106100 131100 133780 147050 153700 161015 164009 168461 180721 180840 191181 193235 209901 232600 259700 259770 600045 600319 600528 601884
3650	Xp22.1	300075 300077 301200 302350 306000 306100 307800 309510 311770 312040 312170 312700 313400
3652	5q22-q23	121050 126150 159000 175100 179095 192974 601596
3653	1q44-qter	

3659	19q13.1	164731 172400 180901 221770 248600 600918 602716
3671	7p21-p15	138079 139191 142959 153880 180104 600994 601622 601649
3683	15q26	180090 600318
3688	10q11.2	154545 164761 188550
3690	12q24.31	181405
3691	6q14	136550 203310 269920 602772
3701	15q21-q22.2	102578 105600 107910 109700 114240 134797 151670 154550 160777 191010 600839 601780 602099
3702	1	
3703	Xq24	300046 300123 301201 301835 301845 307150 310490 311850
3704	8q21.3-q22.1	216550 222745 259730
3705	2q31	100690 120180 120190 142989 156232 178600 266100 600258 600321
3706	22q13.31	250100 250800
3707	3q12-q13	121300 146200 190300 258900 600882
3711	12q22-q23	124200 147440 160781 201470 235800 273300 600175
3712	15q21-q22.2	102578 105600 107910 109700 114240 134797 151670 154550 160777 191010 600839 601780 602099
3729	8q	
3749	19q13.1-q13.2	107741 113900 122720 126340 126391 160900 164731 172400 173850 180901 207750 221770 248600 258501 600918 602716
3773	12q24.2	100650 142410 160781 181405
3782	3p21	139330 139360 150250 164500 182280 600163 600971 601226 601267 601373
3784	5q13.3-q14	139150 143200 181510 600354
3800	4q13-q21	103600 104150 104500 125490 147790 170650 173910 252500
3803	6q14	136550 203310 269920 602772
3831	3q26	165215 222900 600049
3838	10p11.2	600964 602026
3854	1p21	102770 120280 166600 170995 232400 600309 601414 601691 601718 602094
3863	18q21.1	174810 600624 600993 602080
3864	6q	
3871	19p13.3-p13.2	108725 120700 133171 136836 143890 145981 147141 147670 151440 164953 188070 231670 600276 600957 601238 601843 601846 602216 602477
3877	2p21.3-p21.1	120435 182601 601771
3879	19q13.1-q13.2	107741 113900 122720 126340 126391 160900 164731 172400 173850 180901 207750 221770 248600 258501 600918 602716
3887	4q21-q25	103720 104500 125490 137600 138850 147790 157147 163890 173910 189800 217030 248510 252500 600919 601542
3888	1q21-q23	104770 107300 107670 110700 131210 134638 135940 136132 145001 146740 146760 146790 152445 159001 159440 173610 174000 176310 179755 182860 186780

		191030 191315 227400 230800 266200 600897 600923 601105 601412 601652 601863 602491
3908	15q22.3-q23	118485 151670 231680 272800 276700 600374 601780
3911	1q42.1	106150 136850 214500 600996 601975
3917	13	
3918	17q24.3-q25.1	114290 138033 162100 170500 180860 264470
3919	11q14.1-q14.3	133780 203100
3923	1pter-p35	
3926	10q22	126090 129010 142600 250850 601386 601493
3930	17p13.3	113721 247200 600059 601545
3971	4q	
3977	15q15	177070 182500 218000 227220 243500 600839 601800
3993	19p13.3	108725 120700 133171 136836 145981 147141 164953 188070 600957 601238 601846 602216 602477
4001	Xq26.1-q27.2	300085 300123 300700 301201 301590 301845 301900 304340 306900 306955 307150 307700 308000 309000 310490 313850
4003	17p13.3	113721 247200 600059 601545
4008	12p13	103950 120580 131440 139130 142680 176260 190450 200990 216950 600228 600414 600618 602096
4011	16q22.1	103850 114835 116800 140100 192090 245900 276600 600223
4013	10	
4018	16q22.1	103850 114835 116800 140100 192090 245900 276600 600223
4029	6q21-q22	120110 121014 156225 164200 601410 601666 601757 602772
4047	1p32-p31	120950 120960 138140 178300 180069 187040 201450 248610 600101 600309 600650 600722 601676 602522
4054	11q23	107680 107720 133780 147791 159555 168000 186740 186830 188025 203750 261640 600048 601382 602574
4058	12q22-qter	
4061	5q31.3-q32	109690 131400 138491 154500 159000 180071 181460 222600 272750 600807 601596 602089
4085	16q22.1	103850 114835 116800 140100 192090 245900 276600 600223
4093	19q13.4	134790 191044 600040 600138
4100	10q25	167409 278000 600020 600095 602669
4105	17q21	109270 113705 144200 148065 148066 148067 148069 148080 154275 168610 171190 176705 185800 200350 221820 232200 249000 252920 253250 600119 601363 601844
4125	4q21	104500 125490 147790 173910 252500
4128	17p13	138190 254210 271900 600179 600977 601202 601777
4143	19q13.2	107741 113900 122720 126340 126391 160900 164731 173850 207750 248600 258501
4149	4q27	147680 189800 600919
4171	11p15.4	130650 150000 257200
4178	12q22-q23	124200 147440 160781 201470 235800 273300 600175
4185	13q33	133530 601295

4192	1q31	134580 145001 145260 150292 208250 226450 600105 600759 600995 601652
4196	8q24.3	188450
4245	2p12	147200 178640 216900
4261	12p13	103950 120580 131440 139130 142680 176260 190450 200990 216950 600228 600414 600618 602096
4262	12q13-q15	107777 120140 123829 123940 126337 139350 147570 148040 148041 148043 148070 181430 231550 232800 252940 264700 600194 600231 600536 600698 600808 600956 601284 601769 601928 602116 602153
4263	11q22.2-q22.3	133780 203750 208900 261640 602574
4270	1q21.2-q22	104770 107670 110700 145001 146760 146790 159440 186780 191030 191315 600923 601412 601652 601863 602491

Table 5

Library Code	Library Description
	Morton Fetal
H0002	Human Adult Heart
H0004	Human Adult Spleen
H0007	Human Cerebellum
H0008	Whole 6 Week Old Embryo
H0009	Human Fetal Brain
H0011	Human Fetal Kidney
H0012	Human Fetal Kidney
H0013	Human 8 Week Whole Embryo
H0014	Human Gall Bladder
H0015	Human Gall Bladder, fraction II
H0019	Human Fetal Heart
H0022	Jurkat Cells
H0023	Human fetal lung
H0024	Human Fetal Lung III
H0026	Namalwa Cells
H0030	Human Placenta
H0031	Human Placenta
H0032	Human Prostate
H0036	Human Adult Small Intestine
H0037	Human Adult Small Intestine
H0038	Human Testes
H0039	Human Pancreas Tumor
H0040	Human Testes Tumor
H0041	Human Fetal Bone
H0042	Human Adult Pulmonary
H0044	Human Cornea
H0045	Human Esophagus, Cancer
H0046	Human Endometrial Tumor
H0048	Human Pineal Gland
H0050	Human Fetal Heart
H0051	Human Hippocampus
H0052	Human Cerebellum
H0056	Human Umbilical Vein, Endo. remake
H0057	Human Fetal Spleen
H0059	Human Uterine Cancer
H0063	Human Thymus
H0068	Human Skin Tumor
H0069	Human Activated T-Cells
H0071	Human Infant Adrenal Gland
H0074	Human Platelets
H0081	Human Fetal Epithelium (Skin)
H0083	HUMAN JURKAT MEMBRANE BOUND POLYSOMES
H0085	Human Colon
H0086	Human epithelioid sarcoma

H0087	Human Thymus
H0090	Human T-Cell Lymphoma
H0097	Human Adult Heart, subtracted
H0098	Human Adult Liver, subtracted
H0100	Human Whole Six Week Old Embryo
H0101	Human 7 Weeks Old Embryo, subtracted
H0102	Human Whole 6 Week Old Embryo (II), subt
H0105	Human Fetal Heart, subtracted
H0107	Human Infant Adrenal Gland, subtracted
H0108	Human Adult Lymph Node, subtracted
H0116	Human Thymus Tumor, subtracted
H0119	Human Pediatric Kidney
H0122	Human Adult Skeletal Muscle
H0123	Human Fetal Dura Mater
H0124	Human Rhabdomyosarcoma
H0125	Cem cells cyclohexamide treated
H0130	LNCAP untreated
H0131	LNCAP + 0.3nM R1881
H0132	LNCAP + 30nM R1881
H0134	Raji Cells, cyclohexamide treated
H0135	Human Synovial Sarcoma
H0136	Supt Cells, cyclohexamide treated
H0144	Nine Week Old Early Stage Human
H0147	Human Adult Liver
H0150	Human Epididymus
H0153	Human adult lymph node, subtracted
H0156	Human Adrenal Gland Tumor
H0159	Activated T-Cells, 8 hrs., ligation 2
H0163	Human Synovium
H0165	Human Prostate Cancer, Stage B2
H0166	Human Prostate Cancer, Stage B2 fraction
H0169	Human Prostate Cancer, Stage C fraction
H0170	12 Week Old Early Stage Human
H0171	12 Week Old Early Stage Human, II
H0173	Human Cardiomyopathy, RNA remake
H0176	CAMA1Ee Cell Line
H0177	CAMA1Ee Cell Line
H0178	Human Fetal Brain
H0179	Human Neutrophil
H0181	Human Primary Breast Cancer
H0182	Human Primary Breast Cancer
H0183	Human Colon Cancer
H0184	Human Colon Cancer, metasticized to live
H0186	Activated T-Cell
H0187	Resting T-Cell
H0188	Human Normal Breast
H0194	Human Cerebellum, subtracted
H0196	Human Cardiomyopathy, subtracted
H0197	Human Fetal Liver, subtracted

H0200	Human Greater Omentum, fract II remake,
H0201	Human Hippocampus, subtracted
H0204	Human Colon Cancer, subtracted
H0205	Human Colon Cancer, differential
H0207	LNCAP, differential expression
H0208	Early Stage Human Lung, subtracted
H0212	Human Prostate, subtracted
H0213	Human Pituitary, subtracted
H0214	Raji cells, cyclohexamide treated, subtracted
H0216	Supt cells, cyclohexamide treated, subtracted
H0222	Activated T-Cells, 8 hrs, subtracted
H0225	Activated T-Cells, 12hrs, differentially expressed
H0231	Human Colon, subtraction
H0232	Human Colon, differential expression
H0234	human colon cancer, metastatic to liver, differentially expressed
H0235	Human colon cancer, metaticized to liver, subtraction
H0238	Human Myometrium Leiomyoma
H0239	Human Kidney Tumor
H0242	Human Fetal Heart, Differential (Fetal-Specific)
H0244	Human 8 Week Whole Embryo, subtracted
H0247	Human Membrane Bound Polysomes- Enzyme Subtraction
H0250	Human Activated Monocytes
H0251	Human Chondrosarcoma
H0252	Human Osteosarcoma
H0253	Human adult testis, large inserts
H0254	Breast Lymph node cDNA library
H0255	breast lymph node CDNA library
H0257	HL-60, PMA 4H
H0261	H. cerebellum, Enzyme subtracted
H0263	human colon cancer
H0264	human tonsils
H0265	Activated T-Cell (12hs)/Thiouridine labelledEco
H0266	Human Microvascular Endothelial Cells, fract. A
H0267	Human Microvascular Endothelial Cells, fract. B
H0268	Human Umbilical Vein Endothelial Cells, fract. A
H0269	Human Umbilical Vein Endothelial Cells, fract. B
H0271	Human Neutrophil, Activated
H0272	HUMAN TONSILS, FRACTION 2
H0274	Human Adult Spleen, fractionII
H0284	Human OB MG63 control fraction I
H0286	Human OB MG63 treated (10 nM E2) fraction I
H0288	Human OB HOS control fraction I
H0290	Human OB HOS treated (1 nM E2) fraction I
H0292	Human OB HOS treated (10 nM E2) fraction I
H0294	Amniotic Cells - TNF induced
H0295	Amniotic Cells - Primary Culture
H0298	HCBB's differential consolidation
H0305	CD34 positive cells (Cord Blood)
H0306	CD34 depleted Buffy Coat (Cord Blood)

H0309	Human Chronic Synovitis
H0313	human pleural cancer
H0316	HUMAN STOMACH
H0318	HUMAN B CELL LYMPHOMA
H0320	Human frontal cortex
H0321	HUMAN SCHWANOMA
H0327	human corpus colosum
H0328	human ovarian cancer
H0329	Dermatofibrosarcoma Protuberance
H0331	Hepatocellular Tumor
H0333	Hemangiopericytoma
H0334	Kidney cancer
H0340	Corpus Callosum
H0341	Bone Marrow Cell Line (RS4,11)
H0343	stomach cancer (human)
H0345	SKIN
H0351	Glioblastoma
H0352	wilm's tumor
H0354	Human Leukocytes
H0355	Human Liver
H0356	Human Kidney
H0359	KMH2 cell line
H0361	Human rejected kidney
H0369	H. Atrophic Endometrium
H0370	H. Lymph node breast Cancer
H0372	Human Testes
H0373	Human Heart
H0374	Human Brain
H0375	Human Lung
H0376	Human Spleen
H0379	Human Tongue, frac 1
H0380	Human Tongue, frac 2
H0381	Bone Cancer
H0383	Human Prostate BPH, re-excision
H0384	Brain, Kozak
H0386	Leukocyte and Lung, 4 screens
H0390	Human Amygdala Depression, re-excision
H0391	H. Meningioma, M6
H0392	H. Meningioma, M1
H0393	Fetal Liver, subtraction II
H0395	A1-CELL LINE
H0399	Human Kidney Cortex, re-rescue
H0402	CD34 depleted Buffy Coat (Cord Blood), re-excision
H0403	H. Umbilical Vein Endothelial Cells, IL4 induced
H0408	Human kidney Cortex, subtracted
H0411	H Female Bladder, Adult
H0412	Human umbilical vein endothelial cells, IL-4 induced
H0413	Human Umbilical Vein Endothelial Cells, uninduced
H0415	H. Ovarian Tumor, II, OV5232

H0416	Human Neutrophils, Activated, re-excision
H0419	Bone Cancer, re-excision
H0421	Human Bone Marrow, re-excision
H0422	T-Cell PHA 16 hrs
H0423	T-Cell PHA 24 hrs
H0424	Human Pituitary, subt IX
H0427	Human Adipose
H0428	Human Ovary
H0431	H. Kidney Medulla, re-excision
H0433	Human Umbilical Vein Endothelial cells, frac B, re-excision
H0435	Ovarian Tumor 10-3-95
H0436	Resting T-Cell Library,II
H0437	H Umbilical Vein Endothelial Cells, frac A, re-excision
H0438	H. Whole Brain #2, re-excision
H0441	H. Kidney Cortex, subtracted
H0444	Spleen metastatic melanoma
H0445	Spleen, Chronic lymphocytic leukemia
H0453	H. Kidney Pyramid, subtracted
H0455	H. Striatum Depression, subt
H0457	Human Eosinophils
H0458	CD34+ cell, I, frac II
H0459	CD34+cells, II, FRACTION 2
H0461	H. Kidney Medulla, subtracted
H0477	Human Tonsil, Lib 3
H0478	Salivary Gland, Lib 2
H0479	Salivary Gland, Lib 3
H0483	Breast Cancer cell line, MDA 36
H0484	Breast Cancer Cell line, angiogenic
H0485	Hodgkin's Lymphoma I
H0486	Hodgkin's Lymphoma II
H0487	Human Tonsils, lib I
H0488	Human Tonsils, Lib 2
H0489	Crohn's Disease
H0492	HL-60, RA 4h, Subtracted
H0494	Keratinocyte
H0497	HEL cell line
H0506	Ulcerative Colitis
H0509	Liver, Hepatoma
H0510	Human Liver, normal
H0512	Keratinocyte, lib 3
H0517	Nasal polyps
H0518	pBMC stimulated w/ poly I/C
H0519	NTERA2, control
H0520	NTERA2 + retinoic acid, 14 days
H0521	Primary Dendritic Cells, lib 1
H0522	Primary Dendritic cells,frac 2
H0525	PCR, pBMC I/C treated
H0528	Poly[I]/Poly[C] Normal Lung Fibroblasts
H0529	Myeloid Progenitor Cell Line

H0530	Human Dermal Endothelial Cells,untreated
H0535	Human ovary tumor cell OV350721
H0538	Merkel Cells
H0539	Pancreas Islet Cell Tumor
H0540	Skin, burned
H0542	T Cell helper I
H0543	T cell helper II
H0544	Human endometrial stromal cells
H0545	Human endometrial stromal cells-treated with progesterone
H0546	Human endometrial stromal cells-treated with estradiol
H0547	NTERA2 teratocarcinoma cell line+retinoic acid (14 days)
H0549	H. Epididymus, caput & corpus
H0550	H. Epididymus, cauda
H0551	Human Thymus Stromal Cells
H0553	Human Placenta
H0555	Rejected Kidney, lib 4
H0556	Activated T-cell(12h)/Thiouridine-re-excision
H0559	HL-60, PMA 4H, re-excision
H0560	KMH2
H0561	L428
H0562	Human Fetal Brain, normalized c5-11-26
H0563	Human Fetal Brain, normalized 50021F
H0565	HUman Fetal Brain, normalized 100024F
H0569	Human Fetal Brain, normalized CO
H0570	Human Fetal Brain, normalized C500H
H0572	Human Fetal Brain, normalized AC5002
H0574	Hepatocellular Tumor, re-excision
H0575	Human Adult Pulmonary,re-excision
H0576	Resting T-Cell, re-excision
H0579	Pericardium
H0580	Dendritic cells, pooled
H0581	Human Bone Marrow, treated
H0583	B Cell lymphoma
H0584	Activated T-cells, 24 hrs,re-excision
H0585	Activated T-Cells,12 hrs,re-excision
H0586	Healing groin wound, 6.5 hours post incision
H0587	Healing groin wound, 7.5 hours post incision
H0590	Human adult small intestine,re-excision
H0591	Human T-cell lymphoma,re-excision
H0592	Healing groin wound - zero hr post-incision (control)
H0593	Olfactory epithelium,nasalcavity
H0594	Human Lung Cancer,re-excision
H0595	Stomach cancer (human),re-excision
H0596	Human Colon Cancer,re-excision
H0597	Human Colon, re-excision
H0598	Human Stomach,re-excision
H0599	Human Adult Heart,re-excision
H0600	Healing Abdomen wound,70&90 min post incision
H0601	Healing Abdomen Wound,15 days post incision

H0602	Healing Abdomen Wound,21&29 days post incision
H0606	Human Primary Breast Cancer,re-excision
H0609	H. Leukocytes, normalized cot > 500A
H0613	H.Leukocytes, normalized cot 5B
H0615	Human Ovarian Cancer Reexcision
H0616	Human Testes, Reexcision
H0617	Human Primary Breast Cancer Reexcision
H0618	Human Adult Testes, Large Inserts, Reexcision
H0619	Fetal Heart
H0620	Human Fetal Kidney, Reexcision
H0622	Human Pancreas Tumor, Reexcision
H0623	Human Umbilical Vein, Reexcision
H0624	12 Week Early Stage Human II, Reexcision
H0625	Ku 812F Basophils Line
H0626	Saos2 Cells, Untreated
H0627	Saos2 Cells, Vitamin D3 Treated
H0628	Human Pre-Differentiated Adipocytes
H0631	Saos2, Dexamethosome Treated
H0632	Hepatocellular Tumor,re-excision
H0633	Lung Carcinoma A549 TNFalpha activated
H0634	Human Testes Tumor, re-excision
H0635	Human Activated T-Cells, re-excision
H0638	CD40 activated monocyte dendridic cells
H0641	LPS activated derived dendritic cells
H0642	Hep G2 Cells, lambda library
H0643	Hep G2 Cells, PCR library
H0644	Human Placenta (re-excision)
H0645	Fetal Heart, re-excision
H0646	Lung, Cancer (4005313 A3): Invasive Poorly Differentiated Lung Adenocarcinoma,
H0647	Lung, Cancer (4005163 B7): Invasive, Poorly Diff. Adenocarcinoma, Metastatic
H0648	Ovary, Cancer: (4004562 B6) Papillary Serous Cystic Neoplasm, Low Malignant Pot
H0649	Lung, Normal: (4005313 B1)
H0650	B-Cells
H0651	Ovary, Normal: (9805C040R)
H0652	Lung, Normal: (4005313 B1)
H0653	Stromal Cells
H0654	Lung, Cancer: (4005313 A3) Invasive Poorly-differentiated Metastatic lung adenoc
H0656	B-cells (unstimulated)
H0657	B-cells (stimulated)
H0658	Ovary, Cancer (9809C332): Poorly differentiated adenocarcinoma
H0659	Ovary, Cancer (15395A1F): Grade II Papillary Carcinoma
H0660	Ovary, Cancer: (15799A1F) Poorly differentiated carcinoma
H0661	Breast, Cancer: (4004943 A5)
H0662	Breast, Normal: (4005522B2)
H0663	Breast, Cancer: (4005522 A2)
H0664	Breast, Cancer: (9806C012R)

H0665	Stromal cells 3.88
H0666	Ovary, Cancer: (4004332 A2)
H0667	Stromal cells(HBM3.18)
H0668	stromal cell clone 2.5
H0669	Breast, Cancer: (4005385 A2)
H0670	Ovary, Cancer(4004650 A3): Well-Differentiated Micropapillary Serous Carcinoma
H0671	Breast, Cancer: (9802C02OE)
H0672	Ovary, Cancer: (4004576 A8)
H0673	Human Prostate Cancer, Stage B2, re-excision
H0674	Human Prostate Cancer, Stage C, re-excision
H0675	Colon, Cancer: (9808C064R)
H0676	Colon, Cancer: (9808C064R)-total RNA
H0677	TNFR degenerate oligo
H0682	Ovarian cancer, Serous Papillary Adenocarcinoma
H0683	Ovarian Serous Papillary Adenocarcinoma
H0684	Serous Papillary Adenocarcinoma
H0685	Adenocarcinoma of Ovary, Human Cell Line, # OVCAR-3
H0686	Adenocarcinoma of Ovary, Human Cell Line
H0687	Human normal ovary(#9610G215)
H0688	Human Ovarian Cancer(#9807G017)
H0689	Ovarian Cancer
H0690	Ovarian Cancer, # 9702G001
H0691	Normal Ovary, #9710G208
H0693	Normal Prostate #ODQ3958EN
H0694	Prostate gland adenocarcinoma
H0695	mononucleocytes from patient
H0696	Prostate Adenocarcinoma
H0702	NK15(IL2 treated for 48 hours)
L0002	Atrium cDNA library Human heart
L0005	Clontech human aorta polyA+ mRNA (#6572)
L0021	Human adult (K.Okubo)
L0022	Human adult lung 3' directed MboI cDNA
L0040	Human colon mucosa
L0041	Human epidermal keratinocyte
L0053	Human pancreatic tumor
L0054	Human PGasparini
L0055	Human promyelocyte
L0065	Liver HepG2 cell line.
L0096	Subtracted human retina
L0105	Human aorta polyA+ (TFujiwara)
L0140	Human pancreatic cancer (CWallrapp)
L0142	Human placenta cDNA (TFujiwara)
L0143	Human placenta polyA+ (TFujiwara)
L0157	Human fetal brain (TFujiwara)
L0163	Human heart cDNA (YNakamura)
L0167	Human thymus (V.L.Boyartchuk)
L0193	Human osteosarcoma EGracia
L0194	Human pancreatic cancer cell line Patu 8988t

L0351	Infant brain, Bento Soares
L0352	Normalized infant brain, Bento Soares
L0361	Stratagene ovary (#937217)
L0362	Stratagene ovarian cancer (#937219)
L0363	NCI CGAP GC2
L0364	NCI CGAP GC5
L0365	NCI CGAP Phe1
L0366	Stratagene schizo brain S11
L0367	NCI CGAP Sch1
L0368	NCI CGAP SS1
L0369	NCI CGAP AA1
L0370	Johnston frontal cortex
L0371	NCI CGAP Br3
L0372	NCI CGAP Co12
L0373	NCI CGAP Co11
L0374	NCI CGAP Co2
L0375	NCI CGAP Kid6
L0376	NCI CGAP Lar1
L0378	NCI CGAP Lu1
L0381	NCI CGAP HN4
L0382	NCI CGAP Pr25
L0383	NCI CGAP Pr24
L0384	NCI CGAP Pr23
L0386	NCI CGAP HN3
L0387	NCI CGAP GCB0
L0388	NCI CGAP HN6
L0389	NCI CGAP HN5
L0394	H, Human adult Brain Cortex tissue
L0415	b4HB3MA Cot8-HAP-Ft
L0435	Infant brain, LLNL array of Dr. M. Soares 1NIB
L0438	normalized infant brain cDNA
L0439	Soares infant brain 1NIB
L0444	HB3MK
L0455	Human retina cDNA randomly primed sublibrary
L0456	Human retina cDNA Tsp509I-cleaved sublibrary
L0462	WATM1
L0471	Human fetal heart, Lambda ZAP Express
L0475	KG1-a Lambda Zap Express cDNA library
L0483	Human pancreatic islet
L0485	STRATAGENE Human skeletal muscle cDNA library, cat. #936215.
L0493	NCI CGAP Ov26
L0499	NCI CGAP HSC2
L0500	NCI CGAP Brn20
L0502	NCI CGAP Br15
L0503	NCI CGAP Br17
L0504	NCI CGAP Br13
L0505	NCI CGAP Br12
L0506	NCI CGAP Br16
L0507	NCI CGAP Br14

L0508	NCI CGAP Lu25
L0509	NCI CGAP Lu26
L0510	NCI CGAP Ov33
L0511	NCI CGAP Ov34
L0512	NCI CGAP Ov36
L0515	NCI CGAP Ov32
L0517	NCI CGAP Pr1
L0518	NCI CGAP Pr2
L0519	NCI CGAP Pr3
L0520	NCI CGAP Alv1
L0521	NCI CGAP Ew1
L0522	NCI CGAP Kid1
L0523	NCI CGAP Lip2
L0524	NCI CGAP Li1
L0526	NCI CGAP Pr12
L0527	NCI CGAP Ov2
L0528	NCI CGAP Pr5
L0529	NCI CGAP Pr6
L0530	NCI CGAP Pr8
L0532	NCI CGAP Thy1
L0534	Chromosome 7 Fetal Brain cDNA Library
L0539	Chromosome 7 Placental cDNA Library
L0540	NCI CGAP Pr10
L0541	NCI CGAP Pr7
L0542	NCI CGAP Pr11
L0543	NCI CGAP Pr9
L0544	NCI CGAP Pr4
L0545	NCI CGAP Pr4.1
L0553	NCI CGAP Co22
L0558	NCI CGAP Ov40
L0560	NCI CGAP HN12
L0562	Chromosome 7 HeLa cDNA Library
L0563	Human Bone Marrow Stromal Fibroblast
L0564	Jia bone marrow stroma
L0565	Normal Human Trabecular Bone Cells
L0581	Stratagene liver (#937224)
L0583	Stratagene cDNA library Human fibroblast, cat#937212
L0586	HTCDL1
L0587	Stratagene colon HT29 (#937221)
L0588	Stratagene endothelial cell 937223
L0589	Stratagene fetal retina 937202
L0590	Stratagene fibroblast (#937212)
L0591	Stratagene HeLa cell s3 937216
L0592	Stratagene hNT neuron (#937233)
L0593	Stratagene neuroepithelium (#937231)
L0594	Stratagene neuroepithelium NT2RAMI 937234
L0595	Stratagene NT2 neuronal precursor 937230
L0596	Stratagene colon (#937204)
L0597	Stratagene corneal stroma (#937222)

L0598	Morton Fetal Cochlea
L0599	Stratagene lung (#937210)
L0600	Weizmann Olfactory Epithelium
L0601	Stratagene pancreas (#937208)
L0602	Pancreatic Islet
L0603	Stratagene placenta (#937225)
L0604	Stratagene muscle 937209
L0605	Stratagene fetal spleen (#937205)
L0606	NCI CGAP Lym5
L0608	Stratagene lung carcinoma 937218
L0611	Schiller meningioma
L0617	Chromosome 22 exon
L0622	HM1
L0623	HM3
L0626	NCI CGAP GC1
L0627	NCI CGAP Co1
L0628	NCI CGAP Ov1
L0629	NCI CGAP Mel3
L0630	NCI CGAP CNS1
L0631	NCI CGAP Br7
L0634	NCI CGAP Ov8
L0636	NCI CGAP Pit1
L0637	NCI CGAP Brn53
L0638	NCI CGAP Brn35
L0639	NCI CGAP Brn52
L0640	NCI CGAP Br18
L0641	NCI CGAP Co17
L0642	NCI CGAP Co18
L0643	NCI CGAP Co19
L0644	NCI CGAP Co20
L0645	NCI CGAP Co21
L0646	NCI CGAP Co14
L0647	NCI CGAP Sar4
L0648	NCI CGAP Eso2
L0649	NCI CGAP GU1
L0650	NCI CGAP Kid13
L0651	NCI CGAP Kid8
L0652	NCI CGAP Lu27
L0653	NCI CGAP Lu28
L0654	NCI CGAP Lu31
L0655	NCI CGAP Lym12
L0656	NCI CGAP Ov38
L0657	NCI CGAP Ov23
L0658	NCI CGAP Ov35
L0659	NCI CGAP Pan1
L0661	NCI CGAP Mel15
L0662	NCI CGAP Gas4
L0663	NCI CGAP Ut2
L0664	NCI CGAP Ut3

L0665	NCI CGAP_Ut4
L0666	NCI CGAP_Ut1
L0667	NCI CGAP_CML1
L0683	Stanley Frontal NS pool 2
L0686	Stanley Frontal SN pool 2
L0689	Stanley Hippocampus SN pool 1
L0698	Testis 2
L0717	Gessler Wilms tumor
L0720	PN001-Normal Human Prostate
L0731	Soares pregnant uterus NbHPU
L0738	Human colorectal cancer
L0740	Soares melanocyte 2NbHM
L0741	Soares adult brain N2b4HB55Y
L0742	Soares adult brain N2b5HB55Y
L0743	Soares breast 2NbHBst
L0744	Soares breast 3NbHBst
L0745	Soares retina N2b4HR
L0746	Soares retina N2b5HR
L0747	Soares fetal heart NbHH19W
L0748	Soares fetal liver spleen 1NFLS
L0749	Soares fetal liver spleen 1NFLS S1
L0750	Soares fetal lung NbHL19W
L0751	Soares ovary tumor NbHOT
L0752	Soares parathyroid tumor NbHPA
L0753	Soares pineal gland N3HPG
L0754	Soares placenta Nb2HP
L0755	Soares placenta 8to9weeks 2NbHP8to9W
L0756	Soares multiple sclerosis 2NbHMSP
L0757	Soares senescent fibroblasts NbHSF
L0758	Soares testis NHT
L0759	Soares total fetus Nb2HF8 9w
L0761	NCI CGAP_CLL1
L0762	NCI CGAP_Br1.1
L0763	NCI CGAP_Br2
L0764	NCI CGAP_Co3
L0765	NCI CGAP_Co4
L0766	NCI CGAP_GCB1
L0767	NCI CGAP_GC3
L0768	NCI CGAP_GC4
L0769	NCI CGAP_Brn25
L0770	NCI CGAP_Brn23
L0771	NCI CGAP_Co8
L0772	NCI CGAP_Co10
L0773	NCI CGAP_Co9
L0774	NCI CGAP_Kid3
L0775	NCI CGAP_Kid5
L0776	NCI CGAP_Lu5
L0777	Soares_NhHMPu_S1
L0779	Soares_NFL_T_GBC_S1

L0780	Soares NSF_F8_9W_OT_PA_P_S1
L0782	NCI_CGAP_Pr21
L0783	NCI_CGAP_Pr22
L0784	NCI_CGAP_Lei2
L0785	Barstead spleen HPLRB2
L0786	Soares_NbHFB
L0787	NCI_CGAP_Sub1
L0788	NCI_CGAP_Sub2
L0789	NCI_CGAP_Sub3
L0790	NCI_CGAP_Sub4
L0791	NCI_CGAP_Sub5
L0792	NCI_CGAP_Sub6
L0793	NCI_CGAP_Sub7
L0794	NCI_CGAP_GC6
L0796	NCI_CGAP_Brn50
L0800	NCI_CGAP_Co16
L0803	NCI_CGAP_Kid11
L0804	NCI_CGAP_Kid12
L0805	NCI_CGAP_Lu24
L0806	NCI_CGAP_Lu19
L0807	NCI_CGAP_Ov18
L0808	Barstead prostate BPH HPLRB4 1
L0809	NCI_CGAP_Pr28
N0007	Human Hippocampus
N0009	Human Hippocampus, prescreened
S0001	Brain frontal cortex
S0002	Monocyte activated
S0003	Human Osteoclastoma
S0004	Prostate
S0006	Neuroblastoma
S0007	Early Stage Human Brain
S0010	Human Amygdala
S0011	STROMAL -OSTEOCLASTOMA
S0013	Prostate
S0014	Kidney Cortex
S0015	Kidney medulla
S0022	Human Osteoclastoma Stromal Cells - unamplified
S0026	Stromal cell TF274
S0027	Smooth muscle, serum treated
S0028	Smooth muscle, control
S0029	brain stem
S0031	Spinal cord
S0032	Smooth muscle-ILb induced
S0036	Human Substantia Nigra
S0037	Smooth muscle, IL1b induced
S0038	Human Whole Brain #2 - Oligo dT > 1.5Kb
S0040	Adipocytes
S0044	Prostate BPH
S0045	Endothelial cells-control

S0046	Endothelial-induced
S0048	Human Hypothalamus, Alzheimer's
S0049	Human Brain, Striatum
S0050	Human Frontal Cortex, Schizophrenia
S0051	Human Hypothalamus, Schizophrenia
S0052	neutrophils control
S0053	Neutrophils IL-1 and LPS induced
S0106	STRIATUM DEPRESSION
S0112	Hypothalamus
S0114	Anergic T-cell
S0116	Bone marrow
S0122	Osteoclastoma-normalized A
S0126	Osteoblasts
S0132	Epithelial-TNF α and INF induced
S0134	Apoptotic T-cell
S0136	PERM TF274
S0140	eosinophil-IL5 induced
S0142	Macrophage-oxLDL
S0144	Macrophage (GM-CSF treated)
S0146	prostate-edited
S0148	Normal Prostate
S0150	LNCAP prostate cell line
S0152	PC3 Prostate cell line
S0174	Prostate-BPH subtracted II
S0176	Prostate, normal, subtraction I
S0182	Human B Cell 8866
S0188	Prostate, BPH, Lib 2
S0190	Prostate BPH, Lib 2, subtracted
S0192	Synovial Fibroblasts (control)
S0194	Synovial hypoxia
S0196	Synovial IL-1/TNF stimulated
S0206	Smooth Muscle- HASTE normalized
S0208	Mesangial cell, frac 1
S0210	Mesangial cell, frac 2
S0212	Bone Marrow Stromal Cell, untreated
S0214	Human Osteoclastoma, re-excision
S0216	Neutrophils IL-1 and LPS induced
S0218	Apoptotic T-cell, re-excision
S0222	H. Frontal cortex, epileptic, re-excision
S0242	Synovial Fibroblasts (IL1/TNF), subt
S0250	Human Osteoblasts II
S0260	Spinal Cord, re-excision
S0276	Synovial hypoxia-RSF subtracted
S0278	H Macrophage (GM-CSF treated), re-excision
S0280	Human Adipose Tissue, re-excision
S0282	Brain Frontal Cortex, re-excision
S0294	Larynx tumor
S0300	Frontal lobe, dementia, re-excision
S0306	Larynx normal #10 261-273

S0312	Human osteoarthritic, fraction II
S0314	Human osteoarthritis, fraction I
S0318	Human Normal Cartilage Fraction II
S0320	Human Larynx
S0322	Siebben Polyposis
S0328	Palate carcinoma
S0330	Palate normal
S0332	Pharynx carcinoma
S0334	Human Normal Cartilage Fraction III
S0342	Adipocytes, re-excision
S0344	Macrophage-oxLDL, re-excision
S0346	Human Amygdala, re-excision
S0348	Cheek Carcinoma
S0350	Pharynx Carcinoma
S0354	Colon Normal II
S0356	Colon Carcinoma
S0358	Colon Normal III
S0360	Colon Tumor II
S0362	Human Gastrocnemius
S0364	Human Quadriceps
S0366	Human Soleus
S0370	Larynx carcinoma II
S0372	Larynx carcinoma III
S0374	Normal colon
S0376	Colon Tumor
S0378	Pancreas normal PCA4 No
S0380	Pancreas Tumor PCA4 Tu
S0382	Larynx carcinoma IV
S0384	Tongue carcinoma
S0386	Human Whole Brain, re-excision
S0388	Human Hypothalamus, schizophrenia, re-excision
S0390	Smooth muscle, control, re-excision
S0392	Salivary Gland
S0394	Stomach, normal
S0402	Adrenal Gland, normal
S0404	Rectum normal
S0406	Rectum tumour
S0408	Colon, normal
S0410	Colon, tumour
S0414	Hippocampus, Alzheimer Subtracted
S0418	CHME Cell Line, treated 5 hrs
S0420	CHME Cell Line, untreated
S0422	Mo7c Cell Line GM-CSF treated (1ng/ml)
S0424	TF-1 Cell Line GM-CSF Treated
S0426	Monocyte activated, re-excision
S0428	Neutrophils control, re-excision
S0430	Aryepiglottis Normal
S0432	Sinus piniformis Tumour
S0434	Stomach Normal

S0436	Stomach Tumour
S0438	Liver Normal Met5No
S0440	Liver Tumour Met 5 Tu
S0442	Colon Normal
S0444	Colon Tumor
S0446	Tongue Tumour
S0448	Larynx Normal
S0450	Larynx Tumour
S0452	Thymus
S0454	Placenta
S0456	Tongue Normal
S0458	Thyroid Normal (SDCA2 No)
S0460	Thyroid Tumour
S0462	Thyroid Thyroiditis
S0464	Larynx Normal
S0468	Ea.hy.926 cell line
S0472	Lung Mesothelium
S0474	Human blood platelets
S3012	Smooth Muscle Serum Treated, Norm
S3014	Smooth muscle, serum induced,re-exc
S6014	H. hypothalamus, frac A
S6016	H. Frontal Cortex, Epileptic
S6022	H. Adipose Tissue
S6024	Alzheimers, spongy change
S6026	Frontal Lobe, Dementia
S6028	Human Manic Depression Tissue
T0002	Activated T-cells
T0003	Human Fetal Lung
T0006	Human Pineal Gland
T0008	Colorectal Tumor
T0010	Human Infant Brain
T0023	Human Pancreatic Carcinoma
T0039	HSA 172 Cells
T0040	HSC172 cells
T0041	Jurkat T-cell G1 phase
T0042	Jurkat T-Cell, S phase
T0048	Human Aortic Endothelium
T0049	Aorta endothelial cells + TNF-a
T0060	Human White Adipose
T0067	Human Thyroid
T0068	Normal Ovary, Premenopausal
T0069	Human Uterus, normal
T0071	Human Bone Marrow
T0074	Human Adult Retina
T0079	Human Kidney, normal Adult
T0082	Human Adult Retina
T0103	Human colon carcinoma (HCC) cell line
T0104	HCC cell line metastasis to liver
T0109	Human (HCC) cell line liver (mouse) metastasis, remake

T0110	Human colon carcinoma (HCC) cell line, remake
T0114	Human (Caco-2) cell line, adenocarcinoma, colon, remake
T0115	Human Colon Carcinoma (HCC) cell line

Table 6

OMIM ID	OMIM Description
100650	Alcohol intolerance, acute (3) ?Fetal alcohol syndrome (1)
100690	Myasthenic syndrome, slow-channel congenital, 601462 (3)
100710	Myasthenic syndrome, slow-channel congenital, 601462 (3)
100730	Myasthenia gravis, neonatal transient (2)
101000	Malignant mesothelioma, sporadic (3) Meningioma, NF2-related, sporadic (3) Schwannoma, sporadic (3) Neurofibromatosis, type 2 (3) Neurolemmomatosis (3)
102200	Somatotrophinoma (2)
102540	Cardiomyopathy, idiopathic dilated (3)
102578	Leukemia, acute promyelocytic, PML/RARA type (3)
102600	Urolithiasis, 2,8-dihydroxyadenine (3)
102770	Myoadenylate deaminase deficiency (3)
102772	[AMP deaminase deficiency, erythrocytic] (3)
103000	Hemolytic anemia due to adenylate kinase deficiency (3)
103050	Adenylosuccinase deficiency (1) Autism, succinylpurinemic (3)
103581	Albright hereditary osteodystrophy-2 (2) (?)
103600	Analbuminemia (3) [Dysalbuminemic hyperthyroxinemia] (3) [Dysalbuminemic hyperzincemia], 194470 (3)
103720	Alcoholism, susceptibility to (1)
103850	Aldolase A deficiency (3)
103950	Emphysema due to alpha-2-macroglobulin deficiency (1)
104150	[AFP deficiency, congenital] (1) [Hereditary persistence of alpha-fetoprotein] (3)
104311	Alzheimer disease-3 (3)
104500	Amelogenesis imperfecta-2, hypoplastic local type (2)
104614	Cystinuria, 220100 (3)
104770	?Amyloidosis, secondary, susceptibility to (1)
105580	Anal canal carcinoma (2) (?)
105600	Dyserythropoietic anemia, congenital, type III (2)
106100	Angioedema, hereditary (3)
106150	Hypertension, essential, susceptibility to (3) Preeclampsia, susceptibility to (3)
106165	Hypertension, essential, 145500 (3)
106180	Myocardial infarction, susceptibility to (3)
106210	Aniridia (3) Cataract, congenital, with late-onset corneal dystrophy (3) Foveal hypoplasia, isolated, 136520 (3) Peters anomaly (3)
106300	Ankylosing spondylitis (2)
107250	Anterior segment mesenchymal dysgenesis (2)
107271	CD59 deficiency (3)
107280	Alpha-1-antichymotrypsin deficiency (3) Cerebrovascular disease, occlusive (3)

107300	Antithrombin III deficiency (3)
107400	Emphysema (3) Emphysema-cirrhosis (3)
107470	Atypical mycobacterial infection, familial disseminated, 209950 (3) BCG infection, generalized familial (3) Tuberculosis, susceptibility to (3)
107670	Apolipoprotein A-II deficiency (3)
107680	Amyloidosis, 3 or more types (3) ApoA-I and apoC-III deficiency, combined (3) Corneal clouding, autosomal recessive (3) Hypertriglyceridemia, one form (3) Hypoalphalipoproteinemia (3)
107720	Hypertriglyceridemia (3)
107730	Abetalipoproteinemia (3) Apolipoprotein B-100, ligand-defective (3) Hyperbetalipoproteinemia (3) Hypobetalipoproteinemia (3)
107741	Hyperlipoproteinemia, type III (3)
107776	Colton blood group, 110450 (3)
107777	Diabetes insipidus, nephrogenic, autosomal recessive, 222000 (3)
107910	Gynecomastia, familial, due to increased aromatase activity (1) Virilization, maternal and fetal, from placental aromatase deficiency (3)
107970	Arrhythmogenic right ventricular dysplasia-1 (2)
108120	Distal arthrogryposis-1 (2)
108725	Atherosclerosis, susceptibility to (2)
108730	Brody myopathy, 601003 (3)
108800	Atrial septal defect, secundum type (2)
108962	Hypertension, salt-resistant (1) (?)
108985	Atrophia areata (2)
109150	Machado-Joseph disease (3)
109270	Hemolytic anemia due to band 3 defect (3) Renal tubular acidosis, distal, 179800 (3) Spherocytosis, hereditary (3) [Acanthocytosis, one form] (1) [Elliptocytosis, Malaysian-Melanesian type] (3)
109400	Basal cell nevus syndrome (2)
109543	Leukemia, chronic lymphocytic, B-cell (2)
109560	Leukemia/lymphoma, B-cell, 3 (2)
109690	Asthma, nocturnal, susceptibility to (3) Obesity, susceptibility to (3)
109700	Hemodialysis-related amyloidosis (1)
110100	Blepharophimosis, epicanthus inversus, and ptosis, type 1 (2)
110700	Vivax malaria, susceptibility to (1)
112250	Bone dysplasia with medullary fibrosarcoma (2)
112261	Fibrodysplasia ossificans progressiva (1) (?)
112262	Fibrodysplasia ossificans progressiva, 135100 (1) (?)
112410	Hypertension with brachydactyly (2)
113100	Brachydactyly, type C (2)
113300	Brachydactyly type E (2) (?)
113520	Hyperleucinemia-isoleucinemia or hypervalinemia (1) (?)

113705	Breast cancer-1 (3) Ovarian cancer (3)
113721	Breast cancer (1)
113900	Heart block, progressive familial, type I (2)
114130	Osteoporosis (3)
114208	Hypokalemic periodic paralysis, 170400 (3) Malignant hyperthermia susceptibility 5, 601887 (3)
114240	Muscular dystrophy, limb-girdle, type 2A, 253600 (3)
114290	Campomelic dysplasia with autosomal sex reversal (3)
114350	Leukemia, acute myeloid (2)
114400	Lynch cancer family syndrome II (2) (?)
114550	Hepatocellular carcinoma (1)
114835	Monocyte carboxyesterase deficiency (1) (?)
115500	Acatlasemia (3)
115650	Cataract, anterior polar-1 (2) (?)
115660	Cataract, cerulean, type 1 (2)
116600	Cataract, posterior polar (2)
116800	Cataract, Marner type (2)
116806	Colorectal cancer (3)
116860	Cavernous angiomatous malformations (2)
117700	Hemosiderosis, systemic, due to aceruloplasminemia (3) [Hypoceruloplasminemia, hereditary] (1)
118210	Charcot-Marie-Tooth neuropathy-2A (2)
118425	Myotonia congenita, dominant, 160800 (3) Myotonia congenita, recessive, 255700 (3) Myotonia levior, recessive (3)
118470	[CETP deficiency] (3)
118485	Polycystic ovary syndrome with hyperandrogenemia (2)
118504	Epilepsy, benign neonatal, type 1, 121200 (3) Epilepsy, nocturnal frontal lobe, 600513 (3)
118511	Schizophrenia, neurophysiologic defect in (2)
118800	Choreoathetosis, familial paroxysmal (2)
119300	van der Woude syndrome (2)
120070	Alport syndrome, autosomal recessive, 203780 (3)
120110	Metaphyseal chondrodysplasia, Schmid type (3)
120120	Epidermolysis bullosa dystrophica, dominant, 131750 (3) Epidermolysis bullosa dystrophica, recessive, 226600 (3) Epidermolysis bullosa, pretibial, 131850 (3)
120131	Alport syndrome, autosomal recessive, 203780 (3) Hematuria, familial benign (3)
120140	Achondrogenesis-hypochondrogenesis, type II (3) Kniest dysplasia (3) Osteoarthritis, precocious (3) SED congenita (3) SMED Strudwick type (3) Stickler syndrome, type I (3) Wagner syndrome, type II (3)
120150	Ehlers-Danlos syndrome, type VIIA1, 130060 (3) Osteogenesis imperfecta, 4 clinical forms, 166200, 166210, 259420, 166220 (3)

	Osteoporosis, idiopathic, 166710 (3)
120160	Ehlers-Danlos syndrome, type VIIA2, 130060 (3) Marfan syndrome, atypical (3) Osteogenesis imperfecta, 4 clinical forms, 166200, 166210, 259420, 166220 (3) Osteoporosis, idiopathic, 166710 (3)
120180	Aneurysm, familial, 100070 (3) Ehlers-Danlos syndrome, type III (3) Ehlers-Danlos syndrome, type IV, 130050 (3) Fibromuscular dysplasia of arteries, 135580 (3)
120190	Ehlers-Danlos syndrome, type I, 130000 (3)
120215	Ehlers-Danlos syndrome, type I, 130000 (3) Ehlers-Danlos syndrome, type II, 130010 (3)
120220	Bethlem myopathy, 158810 (3)
120240	Bethlem myopathy, 158810 (3)
120250	Bethlem myopathy, 158810 (3)
120260	Epiphyseal dysplasia, multiple, type 2, 600204 (3)
120280	Marshall syndrome, 154780 (3) Stickler syndrome, type III (3)
120290	OSMED syndrome, 215150 (3) Stickler syndrome, type II, 184840 (3)
120435	Colorectal cancer, hereditary, nonpolyposis, type 1 (3) Ovarian cancer (3) Muir-Torre syndrome, 158320 (3)
120436	Colorectal cancer, hereditary nonpolyposis, type 2 (3) Muir-Torre family cancer syndrome, 158320 (3) Turcot syndrome with glioblastoma, 276300 (3)
120470	Colorectal cancer (3)
120550	C1q deficiency, type A (3)
120570	C1q deficiency, type B (3)
120575	C1q deficiency, type C (3)
120580	C1r/C1s deficiency, combined (1)
120620	CR1 deficiency (1) ?SLE susceptibility (1)
120700	C3 deficiency (3)
120810	C4 deficiency (3)
120820	C4 deficiency (3)
120900	C5 deficiency (1)
120920	Measles, susceptibility to (1)
120940	C9 deficiency (3)
120950	C8 deficiency, type I (2)
120960	C8 deficiency, type II (3)
121011	Deafness, autosomal dominant 3, 601544 (3) Deafness, autosomal recessive 1, 220290 (3)
121014	Heterotaxia, visceroatrial, autosomal recessive (3)
121050	Contractural arachnodactyly, congenital (3)
121300	Coproporphyrria (3) Harderoporphyurinuria (3)
121360	Myeloid leukemia, acute, M4Eo subtype (2)
121700	Congenital hereditary endothelial dystrophy of cornea (2)
121800	Corneal dystrophy, crystalline, Schnyder (2)

122000	Corneal dystrophy, posterior polymorphous (2)
122500	[Transcortin deficiency] (1)
122560	ACTH deficiency, 201400 (2)
122720	Coumarin resistance, 122700 (3) Nicotine addiction, protection from (3)
123000	Cranio metaphyseal dysplasia (2)
123101	Craniosynostosis, type 2 (3)
123580	Cataract, congenital, autosomal dominant (3)
123620	Cataract, cerulean, type 2, 601547 (3)
123660	Cataract, Coppock-like (3)
123829	Melanoma (3)
123940	White sponge nevus, 193900 (3)
124030	Debrisoquine sensitivity (3) ?Parkinsonism, susceptibility to (1)
124080	CMO II deficiency (3)
124200	Darier disease (keratosis follicularis) (2)
125270	Porphyria, acute hepatic (3) Lead poisoning, susceptibility to (3)
125490	Dentinogenesis imperfecta-1 (2)
125660	Cardiomyopathy (1) (?) Myopathy, desminopathic (1) (?)
125852	Insulin-dependent diabetes mellitus-2 (2)
126060	Anemia, megaloblastic, due to DHFR deficiency (1) (?)
126090	Hyperphenylalaninemia due to pterin-4a-carbinolamine dehydratase deficiency, 264070 (3)
126150	Diphtheria, susceptibility to (1)
126337	Myxoid liposarcoma (3)
126340	Xeroderma pigmentosum, group D, 278730 (3)
126391	DNA ligase I deficiency (3)
126451	?Schizophrenia, susceptibility to (2)
126452	Autonomic nervous system dysfunction (3) [Novelty seeking personality] (1)
126600	Drusen, radial, autosomal dominant (2)
126650	Chloride diarrhea, congenital, Finnish type, 214700 (3) Colon cancer (1) (?)
128100	Dystonia-1, torsion (3)
129010	Neuropathy, congenital hypomyelinating, 1 (3)
129490	Ectodermal dysplasia-3, anhidrotic (2)
129500	Ectodermal dysplasia, hidrotic (2)
129900	EEC syndrome-1 (2) (?)
130160	Cutis laxa, 123700 (3) Supravalvar aortic stenosis, 185500 (3) Williams-Beuren syndrome, 194050 (3)
130410	Glutaric aciduria, type IIB (3)
130500	Elliptocytosis-1 (3)
130650	Beckwith-Wiedemann syndrome (2)
131100	Carcinoid tumor of lung (3) Multiple endocrine neoplasia I (3) Prolactinoma, hyperparathyroidism, carcinoid syndrome (2)

131195	Hereditary hemorrhagic telangiectasia-1, 187300 (3)
131210	Atherosclerosis, susceptibility to (2)
131242	Shah-Waardenburg syndrome, 277580 (3)
131400	Eosinophilia, familial (2)
131440	Eosinophilic myeloproliferative disorder (2) (?)
132700	Cylindromatosis (2)
132800	Basal cell carcinoma (2) (?) Epithelioma, self-healing, squamous 1, Ferguson-Smith type (2)
133170	Erythremia (1) (?)
133171	[Erythrocytosis, familial], 133100 (3)
133200	Erythrokeratoderma variabilis (2)
133510	Trichothiodystrophy (3) Xeroderma pigmentosum, group B (3)
133530	Xeroderma pigmentosum, group G, 278780 (3)
133540	Cockayne syndrome-2, late onset (2)
133700	Chondrosarcoma, 215300 (3) Exostoses, multiple, type 1 (3)
133701	Exostoses, multiple, type 2 (3)
133780	Vitreoretinopathy, exudative, familial (2)
134370	Factor H deficiency (1) Hemolytic-uremic syndrome, 235400 (3) Membroproliferative glomerulonephritis (1)
134580	Factor XIIB deficiency (3)
134638	Systemic lupus erythematosus, susceptibility, 152700 (3)
134790	Hyperferritinemia-cataract syndrome, 600886 (3)
134797	Ectopia lentis, ?isolated (3) Marfan syndrome, 154700 (3) Shprintzen-Goldberg syndrome, 182212 (3)
134820	Amyloidosis, hereditary renal, 105200 (3) Dysfibrinogenemia, alpha type, causing bleeding diathesis (3) Dysfibrinogenemia, alpha type, causing recurrent thrombosis (3)
134830	Dysfibrinogenemia, beta type (3)
134850	Dysfibrinogenemia, gamma type (3) Hypofibrinogenemia, gamma type (3)
134934	Achondroplasia, 100800 (3) Craniosynostosis, nonsyndromic (3) Crouzon syndrome with acanthosis nigricans (3) Hypochondroplasia, 146000 (3) Thanatophoric dysplasia, types I and II, 187600 (3)
135300	Fibromatosis, gingival (2)
135600	Ehlers-Danlos syndrome, type X (1) (?)
135700	Fibrosis of extraocular muscles, congenital, 1 (2)
135750	Tetramelic mirror-image polydactyly (2) (?)
135940	Ichthyosis vulgaris, 146700 (1) (?)
136132	[Fish-odor syndrome], 602079 (3)
136350	Pfeiffer syndrome, 101600 (3)
136435	Ovarian dysgenesis, hypergonadotropic, with normal karyotype, 233300 (3)
136440	Lymphoma/leukemia, B-cell, variant (1)
136530	Male infertility, familial (1) (?)
136550	Macular dystrophy, North Carolina type (2)

136836	Fucosyltransferase-6 deficiency (3)
136850	Fumarase deficiency (3)
137181	[Gamma-glutamyltransferase, familial high serum] (2)
137350	Amyloidosis, Finnish type, 105120 (3)
137600	Iridogoniodysgenesis syndrome (2)
138030	[?Hyperproglucagonemia] (1)
138033	Diabetes mellitus, type II (3)
138040	Cortisol resistance (3)
138079	Hyperinsulinism, familial, 602485 (3) MODY, type 2, 125851 (3)
138140	Glucose transport defect, blood-brain barrier (3)
138190	Diabetes mellitus, noninsulin-dependent (3)
138320	Hemolytic anemia due to glutathione peroxidase deficiency (1)
138430	Diabetes mellitus, type II (3)
138491	Hyperekplexia and spastic paraparesis (3) Startle disease, autosomal recessive (3) Startle disease/hyperekplexia, autosomal dominant, 149400 (3)
138570	Non-insulin dependent diabetes mellitus, susceptibility to (2)
138571	Glycogen synthase, liver, deficiency of, 240600 (1)
138700	[Apolipoprotein H deficiency] (3)
138720	Bernard-Soulier syndrome, type B (2)
138850	Hypogonadotropic hypogonadism (3)
138971	Kostmann neutropenia, 202700 (3)
138981	Pulmonary alveolar proteinosis, 265120 (3)
139130	Hypertension, essential, susceptibility to, 145500 (3)
139150	Basal cell carcinoma (3)
139190	Gigantism due to GHRF hypersecretion (1) Isolated growth hormone deficiency due to defect in GHRF (1) (?)
139191	Growth hormone deficient dwarfism (3)
139250	Isolated growth hormone deficiency, Illig type with absent GH and Kowarski type with bioinactive GH (3)
139320	McCune-Albright polyostotic fibrous dysplasia, 174800 (3) Pituitary ACTH secreting adenoma (3) Pseudohypoparathyroidism, type Ia, 103580 (3) Somatotrophinoma (3)
139330	Night blindness, congenital stationary (3)
139350	Epidermolytic hyperkeratosis, 113800 (3) Keratoderma, palmoplantar, nonepidermolytic (3)
139360	Pituitary ACTH-secreting adenoma (3)
140100	[Anhaptoglobinemia] (3) [Hypohaptoglobinemia] (3)
141750	Alpha-thalassemia/mental retardation syndrome, type 1 (1)
141800	Erythremias, alpha- (3) Heinz body anemias, alpha- (3) Methemoglobinemias, alpha- (3) Thalassemias, alpha- (3)
141850	Erythrocytosis (3) Heinz body anemia (3) Hemoglobin H disease (3) Hypochromic microcytic anemia (3)

	Thalassemia, alpha- (3)
141900	Erythremias, beta- (3) HPFH, deletion type (3) Heinz body anemias, beta- (3) Methemoglobinemias, beta- (3) Sickle cell anemia (3) Thalassemias, beta- (3)
142000	Thalassemia due to Hb Lepore (3) Thalassemia, delta- (3)
142200	HPFH, nondeletion type A (3)
142250	HPFH, nondeletion type G (3)
142270	Hereditary persistence of fetal hemoglobin (3) (?)
142335	Hereditary persistence of fetal hemoglobin, heterocellular, Indian type (2) (?)
142380	Hepatocellular carcinoma (3)
142410	Insulin-dependent diabetes mellitus (3) MODY, type 3, 600496 (3) Non-insulin-dependent diabetes mellitus-2, 601407 (2)
142470	[Hereditary persistence of fetal hemoglobin, heterocellular] (2)
142600	Hemolytic anemia due to hexokinase deficiency (3)
142680	Periodic fever, familial (2)
142857	Pemphigoid, susceptibility to (2)
142858	Beryllium disease, chronic, susceptibility to (3)
142959	Hand-foot-uterus syndrome, 140000 (3)
142989	Synpolydactyly, type II, 186000 (3)
143100	Huntington disease (3)
143200	Erosive vitreoretinopathy (2) Wagner syndrome (2)
143450	Trifunctional protein deficiency, type II (3)
143890	Hypercholesterolemia, familial (3)
144120	Hyperimmunoglobulin G1 syndrome (2) (?)
144200	Epidermolytic palmoplantar keratoderma (3)
144700	Renal cell carcinoma (2)
145001	Hyperparathyroidism-jaw tumor syndrome (2)
145260	Pseudohypoaldosteronism, type II (2)
145410	Opitz G syndrome, type II (2)
145505	?Hypertension, essential (1)
145981	Hypocalciuric hypercalcemia, type II (2)
146150	Hypomelanosis of Ito (2) (?)
146200	Hypoparathyroidism, familial (2)
146740	Neutropenia, alloimmune neonatal (3) Viral infections, recurrent (3) Lupus erythematosus, systemic, susceptibility, 152700 (1)
146760	[IgG receptor I, phagocytic, familial deficiency of] (1)
146790	Lupus nephritis, susceptibility to (3)
147020	Agammaglobulinemia, 601495 (3)
147050	Atopy (2)
147061	Allergy and asthma susceptibility (2) (?)
147110	IgG2 deficiency, selective (3)
147141	Leukemia, acute lymphoblastic (1)

147200	[Kappa light chain deficiency] (3)
147440	Growth retardation with deafness and mental retardation (3)
147450	Amyotrophic lateral sclerosis, due to SOD1 deficiency, 105400 (3)
147545	Diabetes mellitus, noninsulin-dependent (3)
147557	Epidermolysis bullosa, junctional, with pyloric atresia, 226730 (3)
147570	Interferon, immune, deficiency (1)
147575	Macrocytic anemia refractory, of 5q- syndrome, 153550 (3) Myelodysplastic syndrome, preleukemic (3) Myelogenous leukemia, acute (3)
147660	Interferon, alpha, deficiency (1)
147670	Diabetes mellitus, insulin-resistant, with acanthosis nigricans (3) Leprechaunism (3) Rabson-Mendenhall syndrome (3)
147680	Severe combined immunodeficiency due to IL2 deficiency (1)
147781	Atopy, susceptibility to (3)
147790	Leukemia, acute lymphocytic, with 4/11 translocation (3) (?)
147791	Jacobsen syndrome (2)
148040	Epidermolysis bullosa simplex, Koebner, Dowling-Meara, and Weber-Cockayne types, 131900, 131760, 131800 (3)
148041	Pachyonychia congenita, Jadassohn-Lewandowsky type, 167200 (3)
148043	Meesmann corneal dystrophy, 122100 (3)
148065	White sponge nevus, 193900 (3)
148066	Epidermolysis bullosa simplex, Koebner, Dowling-Meara, and Weber-Cockayne types, 131900, 131760, 131800 (3) Epidermolysis bullosa simplex, recessive, 601001 (3)
148067	Nonepidermolytic palmoplantar keratoderma, 600962 (3) Pachyonychia congenita, Jadassohn-Lewandowsky type, 167200 (3)
148069	Pachyonychia congenita, Jackson-Lawler type, 167210 (3)
148070	?Liver disease, susceptibility to, from hepatotoxins or viruses (1)
148080	Epidermolytic hyperkeratosis, 113800 (3)
148370	Keratolytic winter erythema (2)
148500	Tylosis with esophageal cancer (2)
148900	Klippel-Feil syndrome with laryngeal malformation (2)
150000	Exertional myoglobinuria due to deficiency of LDH-A (3)
150100	Lactate dehydrogenase-B deficiency (3)
150200	[Placental lactogen deficiency] (1)
150210	Lactoferrin-deficient neutrophils, 245480 (1) (?)
150230	Langer-Giedion syndrome (2)
150240	Cutis laxa, marfanoid neonatal type (1) (?)
150250	Larsen syndrome, autosomal dominant (2)
150270	Laryngeal adductor paralysis (2) (?)
150292	Epidermolysis bullosa, Herlitz junctional type, 226700 (3)
150310	Epidermolysis bullosa, Herlitz junctional type, 226700 (3) Epidermolysis bullosa, generalized atrophic benign, 226650 (3)
151385	Leukemia, acute myeloid (3)
151390	Leukemia, acute T-cell (2)
151400	Leukemia/lymphoma, B-cell, 1 (2)
151430	Leukemia/lymphoma, B-cell, 2 (2)
151440	Leukemia, T-cell acute lymphoblastoid (2)

151670	Hepatic lipase deficiency (3)
152200	Coronary artery disease, susceptibility to (1)
152427	Long QT syndrome-2 (3)
152445	Erythrokeratoderma, progressive symmetric, 602036 (3) Vohwinkel syndrome, 124500 (3)
152760	Hypogonadotropic hypogonadism due to GNRH deficiency, 227200 (1) (?)
152780	Hypogonadism, hypergonadotropic (3) Male pseudohermaphroditism due to defective LH (1) (?)
152790	Leydig cell hypoplasia (3) Precocious puberty, male, 176410 (3)
153455	Cutis laxa, recessive, type I, 219100 (1)
153700	Macular dystrophy, vitelliform type (3)
153880	Macular dystrophy, dominant cystoid (2)
153900	Stargardt disease-2 (2)
154275	Malignant hyperthermia susceptibility 2 (2)
154276	Malignant hyperthermia susceptibility 3 (2)
154500	Treacher Collins mandibulofacial dysostosis (3)
154545	Chronic infections, due to opsonin defect (3)
154550	Carbohydrate-deficient glycoprotein syndrome, type Ib, 602579 (3)
154705	Marfan syndrome, type II (2)
155555	[Red hair/fair skin] (3) UV-induced skin damage, vulnerability to (3)
155600	Malignant melanoma, cutaneous (2)
155900	Melkersson-Rosenthal syndrome (2) (?)
156225	Muscular dystrophy, congenital merosin-deficient (3)
156232	Mesomelic dysplasia, Kantaputra type (2)
156490	Neuroblastoma (3)
156570	Methylcobalamin deficiency, cbl G type (3)
156600	Microcoria, congenital (2)
156845	Tietz syndrome, 103500 (3) Waardenburg syndrome, type IIA, 193510 (3) Waardenburg syndrome/ocular albinism, digenic, 103470 (3)
156850	Cataract, congenital, with microphthalmia (2)
157140	Dementia, frontotemporal, with parkinsonism, 601630 (3)
157147	Abetalipoproteinemia, 200100 (3)
157170	Holoprosencephaly-2 (2)
157640	PEO with mitochondrial DNA deletions, type 1 (2)
157655	Lactic acidosis due to defect in iron-sulfur cluster of complex I (1)
157900	Moebius syndrome (2) (?)
158590	Spinal muscular atrophy-4 (2)
158900	Facioscapulohumeral muscular dystrophy-1A (2)
159000	Muscular dystrophy, limb-girdle, type 1A (2)
159001	Muscular dystrophy, limb-girdle, type 1B (2)
159350	Colorectal cancer (3)
159440	Charcot-Marie-Tooth neuropathy-1B, 118200 (3) Dejerine-Sottas disease, myelin P(0)-related, 145900 (3) Hypomyelination, congenital (3)
159555	Leukemia, myeloid/lymphoid or mixed-lineage (2)
159595	Leukemia, transient, of Down syndrome (2)

160760	Cardiomyopathy, familial hypertrophic, 1, 192600 (3) Central core disease, one form (3) (?)
160777	Griscelli disease, 214450 (3)
160781	Cardiomyopathy, hypertrophic, mid-left ventricular chamber type (3)
160900	Myotonic dystrophy (3)
160980	Carney myxoma-endocrine complex (2)
161015	Mitochondrial complex I deficiency, 252010 (1) (?)
162100	Neuralgic amyotrophy with predilection for brachial plexus (2)
162150	Obesity with impaired prohormone processing, 600955 (3)
162400	Neuropathy, hereditary sensory and autonomic, type 1 (2)
163729	Hypertension, pregnancy-induced (2)
163890	Parkinson disease, type 1, 601508 (3)
163950	Cardiofaciocutaneous syndrome, 115150 (2) Noonan syndrome-1 (2)
164009	Leukemia, acute promyelocytic, NUMA/RARA type (3)
164040	Leukemia, acute promyelocytic, NPM/RARA type (3)
164050	Nucleoside phosphorylase deficiency, immunodeficiency due to (3)
164160	Obesity, severe, due to leptin deficiency (3)
164200	Oculodentodigital dysplasia (2) Syndactyly, type III, 186100 (2)
164500	Spinocerebellar ataxia-7 (3)
164731	Ovarian carcinoma, 167000 (2)
164761	Hirschsprung disease, 142623 (3) Medullary thyroid carcinoma, 155240 (3) Multiple endocrine neoplasia IIA, 171400 (3) Multiple endocrine neoplasia IIB, 162300 (3)
164770	Myeloid malignancy, predisposition to (3)
164790	Colorectal cancer (3)
164860	Renal cell carcinoma, papillary, familial and sporadic (3)
164920	Mast cell leukemia (3) Mastocytosis with associated hematologic disorder (3) Piebaldism (3)
164953	Liposarcoma (1)
165215	3q21q26 syndrome (1)
165240	Greig cephalopolysyndactyly syndrome, 175700 (3) Pallister-Hall syndrome, 146510 (3) Postaxial polydactyly type A1, 174200 (3)
165320	Hepatocellular carcinoma (1) (?)
166600	Osteopetrosis, AD, type II (2)
166800	Otosclerosis (2)
167000	Ovarian cancer, serous (2)
167250	Paget disease of bone (2) (?)
167409	Optic nerve coloboma with renal disease, 120330 (3)
167415	Hypothyroidism, congenital, due to thyroid dysgenesis or hypoplasia (3)
168000	Paraganglioma, familial nonchromaffin, 1 (2)
168360	Paraneoplastic sensory neuropathy (1)
168450	Hypoparathyroidism, autosomal dominant(3) Hypoparathyroidism, autosomal recessive (3)
168461	Centrocytic lymphoma (2) Multiple myeloma, 254250 (2)

	Parathyroid adenomatosis 1 (2)
168468	Metaphyseal chondrodysplasia, Murk Jansen type, 156400 (3)
168470	Humoral hypercalcemia of malignancy (1) (?)
168500	Parietal foramina (2)
168610	Parkinsonism-dementia with pallidopontonigral degeneration (2)
169600	Hailey-Hailey disease (2)
170261	Bare lymphocyte syndrome, type I, due to TAP2 deficiency (1)
170500	Hyperkalemic periodic paralysis (3) Myotonia congenita, atypical acetazolamide-responsive (3) Paramyotonia congenita, 168300 (3)
170650	Periodontitis, juvenile (2)
170993	Zellweger syndrome-3 (3)
170995	Zellweger syndrome-2 (3)
171050	Colchicine resistance (3)
171060	Cholestasis, progressive familial intrahepatic, type III, 602347 (3)
171190	Hypertension, essential, 145500 (1) (?)
171650	Lysosomal acid phosphatase deficiency (1) (?)
171760	Hypophosphatasia, adult, 146300 (1) (?) Hypophosphatasia, infantile, 241500 (3)
171860	Hemolytic anemia due to phosphofructokinase deficiency (1)
172400	Hemolytic anemia due to glucosephosphate isomerase deficiency (3) Hydrops fetalis, one form (1)
172411	?Colorectal cancer, resistance to (1)
172471	Glycogenosis, hepatic, autosomal (3)
172490	Phosphorylase kinase deficiency of liver and muscle, 261750 (2) (?)
173360	Hemorrhagic diathesis due to PAI1 deficiency (1) Thrombophilia due to excessive plasminogen activator inhibitor (1)
173370	Plasminogen activator deficiency (1)
173470	Glanzmann thrombasthenia, type B (3)
173510	Platelet glycoprotein IV deficiency (3) [Macrothrombocytopenia] (1)
173610	Platelet alpha/delta storage pool deficiency (1)
173850	Polio, susceptibility to (2)
173870	Fanconi anemia (1) (?) Xeroderma pigmentosum (1) (?)
173910	Polycystic kidney disease, adult, type II (3)
174000	Medullary cystic kidney disease, AD (2)
174810	Osteolysis, familial expansile (2)
174900	Polyposis, juvenile intestinal (2)
175100	Adenomatous polyposis coli (3) Adenomatous polyposis coli, attenuated (3) Colorectal cancer (3) Desmoid disease, hereditary, 135290 (3) Gardner syndrome (3) Turcot syndrome, 276300 (3)
176000	Porphyria, acute intermittent (3)
176010	Porphyria, Chester type (2)
176100	Porphyria cutanea tarda (3) Porphyria, hepatoerythropoietic (3)
176260	Episodic ataxia/myokymia syndrome, 160120 (3)

176261	Jervell and Lange-Nielsen syndrome, 220400 (3)
176300	Amyloid neuropathy, familial, several allelic types (3) Amyloidosis, senile systemic (3) Carpal tunnel syndrome, familial (3) [Dystransthyretinemic hyperthyroxinemia](3)
176310	Leukemia, acute pre-B-cell (2)
176450	Sacral agenesis-1 (2)
176640	Creutzfeldt-Jakob disease, 123400 (3) Gerstmann-Straussler disease, 137440 (3) Insomnia, fatal familial (3)
176705	Breast cancer, sporadic (3)
176730	Diabetes mellitus, rare form (1) Hyperproinsulinemia, familial (3) MODY, one form (3)
176797	Leukemia, acute promyelocytic, PL2F/RARA type (3)
176860	Purpura fulminans, neonatal (1) Thrombophilia due to protein C deficiency (3)
176930	Dysprothrombinemia (3) Hypoprothrombinemia (3)
176943	Apert syndrome, 101200 (3) Beare-Stevenson cutis gyrata syndrome, 123790 (3) Crouzon craniofacial dysostosis, 123500 (3) Jackson-Weiss syndrome, 123150 (3) Pfeiffer syndrome, 101600 (3)
176947	Selective T-cell defect (3)
176960	Pituitary tumor, invasive (3)
177000	Protoporphyrria, erythropoietic (3) Protoporphyrria, erythropoietic, recessive, with liver failure (3)
177070	Hermansky-Pudlak syndrome, 203300 (1) (?) Spherocytosis, hereditary, Japanese type (3)
177900	Psoriasis susceptibility-1 (2)
178300	Ptois, hereditary congenital, 1 (2)
178600	Pulmonary hypertension, familial primary (2)
178640	Pulmonary alveolar proteinosis, congenital, 265120 (3)
179095	Male infertility (1) (?)
179450	Ragweed sensitivity (2) (?)
179605	Butterfly dystrophy, retinal (3) Macular dystrophy (3) Retinitis pigmentosa, digenic (3) Retinitis pigmentosa-7, peripherin-related (3) Retinitis punctata albescens (3)
179615	Reticulosis, familial histiocytic, 267700 (3) Severe combined immunodeficiency, B cell-negative, 601457 (3)
179616	Severe combined immunodeficiency, B cell-negative, 601457 (3)
179755	Renal cell carcinoma, papillary, 1 (2)
179820	[Hyperproreninemia] (3)
180069	Leber congenital amaurosis-2, 204100 (3) Retinal dystrophy, autosomal recessive, childhood-onset (3) Retinitis pigmentosa-20 (3)
180071	Retinitis pigmentosa, autosomal recessive (3)

180072	Night blindness, congenital stationary, type 3, 163500 (3) Retinitis pigmentosa, autosomal recessive (3)
180090	Retinitis pigmentosa, autosomal recessive (3)
180100	Retinitis pigmentosa-1 (2)
180104	Retinitis pigmentosa-9 (2)
180105	Retinitis pigmentosa-10 (2)
180200	Bladder cancer, 109800 (3) Osteosarcoma, 259500 (2) Pinealoma with bilateral retinoblastoma (2) Retinoblastoma (3)
180240	Leukemia, acute promyelocytic (1)
180250	Retinol binding protein, deficiency of (1) (?)
180297	Anemia, hemolytic, Rh-null, suppressor type, 268150 (3)
180380	Night blindness, congenital stationery, rhodopsin-related (3) Retinitis pigmentosa, autosomal recessive (3) Retinitis pigmentosa-4, autosomal dominant (3)
180381	Oguchi disease-2, 258100 (3)
180385	Leukemia, acute T-cell (2)
180721	Retinitis pigmentosa, digenic (3)
180840	Susceptibility to IDDM (1) (?)
180860	Russell-Silver syndrome (2)
180901	Central core disease, 117000 (3) Malignant hyperthermia susceptibility 1, 145600 (3)
181405	Scapuloperoneal spinal muscular atrophy, New England type (2)
181430	Scapuloperoneal syndrome, myopathic type (2)
181460	Schistosoma mansoni, susceptibility/resistance to (2)
181510	Schizophrenia (2) (?)
181600	Sclerolyosis (2) (?)
182138	Anxiety-related personality traits (3)
182280	Small-cell cancer of lung (2)
182290	Smith-Magenis syndrome (2)
182380	Glucose/galactose malabsorption (3)
182381	Renal glucosuria, 253100 (1) (?)
182452	Lung cancer, small cell (3)
182500	Cataract, congenital (2) (?)
182600	Spastic paraplegia-3A (2)
182601	Spastic paraplegia-4 (3)
182860	Elliptocytosis-2 (3) Pyropoikilocytosis (3) Spherocytosis, recessive (3)
182870	Anemia, neonatal hemolytic, fatal and near-fatal (3) Elliptocytosis-3 (3) Spherocytosis-1 (3)
182900	Spherocytosis-2 (3)
183600	Split hand/foot malformation, type 1 (2)
185000	Stomatocytosis I (1) (?)
185430	Atherosclerosis, susceptibility to (3) (?)
185470	Myopathy due to succinate dehydrogenase deficiency (1) (?)
185800	Symphalangism, proximal (2)

186580	Arthrocutaneous granulomatosis (2)
186740	Immunodeficiency due to defect in CD3-gamma (3)
186770	Leukemia, T-cell acute lymphocytic (2)
186780	CD3, zeta chain, deficiency (1)
186830	Immunodeficiency, T-cell receptor/CD3 complex (3)
186855	Leukemia-2, T-cell acute lymphoblastic (3)
186860	Leukemia/lymphoma, T-cell (2)
186880	Leukemia/lymphoma, T-cell (3)
186921	Leukemia, T-cell acute lymphoblastic (2)
186940	[CD4(+) lymphocyte deficiency] (2) Lupus erythematosus, susceptibility to (2)
186960	Leukemia/lymphoma, T-cell (2)
187040	Leukemia-1, T-cell acute lymphoblastic (3)
188025	Thrombocytopenia, Paris-Trousseau type (2) (?)
188040	Thrombophilia due to thrombomodulin defect (3)
188070	Bleeding disorder due to defective thromboxane A2 receptor (3)
188450	Goiter, adolescent multinodular (1) Goiter, nonendemic, simple (3) Hypothyroidism, hereditary congenital (3)
188540	Hypothyroidism, nongoitrous (3)
188550	Thyroid papillary carcinoma (1)
188826	Sorsby fundus dystrophy, 136900 (3)
189800	Preeclampsia/eclampsia (2) (?)
189980	Leukemia, chronic myeloid (3)
190000	Atransferrinemia (1)
190020	Bladder cancer, 109800 (3)
190040	Dermatofibrosarcoma protuberans (3) Giant-cell fibroblastoma (3) Meningioma, SIS-related (3)
190070	Colorectal adenoma (1) Colorectal cancer (1)
190080	Burkitt lymphoma (3)
190100	Geniospasm (2)
190182	Colon cancer (3) Colorectal cancer, familial nonpolyposis, type 6 (3)
190195	Ichthyosiform erythroderma, congenital, 242100 (3) Ichthyosis, lamellar, autosomal recessive, 242300 (3)
190198	Leukemia, T-cell acute lymphoblastic (2)
190300	Tremor, familial essential, 1 (2)
190350	Trichorhinophalangeal syndrome, type I (2)
190450	Hemolytic anemia due to triosephosphate isomerase deficiency (3)
190605	Triphalangeal thumb-polysyndactyly syndrome (2)
190685	Down syndrome (1)
190900	Colorblindness, tritan (3)
191010	Cardiomyopathy, familial hypertrophic, 3, 115196 (3)
191030	Nemaline myopathy-1, 161800 (3)
191044	Cardiomyopathy, familial hypertrophic (3)
191045	Cardiomyopathy, familial hypertrophic, 2, 115195 (3)
191092	Tuberous sclerosis-2 (3)

191100	Tuberous sclerosis-1 (3)
191170	Colorectal cancer, 114500 (3) Li-Fraumeni syndrome (3)
191181	Cervical carcinoma (2)
191290	Segawa syndrome, recessive (3)
191315	Insensitivity to pain, congenital, with anhidrosis, 256800 (3)
191540	[Urate oxidase deficiency] (1)
192090	Breast cancer, lobular (3) Endometrial carcinoma (3) Gastric cancer, familial, 137215 (3) Ovarian carcinoma (3)
192340	Diabetes insipidus, neurohypophyseal, 125700 (3)
192500	Jervell and Lange-Nielsen syndrome, 220400 (3) Long QT syndrome-1 (3)
192974	Glycoprotein Ia deficiency (2) (?) Neonatal alloimmune thrombocytopenia (2)
193235	Vitreoretinopathy, neovascular inflammatory (2)
193300	Renal cell carcinoma (3) von Hippel-Lindau syndrome (3)
193500	Craniofacial-deafness-hand syndrome, 122880 (3) Rhabdomyosarcoma, alveolar, 268220 (3) Waardenburg syndrome, type I (3) Waardenburg syndrome, type III, 148820 (3)
194070	Denys-Drash syndrome (3) Frasier syndrome, 136680 (3) Wilms tumor, type 1 (3)
194071	Adrenocortical carcinoma, hereditary, 202300 (2) Wilms tumor, type 2 (2)
194190	Wolf-Hirschhorn syndrome (2)
200150	Choreoacanthocytosis (2)
200350	Acetyl-CoA carboxylase deficiency (1)
200990	Acrocallosal syndrome (2) (?)
201450	Acyl-CoA dehydrogenase, medium chain, deficiency of (3)
201460	Acyl-CoA dehydrogenase, long chain, deficiency of (3)
201470	Acyl-CoA dehydrogenase, short-chain, deficiency of (3)
201475	VLCAD deficiency (3)
201810	3-beta-hydroxysteroid dehydrogenase, type II, deficiency (3)
201910	Adrenal hyperplasia, congenital, due to 21-hydroxylase deficiency (3)
202010	Adrenal hyperplasia, congenital, due to 11-beta-hydroxylase deficiency (3) Aldosteronism, glucocorticoid-remediable (3)
203100	Albinism, oculocutaneous, type IA (3) Waardenburg syndrome/ocular albinism, digenic, 103470 (3)
203310	Ocular albinism, autosomal recessive (2) (?)
203500	Alkaptonuria (3)
203740	Alpha-ketoglutarate dehydrogenase deficiency (1)
203750	3-ketothiolase deficiency (3)
203800	Alstrom syndrome (2)
204500	Ceroid-lipofuscinosis, neuronal 2, classic late infantile (2)
205100	Amyotrophic lateral sclerosis, juvenile (2)
205900	Anemia, Diamond-Blackfan (2)

207750	Hyperlipoproteinemia, type Ib (3)
207800	Argininemia (3)
208100	Arthrogryposis multiplex congenita, neurogenic (2)
208250	Jacobs syndrome (2)
208400	Aspartylglucosaminuria (3)
208900	Ataxia-telangiectasia (3) B-cell non-Hodgkin lymphoma, sporadic (3) T-cell prolymphocytic leukemia, sporadic (3)
209900	Bardet-Biedl syndrome 2 (2)
209901	Bardet-Biedl syndrome 1 (2)
210900	Bloom syndrome (3)
211420	Breast cancer, ductal (2)
212138	Carnitine-acylcarnitine translocase deficiency (3)
212200	Carnosinemia (2)
213700	Cerebrotendinous xanthomatosis (3)
214300	Klippel-Feil syndrome (2) (?)
214400	Charcot-Marie-Tooth neuropathy-4A (2)
214500	Chediak-Higashi syndrome (3)
215700	Citrullinemia (3)
216550	Cohen syndrome (2)
216900	Achromatopsia (2)
216950	C1r/C1s deficiency, combined (1)
217000	C2 deficiency (3)
217030	C3b inactivator deficiency (3)
217050	C6 deficiency (1) Combined C6/C7 deficiency (1)
217070	C7 deficiency (1)
217800	Macular corneal dystrophy (2)
218000	Andermann syndrome (2)
218030	Apparent mineralocorticoid excess, hypertension due to (3)
219800	Cystinosis, nephropathic (3)
221770	Polycystic lipomembranous osteodysplasia with sclerosing leukencephalopathy (2)
221820	Gliosis, familial progressive subcortical (2)
222100	Diabetes mellitus, insulin-dependent-1 (2) (?)
222600	Achondrogenesis Ib, 600972 (3) Atelosteogenesis II, 256050 (3) Diastrophic dysplasia (3)
222700	Lysinuric protein intolerance (2)
222745	DECR deficiency (2) (?)
222800	Hemolytic anemia due to bisphosphoglycerate mutase deficiency (1)
222900	Sucrose intolerance (3)
223000	Lactase deficiency, adult, 223100 (1) (?) Lactase deficiency, congenital (1) (?)
223360	Dopamine-beta-hydroxylase deficiency (1)
223900	Dysautonomia, familial (2)
224100	Congenital dyserythropoietic anemia II (2)
224120	Dyserythropoietic anemia, congenital, type I (2)
225500	Ellis-van Creveld syndrome (2)

226450	Epidermolysis bullosa inversa, junctional (2)
227220	[Eye color, brown] (2)
227400	Hemorrhagic diathesis due to factor V deficiency (1) Thromboembolism susceptibility due to factor V Leiden (3)
227500	Factor VII deficiency (3)
227600	Factor X deficiency (3)
227645	Fanconi anemia, type C (3)
227646	Fanconi anemia, type D (2)
227650	Fanconi anemia, type A (3)
229000	Fletcher factor deficiency (1)
229300	Friedreich ataxia (3) Friedreich ataxia with retained reflexes (2)
229600	Fructose intolerance (3)
229700	Fructose-bisphosphatase deficiency (1)
230000	Fucosidosis (3)
230200	Galactokinase deficiency with cataracts (3)
230350	Galactose epimerase deficiency (3)
230450	Hemolytic anemia due to gamma-glutamylcysteine synthetase deficiency (1)
230500	GM1-gangliosidosis (3) Mucopolysaccharidosis IVB (3)
230800	Gaucher disease (3) Gaucher disease with cardiovascular calcification (3)
231200	Bernard-Soulier syndrome (3)
231550	Achalasia-addisonianism-alacrimia syndrome (2)
231670	Glutaricaciduria, type I (3)
231675	Glutaricaciduria, type IIC (3)
231680	Glutaricaciduria, type IIA (1)
231950	Glutathioninuria (1)
232000	Propionicacidemia, type I or pccA type (1)
232050	Propionicacidemia, type II or pccB type (3)
232200	Glycogen storage disease I (3)
232400	Glycogen storage disease IIIa (1) Glycogen storage disease IIIb (3)
232600	McArdle disease (3)
232700	Glycogen storage disease VI (3)
232800	Glycogen storage disease VII (3)
233100	[Renal glucosuria] (2)
233690	Chronic granulomatous disease, autosomal, due to deficiency of CYBA (3)
233700	Chronic granulomatous disease due to deficiency of NCF-1 (3)
233710	Chronic granulomatous disease due to deficiency of NCF-2 (1)
234000	Factor XII deficiency (3)
234200	Neurodegeneration with brain iron accumulation (2)
235200	Hemochromatosis (3)
235800	[Histidinemia] (1)
236100	Holoprosencephaly-1 (2)
236200	Homocystinuria, B6-responsive and nonresponsive types (3)
236700	McKusick-Kaufman syndrome (2)
236730	Urofacial syndrome (2)

237300	Carbamoylphosphate synthetase I deficiency (3)
238300	Hyperglycinemia, nonketotic, type I (3)
238310	Hyperglycinemia, nonketotic, type II (1)
238600	Chylomicronemia syndrome, familial (3) Combined hyperlipemia, familial (3) Hyperlipoproteinemia I (1) Lipoprotein lipase deficiency (3)
238970	HHH syndrome (2) (?)
239500	Hyperprolinemia, type I (1)
240300	Autoimmune polyglandular disease, type I (3)
243500	Isovalericacidemia (3)
245000	Papillon-Lefevre syndrome (2)
245050	Ketoacidosis due to SCOT deficiency (3)
245200	Krabbe disease (3)
245349	Lacticacidemia due to PDX1 deficiency (3)
245900	Fish-eye disease (3) Norum disease (3)
246450	HMG-CoA lyase deficiency (3)
246530	Leukotriene C4 synthase deficiency (1)
246900	Lipoamide dehydrogenase deficiency (3)
247200	Miller-Dieker lissencephaly syndrome (2)
247640	Leukemia, acute lymphoblastic (2)
248510	Mannosidosis, beta- (3)
248600	Maple syrup urine disease, type Ia (3)
248610	Maple syrup urine disease, type II (3)
248611	Maple syrup urine disease, type Ib (3)
249000	Meckel syndrome (2)
249270	Thiamine-responsive megaloblastic anemia (2)
250100	Metachromatic leukodystrophy (3)
250800	Methemoglobinemia, type I (3) Methemoglobinemia, type II (3)
250850	Hypermethioninemia, persistent, autosomal dominant, due to methionine adenosyltransferase I/III deficiency (3)
251000	Methylmalonicaciduria, mutase deficiency type (3)
251170	Mevalonicaciduria (3)
252500	Mucopolipidosis II (1) Mucopolipidosis III (1)
252800	Mucopolysaccharidosis Ih (3) Mucopolysaccharidosis Ih/s (3) Mucopolysaccharidosis Is (3)
252920	Sanfilippo syndrome, type B (3)
252940	Sanfilippo syndrome, type D (1)
253000	Mucopolysaccharidosis IVA (3)
253200	Maroteaux-Lamy syndrome, several forms (3)
253220	Mucopolysaccharidosis VII (3)
253250	Mulibrey nanism (2)
253260	Biotinidase deficiency (3)
253270	Multiple carboxylase deficiency, biotin-responsive (3)
253601	Miyoshi myopathy, 254130 (2)

	Muscular dystrophy, limb-girdle, type 2B (2)
253700	Muscular dystrophy, limb-girdle, type 2C (3)
253800	Fukuyama type congenital muscular dystrophy (2) Walker-Warburg syndrome, 236670 (2) (?)
254210	Myasthenia gravis, familial infantile (2)
254770	Epilepsy, juvenile myoclonic (2)
255800	Schwartz-Jampel syndrome (2)
256030	Nemaline myopathy-2 (2)
256100	Nephronophthisis, juvenile (3)
256540	Galactosialidosis (3)
256550	Sialidosis, type I (3) Sialidosis, type II (3)
256731	Ceroid-lipofuscinosis, neuronal-5, variant late infantile (3)
257200	Niemann-Pick disease, type A (3) Niemann-Pick disease, type B (3)
257220	Niemann-Pick disease, type C (3) Niemann-Pick disease, type D, 257250 (2)
258501	3-methylglutaconicaciduria, type III (2)
258870	Gyrate atrophy of choroid and retina with ornithinemia, B6 responsive or unresponsive (3)
258900	Oroticaciduria (3)
259700	Osteopetrosis, recessive (2)
259730	Renal tubular acidosis-osteopetrosis syndrome (3)
259770	Osteoporosis-pseudoglioma syndrome (2)
259900	Hyperoxaluria, primary, type I (3)
261510	Pseudo-Zellweger syndrome (1)
261600	Phenylketonuria (3) [Hyperphenylalaninemia, mild] (3)
261640	Phenylketonuria due to PTS deficiency (3)
261670	Myopathy due to phosphoglycerate mutase deficiency (3)
262000	Bjornstad syndrome (2)
262850	Plasmin inhibitor deficiency (3)
263200	Polycystic kidney disease, autosomal recessive (2)
263700	Porphyria, congenital erythropoietic (3)
264300	Pseudohermaphroditism, male, with gynecomastia (3)
264470	Adrenoleukodystrophy, pseudoneonatal (2)
264600	Pseudovaginal perineoscrotal hypospadias (3)
264700	Pseudo-vitamin D dependency rickets 1 (2)
264900	Factor XI deficiency (3)
266100	Pyridoxine dependency with seizures (1) (?)
266150	Pyruvate carboxylase deficiency (3)
266200	Anemia, hemolytic, due to PK deficiency (3)
266300	[Hair color, red] (2)
266600	Inflammatory bowel disease-1 (2)
267750	Knobloch syndrome (2)
268800	Sandhoff disease, infantile, juvenile, and adult forms (3) Spinal muscular atrophy, HEXB-related (3)
268900	[Sarcosinemia] (2)
269920	Salla disease (2)

270200	Sjogren-Larsson syndrome (3)
270800	Spastic paraplegia-5A (2)
271245	Spinocerebellar ataxia-8, infantile, with sensory neuropathy (2)
271900	Canavan disease (3)
272750	GM2-gangliosidosis, AB variant (3)
272800	GM2-gangliosidosis, juvenile, adult (3) Tay-Sachs disease (3) [Hex A pseudodeficiency] (1)
273300	Male germ cell tumor (2)
273800	Glanzmann thrombasthenia, type A (3) Thrombocytopenia, neonatal alloimmune (1)
274180	Thromboxane synthase deficiency (2)
274270	Thymine-uraciluria (1) Fluorouracil toxicity, sensitivity to (1)
274500	Goiter, congenital (3) Hypothyroidism, congenital (3) Thyroid iodine peroxidase deficiency (1)
274600	Deafness, autosomal recessive 4 (3) Pendred syndrome (3)
275200	Graves disease, 275000 (1) Hyperthyroidism, congenital (3) Hypothyroidism, nongoitrous, due to TSH resistance (3) Thyroid adenoma, hyperfunctioning (3)
275350	Transcobalamin II deficiency (3)
276000	Pancreatitis, hereditary, 167800 (3) Trypsinogen deficiency (1)
276600	Tyrosinemia, type II (3)
276700	Tyrosinemia, type I (3)
276710	Tyrosinemia, type III (1)
276901	Usher syndrome, type 2 (3)
276902	Usher syndrome, type 3 (2)
276903	Deafness, autosomal dominant 11, neurosensory, 601317 (3) Deafness, autosomal recessive 2, neurosensory, 600060 (3) Usher syndrome, type 1B (3)
276904	Usher syndrome, type 1C (2)
277700	Werner syndrome (3)
277730	Wernicke-Korsakoff syndrome, susceptibility to (1)
277900	Wilson disease (3)
278000	Cholesteryl ester storage disease (3) Wolman disease (3)
278250	Wrinkly skin syndrome (2)
278300	Xanthinuria, type I (3)
278700	Xeroderma pigmentosum, group A (3)
278720	Xeroderma pigmentosum, group C (3)
278760	Xeroderma pigmentosum, group F (3)
300011	Cutis laxa, neonatal (3) Menkes disease, 309400 (3) Occipital horn syndrome, 304150 (3)
300029	Retinitis pigmentosa-15 (2)
300031	Mental retardation, X-linked, FRAXF type (3)

300032	Alpha-thalassemia/mental retardation syndrome, type 2, 301040 (3) Juberg-Marsidi syndrome, 309590 (3)
300044	?Wernicke-Korsakoff syndrome, susceptibility to (1)
300046	Mental retardation, X-linked 23, nonspecific (2)
300047	Mental retardation, X-linked 20 (2)
300048	Intestinal pseudoobstruction, neuronal, X-linked (2)
300049	BPNH/MR syndrome (2) Nodular heterotopia, bilateral periventricular (2)
300055	Mental retardation with psychosis, pyramidal signs, and macroorchidism (2)
300071	Night blindness, congenital stationary, type 2 (2)
300075	Coffin-Lowry syndrome, 303600 (3)
300077	Mental retardation, X-linked 29 (2)
300085	Cone dystrophy, progressive X-linked, 2 (2)
300088	Epilepsy, female restricted, with mental retardation (2)
300100	Adrenoleukodystrophy (3) Adrenomyeloneuropathy (3)
300104	Mental retardation, X-linked nonspecific, 309541 (3)
300110	Night blindness, congenital stationary, X-linked incomplete, 300071 (3)
300123	Mental retardation with isolated growth hormone deficiency (2)
300126	Dyskeratosis congenita-1, 305000 (3)
300300	Agammaglobulinemia, type 1, X-linked (3) XLA and isolated growth hormone deficiency, 307200 (3) (?)
300600	Ocular albinism, Forsius-Eriksson type (2)
300700	Albinism-deafness syndrome (2)
301000	Thrombocytopenia, X-linked, 313900 (3) Wiskott-Aldrich syndrome (3)
301200	Amelogenesis imperfecta (3)
301201	Amelogenesis imperfecta-3, hypoplastic type (2) (?)
301300	Anemia, sideroblastic/hypochromic (3)
301310	Anemia, sideroblastic, with spinocerebellar ataxia (2) (?)
301500	Fabry disease (3)
301590	Anophthalmos-1 (2) (?)
301830	Arthrogryposis, X-linked (spinal muscular atrophy, infantile, X-linked) (2)
301835	Arts syndrome (2)
301845	Bazex syndrome (2)
301900	Borjeson-Forssman-Lehmann syndrome (2)
302060	Barth syndrome (3) Cardiomyopathy, X-linked dilated, 300069 (3) Endocardial fibroelastosis-2 (2) Noncompaction of left ventricular myocardium, isolated (3)
302350	Nance-Horan syndrome (2)
302801	Charcot-Marie-Tooth neuropathy, X-linked-2, recessive (2)
302960	Chondrodysplasia punctata, X-linked dominant (2)
303400	Cleft palate, X-linked (2)
303630	Alport syndrome, 301050 (3) Leiomyomatosis-nephropathy syndrome, 308940 (1)
303631	Leiomyomatosis, diffuse, with Alport syndrome (3)
303700	Colorblindness, blue monochromatic (3)

303800	Colorblindness, deutan (3)
303900	Colorblindness, protan (3)
304040	Charcot-Marie-Tooth neuropathy, X-linked-1, dominant, 302800 (3)
304340	Mental retardation, X-linked, syndromic-5, with Dandy-Walker malformation, basal ganglia disease, and seizures (2)
304500	Deafness, X-linked 2, perceptive congenital (2)
304700	Deafness, X-linked 1, progressive (3) Jensen syndrome, 311150 (3) Mohr-Tranebjaerg syndrome (3)
304800	Diabetes insipidus, nephrogenic (3)
305100	Anhidrotic ectodermal dysplasia (2)
305400	Aarskog-Scott syndrome (3)
305435	Heterocellular hereditary persistence of fetal hemoglobin, Swiss type (2)
305450	FG syndrome (2)
305900	Favism (3) G6PD deficiency (3) Hemolytic anemia due to G6PD deficiency (3)
306000	Glycogenosis, X-linked hepatic, type I (3) Glycogenosis, X-linked hepatic, type II (3)
306100	Gonadal dysgenesis, XY female type (2)
306250	Leukemia, acute myeloid, M2 type (1)
306700	Hemophilia A (3)
306900	Hemophilia B (3)
306955	Heterotaxy, X-linked visceral (3)
306995	[?Homosexuality, male] (2)
307150	Hypertrichosis, congenital generalized (2)
307700	Hypoparathyroidism, X-linked (2)
307800	Hypophosphatemia, hereditary (3)
308000	HPRT-related gout (3) Lesch-Nyhan syndrome (3)
308100	Ichthyosis, X-linked (3) Placental steroid sulfatase deficiency (3)
308240	Lymphoproliferative syndrome, X-linked (2)
308300	Incontinentia pigmenti, sporadic type (2)
308310	Incontinentia pigmenti, familial (2)
308380	Combined immunodeficiency, X-linked, moderate, 312863 (3) Severe combined immunodeficiency, X-linked, 300400 (3)
308800	Keratosis follicularis spinulosa decalvans (2)
308840	Hydrocephalus due to aqueductal stenosis, 307000 (3) MASA syndrome, 303350 (3) Spastic paraplegia, 312900 (3)
309000	Lowe syndrome (3)
309200	Manic-depressive illness, X-linked (2) (?)
309300	Megalocornea, X-linked (2)
309470	Mental retardation, X-linked, syndromic-3, with spastic diplegia (2)
309500	Renpenning syndrome-1 (2)
309510	Mental retardation, X-linked, syndromic-1, with dystonic movements, ataxia, and seizures (2)
309548	Mental retardation, X-linked, FRAXE type (3)
309605	Mental retardation, X-linked, syndromic-4, with congenital contractures

	and low fingertip arches (2)
309610	Mental retardation, X-linked, syndromic-2, with dysmorphism and cerebral atrophy (2)
309620	Mental retardation-skeletal dysplasia (2)
309850	Brunner syndrome (3)
309900	Mucopolysaccharidosis II (3)
310300	Emery-Dreifuss muscular dystrophy (3)
310400	Myotubular myopathy, X-linked (3)
310460	Bornholm eye disease (2) Myopia-1 (2)
310490	Cowchock syndrome (2)
311050	Optic atrophy, X-linked (2)
311200	Oral-facial-digital syndrome 1 (2)
311300	Otopalatodigital syndrome, type I (2)
311510	Waisman parkinsonism-mental retardation syndrome (2)
311770	Paroxysmal nocturnal hemoglobinuria (3)
311800	Hemolytic anemia due to PGK deficiency (3) Myoglobinuria/hemolysis due to PGK deficiency (3)
311850	Phosphoribosyl pyrophosphate synthetase-related gout (3)
311870	Muscle glycogenosis (3)
312000	Panhypopituitarism, X-linked (2)
312040	N syndrome, 310465 (1) (?)
312060	Properdin deficiency, X-linked (3)
312080	Pelizaeus-Merzbacher disease (3) Spastic paraplegia-2, 312920 (3)
312170	Pyruvate dehydrogenase deficiency (3)
312700	Retinoschisis (3)
312760	Turner syndrome (1)
312865	Langer mesomelic dysplasia, 249700 (3) Leri-Weill dyschondrosteosis, 127300 (3) Short stature, idiopathic familial (3)
313400	Spondyloepiphyseal dysplasia tarda (2)
313850	Thoracoabdominal syndrome (2)
314250	Dystonia-3, torsion, with parkinsonism, Filipino type (2)
314300	Goeminne TKCR syndrome (2)
314400	Cardiac valvular dysplasia-1 (2)
314580	Wieacker-Wolff syndrome (2)
600020	Prostate cancer, 176807 (3)
600040	Colorectal cancer (3)
600045	Xeroderma pigmentosum, group E, subtype 2 (1)
600048	Breast cancer-3 (2)
600049	Myelodysplasia syndrome-1 (3)
600059	Retinitis pigmentosa-13 (2)
600065	Leukocyte adhesion deficiency, 116920 (3)
600079	Colon cancer (3)
600095	Split hand/foot malformation, type 3 (2)
600101	Deafness, autosomal dominant 2 (2)
600105	Retinitis pigmentosa-12, autosomal recessive (2)
600119	Adhalinopathy, primary (1)

	Muscular dystrophy, Duchenne-like, type 2 (3)
600138	Retinitis pigmentosa-11 (2)
600140	Rubenstein-Taybi syndrome, 180849 (3)
600143	Epilepsy, progressive, with mental retardation (2)
600160	Melanoma, 155601 (3)
600163	Long QT syndrome-3 (3)
600173	SCID, autosomal recessive, T-negative/B-positive type (3)
600175	Spinal muscular atrophy, congenital nonprogressive, of lower limbs (2)
600179	Leber congenital amaurosis, type I, 204000 (3)
600184	Carnitine acetyltransferase deficiency (1) (?)
600185	Breast cancer 2, early onset (3) Pancreatic cancer (3)
600192	Sarcoma, synovial (1)
600194	Ichthyosis bullosa of Siemens, 146800 (3)
600202	Dyslexia, specific, 2 (2)
600211	Cleidocranial dysplasia, 119600 (3)
600221	Venous malformations, multiple cutaneous and mucosal, 600195 (3)
600223	Spinocerebellar ataxia-4 (2)
600228	Pseudohypoaldosteronism, type I, 264350 (3)
600231	Palmoplantar keratoderma, Bothnia type (2)
600234	HMG-CoA synthase-2 deficiency (1)
600243	Temperature-sensitive apoptosis (1)
600258	Colorectal cancer, hereditary nonpolyposis, type 3 (3)
600261	Ehlers-Danlos-like syndrome (3)
600266	Resistance/susceptibility to TB, etc. (1) (?)
600273	Polycystic kidney disease, infantile severe, with tuberous sclerosis (3)
600276	Cerebral arteriopathy with subcortical infarcts and leukoencephalopathy, 125310 (3)
600281	MODY, type 1, 125850 (3) Non-insulin-dependent diabetes mellitus, 125853 (3)
600309	Atrioventricular canal defect-1 (2)
600310	Epiphyseal dysplasia, multiple 1, 132400 (3) Pseudoachondroplasia, 177170 (3)
600318	Diabetes mellitus, insulin-dependent, 3 (2)
600319	Diabetes mellitus, insulin-dependent, 4 (2)
600320	Insulin-dependent diabetes mellitus-5 (2)
600321	Diabetes mellitus, insulin-dependent, 7 (2)
600332	Rippling muscle disease-1 (2)
600354	Spinal muscular atrophy-1, 253300 (3) Spinal muscular atrophy-2, 253550 (3) Spinal muscular atrophy-3, 253400 (3)
600359	Bartter syndrome, type 2 (3)
600364	Cone dystrophy-3, 602093 (3)
600374	Bardet-Biedl syndrome 4 (2)
600414	Adrenoleukodystrophy, neonatal, 202370 (3)
600415	Ataxia with isolated vitamin E deficiency, 277460 (3)
600429	[Ii blood group, 110800] (1)
600430	Brachydactyly-mental retardation syndrome (2)
600467	Malignant hyperthermia susceptibility 4 (2)

600509	Persistent hyperinsulinemic hypoglycemia of infancy, 256450 (3)
600510	Pigment dispersion syndrome (2)
600512	Epilepsy, partial (2)
600525	Trichodontoosseous syndrome, 190320 (3)
600528	CPT deficiency, hepatic, type I, 255120 (1)
600536	Myopathy, congenital (3)
600542	Chondrosarcoma, extraskeletal myxoid (1)
600584	Atrial septal defect with atrioventricular conduction defects, 108900 (3)
600593	Craniosynostosis, Adelaide type (2)
600617	Lipoid adrenal hyperplasia, 201710 (3)
600618	Leukemia, acute lymphoblastic (1)
600623	Prostate cancer, 176807 (2)
600624	Cone-rod retinal dystrophy-1 (2)
600631	Enuresis, nocturnal, 1 (2)
600635	Goiter, familial, due to TTF-1 defect (1)
600650	CPT deficiency, hepatic, type II, 600649 (3) Myopathy due to CPT II deficiency, 255110 (3)
600652	Deafness, autosomal dominant 4 (2)
600678	Cancer susceptibility (3)
600698	Lipoma (3) Lipomatosis, multiple, 151900 (2) (?) Salivary adenoma (3) Uterine leiomyoma (3)
600701	Lipoma (1) (?)
600722	Ceroid lipofuscinosis, neuronal, variant juvenile type, with granular osmiophilic deposits (3) Ceroid lipofuscinosis, neuronal-1, infantile, 256730 (3)
600725	Holoprosencephaly-3, 142945 (3)
600757	Orofacial cleft-3 (2)
600759	Alzheimer disease-4 (3)
600760	Liddle syndrome, 177200 (3) Pseudohypoaldosteronism, type I, 264350 (3)
600761	Liddle syndrome, 177200 (3) Pseudohypoaldosteronism, type I, 264350 (3)
600792	Deafness, autosomal recessive 5 (2)
600805	Epidermolysis bullosa, junctional, Herlitz type (3)
600807	Bronchial asthma (2)
600808	Enuresis, nocturnal, 2 (2)
600811	Xeroderma pigmentosum, group E, DDB-negative subtype, 278740 (3)
600835	AIDS, resistance to (3)
600837	Hirschsprung disease, 142623 (3)
600839	Bartter syndrome, 241200 (3)
600850	Schizophrenia disorder-4 (2)
600852	Retinitis pigmentosa-17 (2)
600856	Beckwith-Wiedemann syndrome, 130650 (3)
600857	Leigh syndrome (3)
600881	Cataract, congenital, zonular, with sutural opacities (2)
600882	Charcot-Marie-Tooth neuropathy-2B (2)
600883	Diabetes mellitus, insulin-dependent, 8 (2)

600884	Cardiomyopathy, familial dilated 1B (2)
600887	Endometrial carcinoma (3)
600890	LCHAD deficiency (3) Mitochondrial trifunctional protein deficiency (1)
600897	Cataract, zonular pulverulent-1, 116200 (3)
600899	Severe combined immunodeficiency, type I, 202500 (1) (?)
600900	Muscular dystrophy, limb-girdle, type 2E (3)
600918	Cystinuria, type III (2)
600919	Long QT syndrome-4 with sinus bradycardia (2)
600923	Porphyria variegata, 176200 (3)
600937	Persistent hyperinsulinemic hypoglycemia of infancy, 256450 (3)
600946	Laron dwarfism, 262500 (3) Short stature, autosomal dominant, with normal serum growth hormone binding protein (3) Short stature, idiopathic (3)
600956	Persistent Mullerian duct syndrome, type II, 261550 (3)
600957	Persistent Mullerian duct syndrome, type I, 261550 (3)
600958	Cardiomyopathy, familial hypertrophic, 4, 115197 (3)
600964	Refsum disease, adult, with increased pipecolicacidemia (2)
600965	Deafness, autosomal dominant 6 (2)
600968	Gitelman syndrome, 263800 (3)
600971	Deafness, autosomal recessive 6 (2)
600974	Deafness, autosomal recessive 7 (2)
600975	Glaucoma 3, primary infantile, B (2)
600977	Cone dystrophy, progressive (2)
600983	Pseudohypoadosteronism type I, autosomal dominant, 177735 (3)
600993	Pancreatic cancer (3)
600994	Deafness, autosomal dominant 5 (2)
600995	Nephrotic syndrome, idiopathic, steroid-resistant (2)
600996	Arrhythmogenic right ventricular dysplasia-2 (2)
600998	Bleeding diathesis due to GNAQ deficiency (1)
601002	5-oxoprolinuria, 266130 (3) Hemolytic anemia due to glutathione synthetase deficiency, 231900 (3)
601011	Cerebellar ataxia, pure (3) Episodic ataxia, type 2, 108500 (3) Hemiplegic migraine, familial, 141500 (3) Spinocerebellar ataxia-6, 183086 (3)
601071	Deafness, autosomal recessive 9 (2)
601072	Deafness, autosomal recessive 8 (2)
601097	Charcot-Marie-Tooth neuropathy-1A, 118220 (3) Dejerine-Sottas disease, PMP22 related, 145900 (3) Neuropathy, recurrent, with pressure palsies, 162500 (3)
601105	Pycnodysostosis, 265800 (3)
601107	Dubin-Johnson syndrome, 237500 (3)
601130	Tolbutamide poor metabolizer (3)
601145	Epilepsy, progressive myoclonic 1, 254800 (3)
601146	Acromesomelic dysplasia, Hunter-Thompson type, 201250 (3) Brachydactyly, type C, 113100 (3) Chondrodysplasia, Grebe type, 200700 (3)
601154	Cardiomyopathy, dilated, 1E (2)

601199	Hypocalcemia, autosomal dominant, 601198 (3) Hypocalciuric hypercalcemia, type I, 145980 (3) Neonatal hyperparathyroidism, 239200 (3)
601202	Cataract, anterior polar-2 (2)
601208	Insulin-dependent diabetes mellitus-11 (2)
601226	Progressive external ophthalmoplegia, type 2 (2)
601238	Cerebellar ataxia, Cayman type (2)
601253	Muscular dystrophy, limb-girdle, type IC (3)
601267	HIV infection, susceptibility/resistance to (3)
601277	Ichthyosis, lamellar, type 2 (2)
601284	Hereditary hemorrhagic telangiectasia-2, 600376 (3)
601295	Bile acid malabsorption, primary (3)
601309	Basal cell carcinoma, sporadic (3) Basal cell nevus syndrome, 109400 (3)
601313	Polycystic kidney disease, adult type I, 173900 (3)
601316	Deafness, autosomal dominant 10 (2)
601318	Diabetes mellitus, insulin-dependent, 13 (2)
601362	DiGeorge syndrome/velocardiofacial syndrome complex-2 (2)
601363	Wilms tumor, type 4 (2)
601369	Deafness, autosomal dominant 9 (2)
601373	HIV infection, susceptibility/resistance to (3)
601382	Charcot-Marie-Tooth neuropathy-4B (2)
601385	Prostate cancer (1) (?)
601386	Deafness, autosomal recessive 12 (2)
601387	Breast cancer (3)
601399	Platelet disorder, familial, with associated myeloid malignancy (2)
601406	B-cell non-Hodgkin lymphoma, high-grade (3)
601410	Diabetes mellitus, transient neonatal (2)
601411	Muscular dystrophy, limb-girdle, type 2F, 601287 (3)
601412	Deafness, autosomal dominant 7 (2)
601414	Retinitis pigmentosa-18 (2)
601471	Moebius syndrome-2 (2)
601472	Charcot-Marie-Tooth neuropathy-2D (2)
601493	Cardiomyopathy, dilated 1C (2)
601494	Cardiomyopathy, familial, dilated-2 (2)
601498	Peroxisomal biogenesis disorder, complementation group 4 (3)
601499	Rieger syndrome, type 2 (2)
601517	Spinocerebellar ataxia-2, 183090 (3)
601518	Prostate cancer, hereditary, 1, 176807 (2)
601542	Rieger syndrome, type 1, 180500 (3)
601545	Lissencephaly-1 (3)
601567	Combined factor V and VIII deficiency, 227300 (3)
601596	Charcot-Marie-Tooth neuropathy, demyelinating (2)
601604	Mycobacterial and salmonella infections, susceptibility to (3)
601606	Trichoepithelioma, multiple familial (2)
601620	Holt-Oram syndrome, 142900 (3)
601621	Ulnar-mammary syndrome, 181450 (3)
601622	Saethre-Chatzen syndrome, 101400 (3)
601623	Angelman syndrome (3)

601649	Blepharophimosis, epicanthus inversus, and ptosis, type 2 (2)
601650	Paraganglioma, familial nonchromaffin, 2 (2)
601652	Glaucoma 1A, primary open angle, juvenile-onset, 137750 (3)
601653	Branchiotoic syndrome (3) Branchiotoicorenal syndrome, 113650 (3)
601666	Insulin-dependent diabetes mellitus-15 (2)
601669	Hirschsprung disease, one form (2) (?)
601676	Acute insulin response (2)
601680	Distal arthrogryposis, type 2B (2)
601682	Glaucoma 1C, primary open angle (2)
601687	Meesmann corneal dystrophy, 122100 (3)
601690	Platelet-activating factor acetylhydrolase deficiency (3)
601691	Cone-rod dystrophy 3 (3) Fundus flavimaculatus with macular dystrophy, 248200 (3) Retinitis pigmentosa-19, 601718 (3) Stargardt disease-1, 248200 (3)
601692	Corneal dystrophy, Avellino type (3) Corneal dystrophy, Groenouw type I, 121900 (3) Corneal dystrophy, lattice type I, 122200 (3) Reis-Bucklers corneal dystrophy (3)
601718	Retinitis pigmentosa-19 (2)
601744	Systemic lupus erythematosus, susceptibility to, 1 (2)
601757	Rhizomelic chondrodysplasia punctata, type 1, 215100 (3)
601768	Leukemia, acute myeloid (3)
601769	Osteoporosis, involutional (1) (?) Rickets, vitamin D-resistant, 277440 (3)
601771	Glaucoma 3A, primary infantile, 231300 (3)
601777	Cone dystrophy, progressive (2)
601780	Ceroid-lipofuscinosis, neuronal-6, variant late infantile (2)
601785	Carbohydrate-deficient glycoprotein syndrome, type I, 212065 (3)
601800	[Hair color, brown] (2)
601841	Protein C inhibitor deficiency (2)
601843	Hypothyroidism, congenital, 274400 (3)
601844	Pseudohypoaldosteronism type II (2)
601846	Muscular dystrophy with rimmed vacuoles (2)
601847	Progressive intrahepatic cholestasis-2 (2)
601850	Retinitis pigmentosa-deafness syndrome (2)
601863	Bare lymphocyte syndrome, complementation group C (1)
601868	Deafness, autosomal dominant 13 (2)
601884	[High bone mass] (2)
601885	Cataract, zonular pulverulent-2 (2)
601889	Lymphoma, diffuse large cell (3)
601916	Pancreatic cancer (2)
601920	Alagille syndrome, 118450 (3)
601928	Monilethrix, 158000 (3)
601941	Insulin-dependent diabetes mellitus-6 (2)
601954	Muscular dystrophy, limb-girdle, type 2G (2)
601969	Glioblastoma multiforme, 137800 (3) Medulloblastoma, 155255 (3)

601975	Ectodermal dysplasia/skin fragility syndrome (3)
601990	Neuroblastoma (1) (?)
602011	Pancreatic endocrine tumors (1) (?)
602014	Hypomagnesemia with secondary hypocalcemia (2)
602023	Bartter syndrome, type 3 (3)
602025	Obesity/hyperinsulinism, susceptibility to (2)
602026	Refsum disease, 266500 (3)
602066	Convulsions, infantile and paroxysmal choreoathetosis (2)
602067	Cardiomyopathy, dilated, 1F (2)
602078	Fibrosis of extraocular muscles, congenital, 2 (2)
602080	Paget disease of bone-2 (2)
602081	Speech-language disorder-1 (2)
602082	Corneal dystrophy, Thiel-Behnke type (2)
602084	Endometrial carcinoma (2)
602085	Postaxial polydactyly, type A2 (2)
602086	Arrhythmogenic right ventricular dysplasia-3 (2)
602087	Arrhythmogenic right ventricular dysplasia-4 (2)
602088	Nephronophthisis, infantile (2)
602089	Hemangioma, capillary, hereditary (2)
602091	Marfan syndrome, atypical (3)
602092	Deafness, autosomal recessive 18 (2)
602094	Lipodystrophy, familial partial (2)
602096	Alzheimer disease-5 (2)
602099	Amyotrophic lateral sclerosis-5 (2)
602116	Glioma (1)
602117	Prader-Willi syndrome (1) (?)
602121	Deafness, autosomal dominant nonsyndromic sensorineural, 1, 124900 (3)
602134	Tremor, familial essential, 2 (2)
602136	Adrenoleukodystrophy, neonatal, 202370 (3) Refsum disease, infantile, 266510 (3) Zellweger syndrome-1, 214100 (3)
602153	Monilethrix, 158000 (3)
602216	Peutz-Jeghers syndrome, 175200 (3)
602218	Townes-Brocks syndrome, 107480 (3)
602221	Stem-cell leukemia/lymphoma syndrome (3)
602225	Cone-rod retinal dystrophy-2, 120970 (3) Leber congenital amaurosis, type III (3)
602235	Epilepsy, benign, neonatal, type 1, 121200 (3)
602279	Oculopharyngeal muscular dystrophy, 164300 (3) Oculopharyngeal muscular dystrophy, autosomal recessive, 257950 (3)
602280	Retinitis pigmentosa-14, 600132 (3)
602363	Ellis-van Creveld-like syndrome (2)
602397	Cholestasis, benign recurrent intrahepatic, 243300 (3) Cholestasis, progressive familial intrahepatic-1, 211600 (3)
602404	Parkinson disease, type 3 (2)
602421	Congenital bilateral absence of vas deferens, 277180 (3) Cystic fibrosis, 219700 (3) Sweat chloride elevation without CF (3)
602447	Coronary artery disease, susceptibility to (3)

602460	Deafness, autosomal dominant 15, 602459 (3)
602475	Ossification of posterior longitudinal ligament of spine (2)
602476	Febrile convulsions, familial, 1 (2)
602477	Febrile convulsions, familial, 2 (2)
602491	Hyperlipidemia, familial combined, 1 (2)
602522	Bartter syndrome, infantile, with sensorineural deafness (2)
602544	Parkinson disease, juvenile, type 2, 600116 (3)
602574	Deafness, autosomal dominant 12, 601842 (3) Deafness, autosomal dominant 8, 601543 (3)
602575	Nail-patella syndrome with open-angle glaucoma, 137750 (3) Nail-patella syndrome, 161200 (3)
602616	Carbohydrate-deficient glycoprotein syndrome, type II, 212066 (3)
602629	Dystonia-6, torsion (2)
602631	Breast Cancer (3) Rhabdomyosarcoma, 268210 (3)
602639	Hypodontia, autosomal recessive (2)
602666	Deafness, autosomal recessive 3, 600316 (3)
602667	Nijmegen breakage syndrome, 251260 (3)
602669	Anterior segment mesenchymal dysgenesis and cataract, 107250 (3) Cataract, congenital (3)
602716	Nephrosis-1, congenital, Finnish type, 256300 (3)
602759	Prostate cancer, hereditary, 2, 176807 (2)
602771	Muscular dystrophy, congenital, with early spine rigidity (2)
602772	Retinitis pigmentosa-24 (2)
602782	Faisalabad histiocytosis (2)
602783	Spastic paraplegia-7 (3)

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the colon cancer antigens in methods which are well known in the art.

The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or a cDNA contained in the ATCC deposit. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y and/or a polypeptide encoded by a cDNA contained in the ATCC deposit. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y and/or a polypeptide sequence encoded by a cDNA contained in the ATCC deposits are also encompassed by the invention.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would unduly burden the disclosure of this application. Accordingly, for each "Contig Id" listed in

the third column of Table 7, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described in the second column of Table 7 by the general formula of a-b, each of which are uniquely defined for the SEQ ID NO:X corresponding to that Contig Id in the fourth column of Table 7. Additionally, specific embodiments are

5 directed to polynucleotide sequences excluding one, two, three, four or more of the specific polynucleotide sequences referenced by Genbank Accession No. for each Contig Id which may be included in column five of Table 7. In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. All references available through these accessions are hereby incorporated by

10 reference in their entirety.

Table 7

SEQ ID NO:X	CLONE ID:Z	CONTIG ID:	GENERAL FORMULA	ACCESSION NUMBERS
1	HTWEP07	390631	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 393 of SEQ ID NO:1, b is an integer of 15 to 407, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:1, and where b is greater than or equal to a + 14.	AL119989, T80240, AA773747, AA809992, AA281432, AF051311, AF053535, AF070615, AF145284, AB014560, U65313, AF145285
2	HODBA26	410299	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 399 of SEQ ID NO:2, b is an integer of 15 to 413, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:2, and where b is greater than or equal to a + 14.	
3	HPMEF95	456200	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 460 of	N76659, T85798, AW379474, AR016730, D50857

4	HCFCY21	456438	<p>SEQ ID NO:3, b is an integer of 15 to 474, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:3, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1829 of SEQ ID NO:4, b is an integer of 15 to 1843, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:4, and where b is greater than or equal to a + 14.</p>	<p>AI866002, AI476046, AI610645, AI561299, AI433976, AI251830, AW085667, AW403717, AI868831, AL045266, AI801325, AL038605, AW117746, AI815855, AI873644, AI674838, AI678599, AI609593, AI498579, AI799199, AI867042, AL039086, AW051107, AI696626, AI174394, AI521012, AI633419, AI890806, AI796743, AW103371, AA640779, AW162071, AI816010, AI480118, AI824557, AI499285, AI340582, AW059837, AW071417, AW132056, AI569616, AI872711, AI872545, AI918655, AI955917, AI620003, AI862139, AI696612, AW081036, AI289937, AI274508, AI434468, AI284131, AW082040, AW302988, AI890833, AI926790, AI568870, AW102785, AW103893, AI564719, AI281772, AI889376, AI524671, AW051258, AI919345, AI554245, AI921248, AI611738, AW002342, AI619502, AI677796, AI632408, AI802542, AI308035, AI886753, AI933589, AW026882, AI636719, AI476109, AI923768, AI783504, AL079963, AL036396, AI567351, AI620284, AL119863, AI500039, AI274013, AW301505, AI922365, AW195968, AI587288, AI345587, AI433157, AI702073, AL036759, AI366549, AI446373, AW238730, AI500706, AI537677, AW083804, AI520931, AI500662, AI633125, AW161579, AL041772, AI648663, AI500523, AI682841, AW005858, AI284517, AW129916, AI242249, AI888944, AW050522, AW192375, AA494167, AW268220,</p>
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				AI570781, AI491897, AI349645, AI364788, AI224992, AI318280, AI284509, AL036146, AI799472, AI953562, AL042628, AI673256, AI559296, AI538085, AL036403, AI250663, AI554218, AA427700, AI571909, AI702433, AI591316, AI922901, AI362637, AI924971, AI569583, AI554427, AI273142, AL040241, AW088134, AI269862, AI500553, AI345347, AL119836, AI612759, AW150578, AW190042, AI269696, AI922676, AI800453, AI800433, AI921176, AI888953, AI886124, AI499463, AI874166, AI445165, AI963216, AI590120, AI308032, AW149227, AI828731, AI282326, AI590118, AW079159, AI287326, AI343059, AA572758, AW023590, AW169653, AI648684, AI687065, AI608676, AI811845, AI349933, AI863014, AI468872, AI950664, AI280661, AI345608, AL120853, AI340603, AI680498, AI537617, AW088903, AI567360, AI499381, AI281779, AI348897, AW168650, AI349004, AW081255, AI383919, AI280637, AI539153, AI539771, AI824444, AI608936, AI866608, AI611743, AI687362, AI862144, AC006373, AC009501, AC004808, AL035407, AC006313, AC008014, AC004470, Z98036, AC004159, AC006039, AL022394
5	HMKCO08	467315	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 457 of SEQ ID NO:5, b is an integer of 15 to 471, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID</p>	AI905893, AI905911, D50640, Z22867

6	HBAGS04	471563	<p>NO:5, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 891 of SEQ ID NO:6, b is an integer of 15 to 905, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:6, and where b is greater than or equal to a + 14.</p>	<p>AA148799, AA148530, AA463550, AI979134, AW264037, AA252163, AC004158, AL031118, AC006484, Z75888, Y10196</p>
7	HALSQ75	488131	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 398 of SEQ ID NO:7, b is an integer of 15 to 412, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:7, and where b is greater than or equal to a + 14.</p>	<p>AI352096, AA376070, T81033</p>
8	HMVBD21	490848	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 738 of SEQ ID NO:8, b is an integer of 15 to 752, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID</p>	<p>AI767324, AL121194, AA972628, AI095851, AA743343, AW366882, D20570, AC009802</p>

9	HKIMD67	500696	<p>NO:8, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 628 of SEQ ID NO:9, b is an integer of 15 to 642, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:9, and where b is greater than or equal to a + 14.</p>	<p>T71949, N95702, AI306688, AW451579, AI341434, AI223407, AA885055, AA846712, AA379446, AW362461, H42165, D80959, AI928895, AA081721, D87459, AF134303</p>
10	HOOAE34	504559	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 197 of SEQ ID NO:10, b is an integer of 15 to 211, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:10, and where b is greater than or equal to a + 14.</p>	<p>AI380563, AI004009, AI625234, AW337321, AA321125, AA937785, AA363438</p>
11	HHSD62	506406	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 518 of SEQ ID NO:11, b is an integer of 15 to 532, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID</p>	<p>AW409739, AA773074, AI083705, AI870827, AI126674, W94001, AI273489, AI275482, AI264045, AI423593, AI350937, AI393684, R76773, AA483544, AW131780, AI091146, AA130101, AA255799, AA976695, AA774090, R76460, AI206751, AI350938, AA418479, AI669701, AA669454, H04098, AA460849, AI784675, R49064, AA130100, AA639898, AA639917, AA700950, AA082299, AA702716, X07233, X15051, X15052</p>

12	HSLGZ32	506619	<p>NO:11, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1106 of SEQ ID NO:12, b is an integer of 15 to 1120, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where b is greater than or equal to a + 14.</p>	AA316122, AA314900, AF121202
13	HCENL15	507852	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 586 of SEQ ID NO:13, b is an integer of 15 to 600, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where b is greater than or equal to a + 14.</p>	<p>N40063, AA233205, R46529, AI015135, AW130559, AA324511, AI460380, AA346401, AA604942, AI125644, AI703464, T67213, AW103052, AI452537, AI050784, AI949725, AI052071</p>
14	HCQAI38	509423	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 793 of SEQ ID NO:14, b is an integer of 15 to 807, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID</p>	<p>AW118906, AA134595, N40901, AA134594, ALI38019, AW274753, T35439, T10802</p>

15	HPMDT48	509734	<p>NO:14, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 402 of SEQ ID NO:15, b is an integer of 15 to 416, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where b is greater than or equal to a + 14.</p>	AA315821	
16	HADFX66	509856	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 738 of SEQ ID NO:16, b is an integer of 15 to 752, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:16, and where b is greater than or equal to a + 14.</p>	AA845353, N31960, AA617724, AA307653, AA862795, N92883, R60191, AA321715, AI802963, W23451, AA905145, W25563, AA469079, R60190, R18173	
17	HONAI01	524721	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 467 of SEQ ID NO:17, b is an integer of 15 to 481, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID</p>	AA362921, AA436291, AA425301, AL079672, AW361081, AW341687, AA284486, AI880015, AI379662, AI935013, AA436164, AI066555, AA837415, AA706542, AI126021, AB028996	

18	HEBBT54	524901	<p>NO:17, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 898 of SEQ ID NO:18, b is an integer of 15 to 912, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where b is greater than or equal to a + 14.</p>	<p>T85603, AA132177, AA314644, AA133670, T99921, AL039938, R01637, AA046158, AP000497, D88153</p>
19	H2CBG63	527600	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 493 of SEQ ID NO:19, b is an integer of 15 to 507, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:19, and where b is greater than or equal to a + 14.</p>	<p>AA307234, R60594, AC007327</p>
20	HHSBA79	527827	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 396 of SEQ ID NO:20, b is an integer of 15 to 410, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID</p>	<p>AA247517, AI915163, AI690026, AC004817, AL132774, AL078602, AC003999, AL136168, AL022396, Z68325, AL035414, AB020868, U95740, AC007685, AL049712, AP000067, AC002992, AL022148, U95741, U95743, AC007304, AC002390, AC005482, Z82188, AC005477, AC005295, AL035408, AC007028, AL035608, AC004917, AL132992, AC002385, AC007064, AC004825</p>

21	HCQAQ89	529050	<p>NO:20, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 482 of SEQ ID NO:21, b is an integer of 15 to 496, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where b is greater than or equal to a + 14.</p>	
22	HELGJ91	529465	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 349 of SEQ ID NO:22, b is an integer of 15 to 363, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to a + 14.</p>	
23	HADBE91	530612	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 225 of SEQ ID NO:23, b is an integer of 15 to 239, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID</p>	AW392520

24	HSAAX52	530773	<p>NO:23, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 447 of SEQ ID NO:24, b is an integer of 15 to 461, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where b is greater than or equal to a + 14.</p>	AA299283, AW379368, AA374069, D61135, D60581
25	HACCE33	532810	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 439 of SEQ ID NO:25, b is an integer of 15 to 453, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where b is greater than or equal to a + 14.</p>	AA305030, AI207985, AA469325, AA420424, D10040, L09229
26	HE8DA85	533242	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1926 of SEQ ID NO:26, b is an integer of 15 to 1940, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID</p>	<p>AI052713, AA993209, AI133542, AI160185, AI110772, AA443423, AA406485, AI806057, AI114495, AA410346, AI436310, AI370818, AL035763, T11697, C21213, AA707071, N54577, H52269, R89600, F06943, R98692, R97937, W84760, R98918, AA358620, AI207561, H65229, AI123345, H60435, R98546, AA010003, R98713, AA332857, AI131251, T75531, H52507, T29077, AW440733, R98714, T53093, H80150, H78893, H79897, AA010004, R20093, W84755, AI351429, AI185625,</p>

27	HSKII86	541126	<p>NO:26, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 850 of SEQ ID NO:27, b is an integer of 15 to 864, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where b is greater than or equal to a + 14.</p>	<p>R98547, AA628869, N76658, T75490, N52438, F03211, AA026133, AA342031, H65230, H60481, T55303, H79803, N77400, T81302, AA029616, R97938, AL035762, T11698, T52339, T55135, C21277, AI056662, T52412, AA699919, R88921, X60364, X56352, AF086786, M15268, D86297, M63244, Z83821, AL020991, AF068624</p> <p>AA305909, AA354725, AA296543, AA347633, AA100063, AA424070, AA296485, AI795779, AW239153, AA337079, T87056, AA263171, AA044017, AA044192, AI683358, AW363341, AW138402, AA294979, AA424397, AW134673, T75498, AA827350, M55542, M55543, AR035947, M55544, M63961, AF109168, AJ007970, AF077007, M80367, AR035948</p>
28	HUSGI39	542268	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 689 of SEQ ID NO:28, b is an integer of 15 to 703, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:28, and where b is greater than or equal to a + 14.</p>	<p>AW407143, AA213542, AA284733, AA485799, AI761438, AC005368</p>
29	HKIMB44	547920	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a</p>	<p>AI985978, AW070887, R76142, AW089184, N31775, AI687598, AI963830, AL035869, AI697270, R83410, W94030, AW083686, AI188661, AA653485, AA165514, AW188780, AA989157, AI473469, H69762, AI925548, AA908930, AA340369, AI682723, AI950093,</p>

		<p>is any integer between 1 to 323 of SEQ ID NO:29, b is an integer of 15 to 337, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where b is greater than or equal to a + 14.</p>	<p>AW438743, AI654303, H70528, T82154, H63221, AI954998, AI186315, W85840, W26638, AW190908, AA496463, AA961655, D55762, D55763, D54646, D54319, AA089984, D53696, D52797, W94645, W28832, D55240, AA729249, C15803, AA165556, AA524229, AW194507, AI110844, AI434080, AA100718, AI821986, AI085242, AA903287, AA024410, AI536908, AA053088, AI421841, AI821788, AI821745, T52103, AI540625, AA011625, AI343076, AA167055, AA572953, AW206369, AA284416, J05032, AC003666, Z69838, AC005952, AL031679, AL024474, AC000112, AP000361, AL021977, AC005215, AC004903, AC006238, AF090940, AL050318, AC006211, AC006077, AF113009, AF095901, AL049636, AC004551, Z99289, AC005796, AL136520, AC003104, AF015148, AP000214, Z81310, AP000255, AC004851, AP000135, AC006344, AC007245, AL031983, AL034554, AP000031, AC005520, AC005154, AL133353, AC005737, AL049779, AF055481, AC005335, AL034418, AC002382, AC005037, AC007240, AC005594, AC005018, AF207550, AF038633, AC005779, AF037338, AC004257, AL021878, AC005999, AL132641, Z84488, AF001549, AC006453, AL008639, AC004099, AC007463, AC008163, Z98044, AC007387, AF141976, AC002365, L30117, U73023, AL033543, AC007160, AC003119, AL078581</p>	
30	HBMVJ62	549642	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 617 of SEQ ID NO:30, b is an integer of 15 to 631, where both a and b correspond to the positions of</p>	<p>AI523366, AA856766, AI690026, AA856757, AA486994, AA491240, AA214142, AI032325, R10942, AW023137, R10519, AW237618, AL049712, AC007388, AC007002, Z68192, AC004104, AC007425, AC007182, AC004216, AC005532, AL132774, AC005102, AF196970, U95740, AL031407, AL031767, AC002390, AL133404, AL121840, AC005731, AC005245, AC005291, AF002994, AC006991, AC002394, AB020863, Z82210, AP001058, AC005609, AC004388,</p>

31	HBXFC78	550207	nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.	AC001526, AL031073, AL049828, U69730, AC005057, Z69648, AC007685, AL096861, AL079304, AC005011, AL022578, AC004858, AC008064, AF109907, AP000338, AP000216, AL136168, AC005821, AC003964, AB020868, AC007656, AC007437, AC006210, AL035414, AC004103, AC005971, AP000067, AC005697, AC009946, AC005953, AC002331, Z97054, Z82188, AC004791, AC005380, AC005616, AC004679, Z97055, AC003991, AC007263, AC007280
			Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 557 of SEQ ID NO:31, b is an integer of 15 to 571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:31, and where b is greater than or equal to a + 14.	AW150151, AI689429, AI952267, AI521422, AI920793, N70051, AI743691, AI769315, AI168431, N50902, AI291826, AI123242, AA814094, H23837, AI915645, N50944, AA113864, AA479473, AW028954, AW079750, AI783813, AI824715, AA479362, AW051241, AI566595, C21435, AI269275, AL050285
32	HE2FR32	552115	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 410 of SEQ ID NO:32, b is an integer of 15 to 424, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to a + 14.	CI9093, AA479586, AI417611, AA477425, W07367, AW403461, AA292357, N32437, AA258489, U69127
33	HKACD58	552465	Preferably excluded from the present invention are one or more	AA877796, AW027434, AI335269, N46240, AW402301, AI525602, H38504, AW390227, AI365603, AI819188,

		<p>polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1612 of SEQ ID NO:33, b is an integer of 15 to 1626, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and where b is greater than or equal to a + 14.</p>	<p>AW390207, AW368379, R53778, AA370005, AA134615, AA354527, R69656, AI524965, AA425001, F37313, AI829975, AW339374, AA227281, F27458, AA495894, R78049, AA355898, AI360437, AA149032, R55146, T74386, R54897, AI204915, R88102, H21738, AI971329, AI193372, AA380842, AA343322, AI908997, AI096656, AI367032, AA121830, H22385, AI085242, AA149757, AI433008, AA814721, AA555145, T27702, AI249880, AI434080, AI561147, AL039478, AW151664, AL046021, AI627436, AI732975, AL110373, AA853473, AI805349, AA903287, R46841, AA551390, AA662117, AI821062, AA722215, AI088768, AI368745, AA688217, AW081103, AA019257, F00107, AL046262, AI557808, AI064787, AA618452, AI110708, AL040077, AA653459, AA764903, AI627181, AA235975, AI823716, AA877935, AA659232, AI821259, AI887241, AL110402, AW089171, AA937752, AI874222, AL138455, N52358, AW079659, AI133029, AI111171, AA806438, AI345797, AL042753, AW083846, T62495, AL042853, AI114443, AL042567, AW105519, AL041318, AI440117, AA828395, AI821788, AI821745, AI207728, AW104715, AI249447, AI039141, AI369580, AW167385, AI821986, AW160760, AL038134, AL042731, AL038182, AL050037, AC006455, AF075046, AC005778, AL031282, AP000250, U73023, AL078598, AP000211, AP000133, AP000030, AC009300, AC005520, AC006017, AF095901, AP000080, AL117354, AC004990, AF003738, V00744, J00629, AP000361, AL136130, AC002078, Z84489, AC007748, AC003042, AC007242, AC004974, AC005095, AC006458, AL031274, Z82206, Z99495, AL117337, Z83844, AC009044, AC005284, AC002531, AC005036, AC006205, J00349, Z98036, AL031774, AC004093, AC011013, AC005006, AC005078, AC002382,</p>
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	AL021391, AF053356, AF162270, AL049742, U67221, AC005074, AF090940, L30117, J05032, AF045527, AL031720, AF057280, AF126531, X91656, AC004400, AC005793, Z82250, AC004170, AF045450, AC004213, AC004209, AC000394, AC003005, AC006139, AF184110, AL121915, U89335, AL033543, AL049576, AL031662, AF024533, AC005353, Z99714, Z93784, AC002564, AL022315, AC002467, AP000206, AC002301, AL049761, Z98748, AL031656, AC004900, AL109807, AC005741, AC004858, AC007114, AC006344, AC008071, AC007390, AC005295, AC006965, AL035067, AL020994, U95742, AC004936, AC005479, AC004671, AC002432, AL022723, AC005527, AC004888, AC004626, AC004894, AC002060, AC008014, AC004544, AL136520, AC006160, Z99289, AC005296, AC006296, AF109907, AC005529, S75940, AP000319, AP000167, AP000052, AP000120, AL031667, AC000053, AF206503, AP000569, AC005057, AC007216, AL050309, AL109865, AC006956, AL031346, AF110520, AC007049, AC002482, AL079340, AC006480, AP000350, AC005386, AC002086, AF135026, AC004589, Z49235, AF195658, AC004210, AC002559, AC005667, AC004854, AP000508, AC002462, AL034553, Z92543, Z83840, AL031281, AC005886, AL034554, AC006029, AC007671, AL021918, AL035086, AC005209, AC007385, AC007055, AC006530, D84394, AC002428, AC007877, AC006944, AF200465, Z99297, AB012260, U73638, AC000022, AC003688, AL133371, AL031681, AC007461, AC005992, D83989, S75201, AF088219, AC006582, AC004989, AB012179, AC004972, AC003048, U67233, AL137293, AL079342, AF003737, AF113015, AL122021, AC000025, X58156, D38178, M38180, U89387, Y11740, Z49258, AC004760, AC004536, AL035450, AC004940, AL080245, X66401, AC004769,

34	HDAAB62	554369	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 436 of SEQ ID NO:34, b is an integer of 15 to 450, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where b is greater than or equal to a + 14.</p>	AC006221, AC004009, AP000338, AL022399, AL022393, AL033523, AC005008, AC005250, AL096770 AA308748, AA307995, AA312596, AA307928, AA314740, AA307129, AA102186, AA343955, AA353457, AA361582, AA362045, N86980, AA227387, AA172125, AL046225, AI241561, N66944, N66930, AA553392, Z27098, AL045756, C17672, AA484304, AA484273, AI673070, AA622421, AA662921, T07307, AA487199, AA769512, AA587021, AA151746, AW089861, N68288, AI590255, AI689532, AW135366, W61121, W52658, W81691, AI821039, AI361845, AA743299, AA196412, X16396, AL024507, AC004894, M63439, J04627, AC005803, AJ003147, AC008040, AC005602, AC000378, AL135783, AC005328, U07562, AC004813, AL031666, Z82198, D13631, D25304, AL021328, AC003072, Z98256, AL031320, AC000353, AC007172, AF001549, AC003957, AP000687, AP000688, AC005229, AL109758, U40369, AP000302, AL049919, AC002398, X55448, AC002352, AB003151, AC005737, L44140, AL009183, AC003029, AC004453, AL035447, AF051976, AL035398, AC002492, AC007938, AC007382, AC005288, Z84469, AC005837, AC009498, AC005899, AL078602, AC003102, AL023575, AC002425
35	HEPBA24	557152	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 946 of SEQ ID NO:35, b is an integer of 15 to 960, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where b is greater than or equal to a + 14.</p>	AA632191, AW151795, R59316, AI338706, AI276888, AI366798, AI471791, AA565616, AI248949, AI269722, AI393882, AA504204, AA813608, AI335657, AA682615, AI039562, AA400139, AA187165, AI376431, AA454074, AA128383, AI002866, AA929034, R46374, AA810231, AI241427, AA865170, AI567959, W93122, N47805, AA335391, AI919230, AI242499, AA401552, T28382, AA453654, AA335614, AA336149, AA335946, R41308, T24710, AI017254, D26018

36	H0GBL08	557230	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 516 of SEQ ID NO:36, b is an integer of 15 to 530, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where b is greater than or equal to a + 14.</p>	AA151092, AA367221, F09233, AA442256, AA442255, AA933632, W80475, H22100, AI274366, AA909429, AI918108, AI499770, AI278711, AA948413, AA831784, AI470908, AA936238, W94676, AI002684, AI050788, AI264677, AI246792, AI276574, AI352684, AA428287, AI952002, AI890744, AI806291, T18857, AI819539, R43330, AI749667, R71480, AI262455, N75456, AI869496, AA826541, AA436899, AI187706, AI135960, AJ131016, U21049, AC006487, U80460
37	HCYBD62	558366	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 524 of SEQ ID NO:37, b is an integer of 15 to 538, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:37, and where b is greater than or equal to a + 14.</p>	AA305096, AA424823, AA995932, AW001055, AI016665, AI399850, AI636182, AI949894, AW361640, AI634640, AW377132, AW377117, AW388099, W07829, AA993439, X89602, X67098
38	H2CBD20	570796	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1242 of SEQ ID NO:38, b is an integer of 15 to 1256, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:38, and where b is greater than or equal to a + 14.</p>	AA307235, AI002535, H49502, AL110292

39	HCQAT53	573181	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 652 of SEQ ID NO:39, b is an integer of 15 to 666, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:39, and where b is greater than or equal to a + 14.</p>	<p>AI761465, AW270500, AA290850, AA953717, H57392, AI127126, T82331, AW293000, AA973625, AI298354, AW451105, Z64718, Z64717</p>
40	HETDN09	573199	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1002 of SEQ ID NO:40, b is an integer of 15 to 1016, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:40, and where b is greater than or equal to a + 14.</p>	<p>AI022684, AI807626, AI032750, AI026655, AA931238, AI806336, AI683663, AA062961, AA035619, AA701296, AW351549, AA632626, AA620715, AI690779, AA613277, AA918186, AI500592, AA812859, AI339340, AA911056, AI138829, AA962373, AI826452, AI620160, AI621126, AA642617, AI263569, AA158084, AW183356, AI311751, AI862278, AI305952, AI377600, AI345876, AI340524, AI284742, AI311267, AI310838, R71902, AI311602, H72019, AW301795, AI344075, AI344264, AA863452, R71938, AI311175, AI345015, H72018, AI305761, J04131, X60069, M24087, M24903, E02290, J05235, L20490, L20493, L20492, L20491, AP000356, AC008132, AP000550, AC008018, AC011718, AC007981, AC012330, X98922, AC000051, D87002, AC012331, AC002308, M30474, AP000354, X15443, M33822, M33821, AC007325, M30479, L10395, L10394, L10398, L10399, L10397, L10396, Z93345, Z93348, Z93344, Z93343, AJ007380, Z93342, Z93346, Z93347, M30475, M30478, M30477, M30476, Y09833, AJ006789</p>
41	HCYBE04	573793	<p>Preferably excluded from the present invention are one or more</p>	<p>AA305129, AA768244, AA310241</p>

42	HDPFI14	573796	<p>polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 409 of SEQ ID NO:41, b is an integer of 15 to 423, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:41, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 947 of SEQ ID NO:42, b is an integer of 15 to 961, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:42, and where b is greater than or equal to a + 14.</p>	<p>AA316491, AA704220, R80096, AA305136, R57983, AW009438, D83243, X97186, U58852, D89853, D89852, D89851</p>
43	HJBCD90	574094	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 531 of SEQ ID NO:43, b is an integer of 15 to 545, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where b is greater than or equal to a + 14.</p>	<p>AA311657, N88312, AA307717, Z21301, AA551523, AA631395, D80164, D80212, C14389, D59502, D80391, D59787, D80439, D80196, AA305409, D80268, D51799, D59859, D51060, C15076, D59610, D80022, D80166, C14014, D80195, D59619, D80247, D58283, D51022, D80210, D80240, AA514188, C06015, D50995, C14331, D59467, D51423, D80133, D59275, D80253, D80038, D80043, D80227, D81026, D80522, D59927, D81030, D80219, D80269, D80024, D80366, D80188, D80248, AA514186, D50979, D51103, AA305578, D80157, D80241, D80193, D57483, T03116, D80045, D59889, D51759, D80302, D45260, D81111, C03092, AW377671, D80378, D59551, AW177440, AW178893, C14429, AI525923,</p>

	D80251, F13647, D59503, AA809122, C14227, T11417, D58101, AW375405, AW360844, T03269, D59317, H67854, H67866, AW360811, C14973, D80014, C14344, AW360817, AW360834, D58246, D59627, AI525917, D80258, D80064, D51221, D59474, AW178906, AW177511, AI535686, AI525920, Z30160, AW177501, AW179328, D59695, AW179020, T48593, AW377676, AW375406, AW378534, AI525235, AW352171, AW179332, AW377672, AW179023, AW178905, AW179013, Z21582, AW177731, AI525925, AI525227, AW378528, AW178762, AW178754, AW179019, AW360841, AW179024, AW378533, AI557774, AW378532, AW352120, AA514184, AW352117, D60214, C14407, AW378539, AW177505, AW178775, C14046, AW178909, H67858, AW177456, AW179004, AW352170, AW178986, AI525215, D51250, AW178907, AW177733, AW178908, AW179018, AW352158, AW178971, D31458, AW178914, AW178774, AW178781, AW378543, AW378540, AI525242, AI525912, AA285331, AW177734, AI557751, D45273, AW179017, C06084, C13958, AW367950, C16955, D80168, AW178759, AW179009, AW179012, AW178980, Z33452, T02974, AI525237, AI535665, D80949, AW378542, C05763, D52291, C14298, D51213, AW178911, C14077, AW378525, AW352163, AW360855, T02868, AW177728, T03048, AW369651, AI525228, T11191, AI525914, AC007262, A82595, AR060385, AB028859, AJ132110, AR018138, A84916, AB002449, A62300, A62298, AR008278, AF058696, I50126, I50132, I50128, I50133, I14842, AR054175, AR016514, X67155, Y17187, AR060138, A45456, Y17188, A94995, D26022, AR008277, AR008281, A26615, AR052274, A43192, Y12724, A63261, A43190, AR038669, A25909, AR066488, Y09669, AR066487, A70867, A67220, D89785, A78862, D34614, A30438, AR062872, AR008443, AR016691,

44	HAIAB40	574927	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 363 of SEQ ID NO:44, b is an integer of 15 to 377, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:44, and where b is greater than or equal to a + 14.</p>	<p>AR016690, I79511, U46128, A64136, A68321, X64588, D88547, D50010, X68127, X82626, AR008408, AR025207, AF123263, AR060133</p> <p>AA280602, AA316028</p>
45	H2MCA74	575139	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 426 of SEQ ID NO:45, b is an integer of 15 to 440, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:45, and where b is greater than or equal to a + 14.</p>	<p>AA316835, AA112812, AI028747, W87680, AI082423, AA068997, H73681, AW193615, AC005669, U15177, U71148, AL035458, AC006115, Z49237, AB026898, AP000498, Z21853, AC004706, AL133162, AC004034, AC002054, AC006369, AC007664, AC002049, AC008018, AL122127, AL035086, AC002472, AJ223364, AF017732, AL032821, AP000345, AC004045, AP000346, AB019438, Z97634, AF118808, AC005515, AL021155, AF196969, AF017187, AC004976, AF017188, AC005037, AL031228</p>
46	HWBAX42	575591	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 511 of SEQ ID NO:46, b is an integer of 15 to 525, where both a and b correspond to the positions of</p>	<p>AW068735, AA853585, AA380263, AL121408, AL121410, X64330, U18197, L27075, J05210, L47278</p>

47	HLMMR55	576132	nucleotide residues shown in SEQ ID NO:46, and where b is greater than or equal to a + 14. Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 400 of SEQ ID NO:47, b is an integer of 15 to 414, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where b is greater than or equal to a + 14.	
48	HNFGN91	577390	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 309 of SEQ ID NO:48, b is an integer of 15 to 323, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where b is greater than or equal to a + 14.	AJ011930
49	HTWDI90	577685	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 827 of SEQ ID NO:49, b is an integer of 15 to 841, where both a and b correspond to the positions of	AI743511, AI807252, AA769584, AW340026, AW340029, AA970935, AI807551, AA934884, AA769047, AA804530, AW340028, AA286746

50	HCQAB18	578079	nucleotide residues shown in SEQ ID NO:49, and where b is greater than or equal to a + 14. Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 520 of SEQ ID NO:50, b is an integer of 15 to 534, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:50, and where b is greater than or equal to a + 14.	AA721676, AI632745, AI478171, AI719338, AA761073, AI766631, AA485859, AW059674, AI797505, AI709367, AC000123, AC000127
51	HELHI45	578660	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 303 of SEQ ID NO:51, b is an integer of 15 to 317, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:51, and where b is greater than or equal to a + 14.	N36929, AA771779, AW196937, AA342301, AI808034, AI432219, AI694329
52	HNHDV16	580860	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1775 of SEQ ID NO:52, b is an integer of 15 to 1789, where both a and b correspond to the positions of	AL049874, Z84488, AC002549, AC003035

53	HOAAD32	581143	nucleotide residues shown in SEQ ID NO:52, and where b is greater than or equal to a + 14. Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 640 of SEQ ID NO:53, b is an integer of 15 to 654, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:53, and where b is greater than or equal to a + 14.	AA307601, AI760475, AI972520, AI990288, AI675118, AI669210, AW003506, AW016052, AI984626, AI880850, AA807606, AI685689, AA766936, AI342189, AI824926, AI770146, AI202899, AI075305, AI637764, AI611102, W19739, AI206868, AA825282, AI300737, AI419015, W95671, AA234976, AI052432, AI766516, AI830638, AI830514, W95767, AI341456, AI342005, AI695951, R33457, AA935544, AI738445, AA648791, AI625335, R68590
54	HSAVM80	584899	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 320 of SEQ ID NO:54, b is an integer of 15 to 334, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:54, and where b is greater than or equal to a + 14.	AI902580
55	HWLMA5 I	600669	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 460 of SEQ ID NO:55, b is an integer of 15 to 474, where both a and b correspond to the positions of	AI341167, AI652526, AI990232, Z22968, Z22969, Z22971, Z22970, Y18391, Y18392, Y18390

56	HE8BQ01	611839	nucleotide residues shown in SEQ ID NO:55, and where b is greater than or equal to a + 14. Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 353 of SEQ ID NO:56, b is an integer of 15 to 367, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:56, and where b is greater than or equal to a + 14.	AI267198, AW242820, H89792, T98720, AI743953, AA034283, AI912188, AI268316, AA282592, AI955322, AI680802, AI138929, AA854852, AW340279, AI633670, AI140173, AI914144
57	HELHD03	614078	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 550 of SEQ ID NO:57, b is an integer of 15 to 564, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57, and where b is greater than or equal to a + 14.	AW028557, AW008015, AA279640
58	HBMCT70	614554	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 430 of SEQ ID NO:58, b is an integer of 15 to 444, where both a and b correspond to the positions of	N31002, AA504707, AL041182, M78574

59	HLYDF04	615029	nucleotide residues shown in SEQ ID NO:58, and where b is greater than or equal to a + 14. Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 333 of SEQ ID NO:59, b is an integer of 15 to 347, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:59, and where b is greater than or equal to a + 14.	AI972404, AW172842, AL079983, AI769801, AI769431, AI472252, AA036804, D79445, AI282586, AI935375, AI569290, AA450323
60	HDSAP04	615590	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 308 of SEQ ID NO:60, b is an integer of 15 to 322, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:60, and where b is greater than or equal to a + 14.	AI732729, AI858825, AI625874, AI266164, AA402921, AA426648, AI039796, AI567237, AW090009, AC000064, AC007566
61	HWBFZ21	630230	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 820 of SEQ ID NO:61, b is an integer of 15 to 834, where both a and b correspond to the positions of	AW369648, AI904452, AF098799, AL137335

62	HCQBH72	637548	nucleotide residues shown in SEQ ID NO:61, and where b is greater than or equal to a + 14. Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1782 of SEQ ID NO:62, b is an integer of 15 to 1796, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62, and where b is greater than or equal to a + 14.	AA640538, AA649644, AA649707, R31618, AA652004, R32348
63	HELGH31	637605	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1362 of SEQ ID NO:63, b is an integer of 15 to 1376, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:63, and where b is greater than or equal to a + 14.	N98658, AI967961, AA888070, AA653693, AI985864, AI342233, AI201196, N66161, AW117713, AW117695, N30234, N34009, H98804, AA969760, AI017192, AW242529, AW087505, R77266, R67143, AA310805, AI188021, N66135, AA300547, C16517, H01413, AA972789, D12299, H99892, R77313, N57126, N24566, N25024, AA633387, N98686, AA334492, H01414, D12297, AI217112, AA724744, AA482680, AA480427, R66409, C16522, C16404, H87992, C16332, AA280332, AL035410
64	HNHEU34	638125	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 560 of SEQ ID NO:64, b is an integer of 15 to 574, where both a and b correspond to the positions of	AC004876, Y12661, M60522, M60525, M74223

65	HJMAF30	638188	nucleotide residues shown in SEQ ID NO:64, and where b is greater than or equal to a + 14. Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 589 of SEQ ID NO:65, b is an integer of 15 to 603, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:65, and where b is greater than or equal to a + 14.	AI090108, AA810218, AA513307, AW028090, AI572270, AW451013, AI373062, AI492435, AI141965, AI161216, AI952357, AI420596, AI804945, AI123032, AI478408, AI830622, AI984276, AA588635, C15098, AI580816, AA430124, AA902480, AI611205, AI928306, AI824182, AA368086, AA731886, AA358722, AA732765, AW383478, AA470116, AI928316, AW383528, AA358723, AW383489, AL046849, AI075391, AA974899, AI630005, AC008126
66	HWBBK93	638249	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1758 of SEQ ID NO:66, b is an integer of 15 to 1772, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:66, and where b is greater than or equal to a + 14.	AI188389, AI763238, AI188787, AA479523, AI423154, AI346520, AW005918, AI682996, AA781395, AI394520, AI700522, AA778127, AW338995, AI348157, AI139369, AA858416, AW291338, AI061441, AI928073, N40533, AA771952, AA835017, AA479526, AA430584, AI276159, AA576421, T34153, AA418766, AI272728, AA563878, AA528124, AI050707, AA433929, AI218374, AA150587, AI422109, AI075212, AI338694, AA418722, AA969029, AA505360, AA782389, AI348193, AA662690, AA904379, AI743240, AI126395, AI090901, AA304971, AI908134, N64614, AA465703, AA505543, AA771799, AI917748, AW271730, AI248295, AA215970, AI811574, R52412, AA971867, AI333671, AI380868, AA574396, R35114, N33899, AW194812, AI280563, R16040, D45470, AW195236, R24139, R79672, W30758, R18084, AA761523, R16039, AI365169, AI864209, N98221, Z40957, T85033, AA725308, AA618381, N99709, AI926895, R02608, R42978, N79943, Z45240, AA320674, N71980, AI630495, T30798, AI886691,

67	HFXAK32	638319	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1815 of SEQ ID NO:67, b is an integer of 15 to 1829, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:67, and where b is greater than or equal to a + 14.</p>	<p>AW089148, R49502, R01668, R24146, AA650492, R79861, AI589880, AA705913, AI247102, AI569369, F02495, T91981, AA248224, T25009</p> <p>AI291718, AI751557, R55888, R52001, H65731, T55784, H65732, T79985, AB001103, U59288, U59289, AL021154, AL034429, Z93016, AC008008, AC002350, AC006948, AC006509, AC005722, AC007182, AF222686, AP0000696</p>
68	HUSIT18	651380	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1674 of SEQ ID NO:68, b is an integer of 15 to 1688, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:68, and where b is greater than or equal to a + 14.</p>	<p>AW294097, AI279800, AA316672, N25621, N34219, AA115172, AI125602, W16706, AA228116, AI348328, AA322714, R59092, AI699089, R51246, AI086372, AA383008, AW339394, AA344347, AA227730, R51245, AB011123</p>
69	HMWVBH5 1	651876	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 551 of SEQ ID NO:69, b is an integer of 15 to 565, where both a and b correspond to the positions of</p>	<p>AI554920, AI469981, AI539465, AA425263, T28976, AA812162, AI740449, W21091, AW242010, W23635, AW275702, AA476848, AI808924, AW117295, AI148939, AA811229, AI343010, AI630793, I96178, A50906, L00049, X85754, U09793, K01912, Z12125, E00392, E00393, I01060, M35504, M35505, X02456, X00485, L00047, X02454, U76425, U76426</p>

70	HCQAW11	653175	nucleotide residues shown in SEQ ID NO:69, and where b is greater than or equal to a + 14. Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 661 of SEQ ID NO:70, b is an integer of 15 to 675, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:70, and where b is greater than or equal to a + 14.	AL041795, AI590066, AI457168, AA126363, AA463388, AA767754, AA463880, AA886811, AW079539, AI884597, H23284, AA907711, AA789127, AI636922, AI039001, AI681335, AA126259, AL050120, AC004925
71	HPRAS01	655544	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 256 of SEQ ID NO:71, b is an integer of 15 to 270, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:71, and where b is greater than or equal to a + 14.	AA370716, AA888839, AI817753, AW131538, AA860117, AI479976, AI568675, AI922252, AW084473, AA370730, AA740955, AA935921, AI566265, AI092718, AA854646, AA724492, AW439983, AL109984
72	HWBBC13	656722	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 524 of SEQ ID NO:72, b is an integer of 15 to 538, where both a and b correspond to the positions of	Z69042

73	HNTBM67	659801	nucleotide residues shown in SEQ ID NO:72, and where b is greater than or equal to a + 14. Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1057 of SEQ ID NO:73, b is an integer of 15 to 1071, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:73, and where b is greater than or equal to a + 14.	AL134955, AA307472, M78461, D56412, AW382561, AW382555, AW382532, AW382562, AW382559, AA223890, AI536122, AA826373, AW382553, AB014509, AB011159, D84346, X80029
74	HDPKCI5	660020	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 626 of SEQ ID NO:74, b is an integer of 15 to 640, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:74, and where b is greater than or equal to a + 14.	AL037983, AL046549, AA630672, AL137998, AA829036, T92347, AW022608, AA570230, AL041706, AW294985, AA629872, T41259, AA588001, AA700032, AA746659, AI002744, AA346467, AI907530, H25921, T41354, AA812141, AL120086, AA570797, AA601125, AA568198, AL047429, AL138182, AI249473, AA515462, AA515443, AI619436, R99735, AI922803, T47572, AC005034, AL133163, AJ006997, AL133244, AL009174, AC003036, AL035079, AC007193, AC005702, AP000962, AC005296, Z85996, AC005783, AC004217, AL080317, AL034386, AC002067, AP000690, Z84487, AL121603, AC006120, AC006016, AL035411, AC006077, AP000346, Z97987, AC007919, AC002485, AC005031, AC009498, AC004540, AL021367, U95740, U80017, AP000251, AL031848, AF029308, AC006042, Z69917, AC004856, AL121748, AP000030, AL117344, Z73358, AP000511, AC002310, AL109984, AL034350, Z82194, AL023284, AC005014, AC005920, AC008122, AC007666, AC002299, AC000052, AC004019, U66083, AF091512, AC006262, L14752, AC002351, AC007386, AC006196, AC000070,

75	HMAHP16	661600	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 493 of SEQ ID NO:75, b is an integer of 15 to 507, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:75, and where b is greater than or equal to a + 14.</p>	<p>AP001051, AC004967, AC005332, AC005538, AL109854, AP000694, AC005940, AC007011, Z81450, AC004652, AC005202, AL049544, AF196970, Z84476, AC005519, AF126403</p> <p>AL135342, AL135338, AI682468, AI984021, H99774, AW087983, AA911190, AA923049, AI804789, AW269257, AA343320, AA599673, AA906706, AW002696, N28500, AI458578, AI168801, AW002691, AI276029, AI753280, T63417, R99573, N52383, AA350643</p>
76	HCEID45	664481	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1376 of SEQ ID NO:76, b is an integer of 15 to 1390, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:76, and where b is greater than or equal to a + 14.</p>	<p>AI633731, AA742535, AA928586, AW024580, AI031748, AA287493, AW139368, AA235073, AI342861, AA024783, AI122951, N47975, AA235180, AA936068, AW083549, AA953192, T96536, AW297014, AI554540, R68510, AA287388, T96535, H43420, R75691, AI206677, C05105, AW372944, Z41074, N89741, AI656081, H43421, N74128, AA612838, AI061189, AW021549, AA811399, AW073662, D52513, AI862684, D53036, AA677516, AI382574, M79140, T97144, F03274, AA356468, N89554, R75606, N51175, AC005003, AL096880, A81324, A81326, AF181071</p>
77	HBIBV81	665154	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 768 of SEQ ID NO:77, b is an integer of 15 to 782, where both a and b</p>	<p>AL080003, AW302605, AW178402, AI701581, AI949784, AA506438, AA176780, AW340099, AI810668, AW008216, AI949793, AI570129, AA025230, W37867, AI564486, AI252216, AI499109, AW242964, AI480359, AA774674, AI026080, AA931127, AA126008, AA629404, AI264043, T91992, AW169773, AI350790, AA960795, AA300132, AA134208, AI695964, AI824322, AI377546,</p>

78	HSXBP02	666790	correspond to the positions of nucleotide residues shown in SEQ ID NO:77, and where b is greater than or equal to a + 14.	AI687600, AA468788, AI380078, AA910317, AI061219, AI915290, AI277301, AA887251, AI298724, AA353348, AA419130, AA937303, AI025658, AA864265, H17773, AA931728, R50817, R27626, AA419069, AA897064, H17656, AI580298, AI521898, AW086126, AA626445, AI918844, F10191, F10115, T63745, R88235, AA721159 W24040, N95428
79	HCQCO19	668040	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 264 of SEQ ID NO:78, b is an integer of 15 to 278, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:78, and where b is greater than or equal to a + 14.	AA837754, AA581115, AC004466
80	HHENT19	668586	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a	AC004998, AF130343

81	HMTMB52	668717	<p>is any integer between 1 to 328 of SEQ ID NO:80, b is an integer of 15 to 342, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:80, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 523 of SEQ ID NO:81, b is an integer of 15 to 537, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:81, and where b is greater than or equal to a + 14.</p>	AA031331, AA447922, AA878870, AA625391, AA026657, AI476276, AA305075, AA148792, AA446846, AW169122, AW149768, AI796276, AA603456, AA090696, AI566470, AA026887, AA455761, AA046950, AA837404, AW196971, AI636657, AA279066, AA321648, AA046476, AI025283, T30865, N40879, AA446847, AA845528, AI879232, AA188287, AA403246, H90077, AA128964, AA031332, H78109, N78226, T36197, AA936074, H37884, AA256024, T34431, T34451, AA308443, W51863, AA568448, AA877372, AI358381, AI351514, AA030022, H27053, AL048514, AF110777, AF151895, AF195950, U21858, I23471 AA916322, AA244285, R57426, T67759, AF161472, AL117545, AL117608
82	HOGAL19	668753	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 278 of SEQ ID NO:82, b is an integer of 15 to 292, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:82, and where b is greater than or equal to a + 14.</p>	
83	HCQAG50	671361	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by</p>	W27182, W31603, W76194, AI057607, AA203214, N43872, AI719074, AW009568, AW418865, R23692, AA136421, H27226, AA055206, AW372559, AW372556, AW372575, AW372567, AW195824, AI057563,

84	HDPLC22	674203	<p>the general formula of a-b, where a is any integer between 1 to 338 of SEQ ID NO:83, b is an integer of 15 to 352, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:83, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 390 of SEQ ID NO:84, b is an integer of 15 to 404, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:84, and where b is greater than or equal to a + 14.</p>	<p>AW372571, I95748</p> <p>AI936345, AA887285, AI678802, AI418187, AW058484, AI978830, AA614465, AI634784, AA508486, AW299537, AI361913, AW299894, AI359657, AI659077, AI718694, AI686164, AA533665, AI469389, T90037, AA878577, AI739343, AA903695, AI934233, AI444978, AA910595, C00551</p>
85	HBMXO90	674745	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1541 of SEQ ID NO:85, b is an integer of 15 to 1555, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:85, and where b is greater than or equal to a + 14.</p>	<p>AI819368, AW043804, AA995625, AA158255, AI989534, AI632079, AI632177, AW385262, AI436651, AA579669, W92990, AA583087, AA702208, AI767610, AI022894, AI694633, AI687149, AA811023, AW207705, AA043498, AA062551, AA024830, AA043234, AA024786, AI636005, AA063156, AI564317, N99809, AI023039, W93177, AA583864, AA210642, AW388581, AI630114, AW352131, T95281, AW388505, AW016381, AW376106, AW376098, AW082627, AA074329, AW339405, AI479095, AA215346, AB011098, Y08686, AF004830, U27455, X95642, U15555, AF111168</p> <p>AA320525, AW025411, AI653685, AI684617</p>
86	HLMIS22	674761	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by</p>	

87	HE8AG73	677212	<p>the general formula of a-b, where a is any integer between 1 to 441 of SEQ ID NO:86, b is an integer of 15 to 455, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:86, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 661 of SEQ ID NO:87, b is an integer of 15 to 675, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:87, and where b is greater than or equal to a + 14.</p>	AA287561, AA307431, AA331618, AA287878, AF136450
88	HCBYBF14	683259	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 479 of SEQ ID NO:88, b is an integer of 15 to 493, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:88, and where b is greater than or equal to a + 14.</p>	AA305210, AW015627, AI580368, AI830042, AI769572, AI741672, AA854575, AI073885, AA834403, AA962811, AA757628, AI923528, N32611, R79828, AW241940, AA961638
89	HKAAS37	685895	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by</p>	

90	HBXFP72	688040	<p>the general formula of a-b, where a is any integer between 1 to 402 of SEQ ID NO:89, b is an integer of 15 to 416, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:89, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1453 of SEQ ID NO:90, b is an integer of 15 to 1467, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:90, and where b is greater than or equal to a + 14.</p>	<p>AA977676, AA039596, AI871723, AA039597, AI201016, AW338088, AI923596, AW268550, AI016244, AA826433, AAI65179, AA876424, AW130871, AI168822, AA743485, AI039963, R81034, AA526606, R80933, AW131872, AA367044, AA278895, AI352299, AI688836</p>
91	HFIYP15	688044	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1779 of SEQ ID NO:91, b is an integer of 15 to 1793, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:91, and where b is greater than or equal to a + 14.</p>	<p>N71063, W94295, N66037, H63245, AI568915, N73616, AA773642, W02603, AA907572</p>
92	HEBAG86	688077	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by</p>	<p>AI312130, N98607, AA062994, W52082, W68173, W67714, AI127084, AA406051, AA305034, AA836397, AA978358, AI347575, AA405217, AA764978, AI375843, W90774, AA649214, AA824648, AA258212,</p>

93	HLDNM81	691124	<p>the general formula of a-b, where a is any integer between 1 to 524 of SEQ ID NO:92, b is an integer of 15 to 538, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:92, and where b is greater than or equal to a + 14.</p>	<p>AI190424, AI719533, AI277627, W24232, AI095177, AA926760, AA927352, AA909449, AA284241, W56767, D54052, F19566, AI342704, H01228, AA514925, AA905893, F36912, D55269, H00845, R95095, F32474, AA887548, AI240810, AA894366, T79247, AA579420, D52953, AA468124, D54053, AI081229, AA947003, T36306, AI597616, AA729251, W90739, F33384, F28057, AI370811, R16001, AI144512, AA988588, AA033634, AA034341, R16102, AA826454, F27110, F31119, D52954, AA631119, AA894720, AI368559, F29378, AA489478, AA483450, F36024, D54336, T31368, T79165, C00350, AA594514, AA062620, N76784, D57671, W56721, H54408, D59289, F00481, F32076, Z24770, AA301716, R05397, AW301847, F25224, AW054814, AA372016, AA485014, AA318851, AI302407, AF047440, AR048128</p>
94	HARNC71	691721	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 469 of SEQ ID NO:93, b is an integer of 15 to 483, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:93, and where b is greater than or equal to a + 14.</p>	<p>AA345522, AI908286, AA484151, C20958, AA913510, AI678105</p>
94	HARNC71	691721	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 705 of SEQ ID NO:94, b is an integer of 15 to 719, where both a and b</p>	<p>H92130, AA468843, AA468855, AW244043, AA935265, F13685</p>

95	HE2OC31	693582	correspond to the positions of nucleotide residues shown in SEQ ID NO:94, and where b is greater than or equal to a + 14. Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 599 of SEQ ID NO:95, b is an integer of 15 to 613, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:95, and where b is greater than or equal to a + 14.	AA425207, AA328348, AI422986, AW085230, AJ223956, X86000, Y09488
96	HTXKQ20	696007	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 802 of SEQ ID NO:96, b is an integer of 15 to 816, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:96, and where b is greater than or equal to a + 14.	AA167034, AA167085, AA037278, AA114130, AI128866, AA291957, AA009438, AA723387, AA766022, AA299755, AA991579, AA291956, AW160699, AI083889, H38599, AA811428, AI348079, AA635954, AA039390, R34160, R34159, AA009919, AI829155, AA010462, AI081871, AI674507, AI082075, AA039391, AC005041, AL049296
97	HE2OK20	697955	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 563 of SEQ ID NO:97, b is an integer of 15 to 577, where both a and b	AA328692, AW244141, AI435184, AC005084, AC003093

			correspond to the positions of nucleotide residues shown in SEQ ID NO:97, and where b is greater than or equal to a + 14.	
98	HMWIW31	698068	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 470 of SEQ ID NO:98, b is an integer of 15 to 484, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:98, and where b is greater than or equal to a + 14.	W01234, AP000500
99	HCEEH33	702853	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 427 of SEQ ID NO:99, b is an integer of 15 to 441, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:99, and where b is greater than or equal to a + 14.	AI436583
100	HAGBL85	703700	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 510 of SEQ ID NO:100, b is an integer of 15 to 524, where both a and b	AI582864, AW138272, AA976107, AA781938, AI093184, AA535789, AI803509, AA412322, AI216808

101	HLWAY38	705461	<p>correspond to the positions of nucleotide residues shown in SEQ ID NO:100, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 600 of SEQ ID NO:101, b is an integer of 15 to 614, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:101, and where b is greater than or equal to a + 14.</p>	<p>AA143160, AA283147, AA142881, N39722, N28707, AA232819, AA233368, AI245977, AI435939, N23044, AI739455, AC007785</p>
102	H2LAN34	705692	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 530 of SEQ ID NO:102, b is an integer of 15 to 544, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:102, and where b is greater than or equal to a + 14.</p>	<p>AA314140, AI623759, AA768701, AW005593, AI420537, H65282, D58283, D80043, D57483, D80253, D80164, D80366, D80022, C14331, D59467, D51423, D59859, D81030, D80391, D59787, D80166, D80195, D59275, D59619, D80210, D51799, D80240, C15076, D80227, D80188, D80024, D59502, D50995, D80196, D59889, D80212, C14389, D80219, D59927, D80269, D80038, D50979, D80193, D59610, D80378, C14429, AA305409, D80241, D80045, C14014, T03269, AW178893, D51060, C75259, D80522, D51022, AW179328, D80134, AW178775, D59695, D80251, D81026, AW177440, AW378532, AA305578, D58253, D51250, AW377671, F13647, AW369651, AW352158, D51079, D80168, D52291, D80248, C14227, AW178762, AW360811, AA514188, C14298, D81111, D80064, AW177501, AI910186, AW177511, C14407, Z21582, AA514186, D80133, AW177505, AI905856, C05695, D80247, AW352117, D80132, AW176467, AW375405, AW378540, D80268, AW179024, AW366296, AW360844, AW360817, AW375406,</p>

			<p>AW378534, AW179332, AW377672, AW179023, AW178905, AA285331, AI557751, AW360834, D51097, AW352170, D80302, AW352171, T11417, D80439, AW377676, AW178906, AW177731, AW178907, AW179019, AW179018, D59373, AW179020, AW360841, AW178909, AW177456, AW178980, AW179329, AW352174, D80014, AW179220, AW177733, AW378528, AW178908, AW178754, AW179004, AW179012, D51103, AW178914, AW378525, AW367967, D80157, AW177722, AW177728, AW179009, D51759, AW178774, AW178911, AW378543, AW352163, C14077, D59627, D58246, AW178983, AW352120, C06015, D80258, D59503, AW178781, T48593, D58101, D45260, T03116, AI557774, AW177723, AA809122, AC012627, AC007204, A62300, A62298, A84916, AJ132110, AR018138, X67155, A25909, Y17188, D26022, A67220, D89785, A78862, D34614, AF058696, D88547, AR008278, X82626, I82448, AB028859, AR025207, Y12724, AB012117, X68127, A82595, A94995, AB002449, A85396, AR066482, AR060385, A44171, A85477, AR008443, I19525, A86792, U87250, X93549, I50126, I50132, I50128, I50133, AR066488, AR016514, AR060138, A45456, A26615, AR052274, AR054175, AR066490, Y09669, A43192, A43190, AR038669, AR066487, I18367, A30438, D88507, I14842, D50010, Y17187, AF135125, AR008277, AR008281, A63261, X64588, AR008408, AR062872, A70867, AR016691, AR016690, U46128, D13509, AB033111, A64136, A68321, AR060133, I79511, AR064240, U87247, AB023656, U79457, AF123263, AR032065, Z82022, A63887, X93535, AR008382</p>
103	HBMXT67	706204	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by</p> <p>AA195264, AI918088, AI392950, AI991206, N51725, AI140306, AI264604, AW304477, AI800326, AI186691, AI356850, AA489331, AA026607, AI383508, AI523998, AI276615, AA884388,</p>

			<p>the general formula of a-b, where a is any integer between 1 to 1873 of SEQ ID NO:103, b is an integer of 15 to 1887, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:103, and where b is greater than or equal to a + 14.</p>	<p>AI356867, AI378377, AI589019, AI361250, AA026719, AA580169, H17664, AA565144, AA514880, AI766245, AA557471, AA632253, W95296, N68920, AI985972, R53701, W95553, AA736984, AI807975, W00561, AW128999, H06890, AA470666, R44101, R19059, Z41259, AI283474, T64963, AA312893, F05870, AA322544, R52922, AI204157, F08182, F02161, T85379, R07731, M96606, F02113, R07732, F05911, AA325154, AA644479, T85478, T92165, F05899, R70373, N51810, AA091065, T93592, AW103327, AA936051, AA876718, H06849, U76421, U76422, AF001042</p>
104	HE2IE28	707161	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 239 of SEQ ID NO:104, b is an integer of 15 to 253, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:104, and where b is greater than or equal to a + 14.</p>	<p>H25350, H28544, AI9555873, N29938, R12730, AL120665, AW104398, AC000064, AC007566</p>
105	HBXCG73	707464	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 691 of SEQ ID NO:105, b is an integer of 15 to 705, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:105, and where b is greater than or equal to a + 14.</p>	<p>AW390194, W86403, R24772, C75131, AA496772, AW383256, AA322376, AA313543, AW068217, AA232072, AL121084, AI983937, R14521, AW401961, N83156, AA385863, AA285265, AF001628, AF006516, U87166, AF176784, U17698</p>

106	HATAN68	709015	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 906 of SEQ ID NO:106, b is an integer of 15 to 920, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:106, and where b is greater than or equal to a + 14.</p>	<p>AI796967, AW195747, AI740869, AA191594, AI498701, N64011, W86388, AI948435, AI125704, W86389, AI282275, AA887501, D61002, AI197956, H80459, AW204689, AI003139, AA219621, AI985257, H99275, H81379, AA346169, R20553, H05031, R41899, AI912734, T30719, AI197904, AW386705, AA779217, AL046187, T24891, AI864073, AL046188, AA992514, C00222, AW020592, AW020634, AI568293, AI525653, AW020397, AI263584, AI499570, AW023863, AW021178, AW022826, AI538564, AW019988, AI522052, AW023351, AW020931, AW020328, AI636727, AI871660, AW004606, AI884318, AW022308, AI579901, AW152182, N25033, AW020425, AW021693, AW022299, AI557238, AI633125, AW022981, AW020406, AW021182, AI701097, AA282824, AI935799, AI557808, AI909697, AI887381, AI541321, AW023469, AI283760, AI744268, AI524626, AI571439, AW023884, AI915291, AW020629, AI696714, AI525669, AW022593, AI473536, AW021059, AI812091, W45039, AW020480, AW021466, AI359744, AI828682, AW021561, AI590043, AW020876, AI254731, AW020710, AI432030, AW198090, T69241, AI674423, AI932966, N21402, AI810544, AI889189, AL042722, AI536638, AI473150, AW023617, AW020295, AI925502, AW080157, AI866469, AI687362, AI687624, AA830709, N64568, AI282673, AI625256, W74529, AA872507, AI368691, AW105296, AI341690, AI824688, AW022168, AW023955, AI699823, AW021717, AI539545, AA554929, AW021777, AW020403, AW022760, AI613270, AW022874, AI469262, AW021930, AI421903, AW163834, AI582932, AI818980, U06944, AF122922, AL117587, A77033, A77035, L35261, A52184, AL137533, A44314, Z13966, AF200464, AF060555, AF124396, I32738</p>
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107	HAGDD59	709518	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 452 of SEQ ID NO:107, b is an integer of 15 to 466, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:107, and where b is greater than or equal to a + 14.</p>	<p>AA454978, AA132519, AW135352, AA179230, AW024761, AW004924, AI127068, AI985072, N45125, AI867004, AA857184, AI985060, AI361206, R54585, AI272727, AI766581, AI940540, AA923780, Z38507, AW192986, AC004685</p>
108	HBJFI65	711769	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 309 of SEQ ID NO:108, b is an integer of 15 to 323, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:108, and where b is greater than or equal to a + 14.</p>	<p>AI740525, AI800754, AI189295, AA878902, AI262709, AW169159, AA495986, AI469879</p>
109	HSNAL84	711840	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 434 of SEQ ID NO:109, b is an integer of 15 to 448, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:109, and where b is greater than or equal to a + 14.</p>	<p>N40932, AI339840, AW044507, AI216527, AI620878, AW316937, AI292180, AI358083, AI954691, AW006263, AA321122, AA321123, AI654341, N46790, AI953114, N69895, AI970523, AA226346, AA226347, AF196969</p>

110	HCRND41	711878	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 835 of SEQ ID NO:110, b is an integer of 15 to 849, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:110, and where b is greater than or equal to a + 14.</p>	AA442729, AI146478, AL042373, AI792521, AW237905, AI625604, AL153777, AI755214, AI754105, AI754567, R72224, AW151541, AL046519, AI440117, AI792575, AW304580, AW438542, AI333387, AL079734, AI114733, AI133552, AA904211, AA503298, AI380617, T74524, AI627614, AI521525, AW328331, AA831638, AW328202, AI754170, AI053688, AA916430, AI251203, AI251034, AA600202, AW068596, AA700943, AA526542, AI284543, AA456937, AA501461, AW270385, AI859438, AW303098, AI613389, AA714110, AL042667, AL042670, AI251284, AI890324, AA833875, AA833896, AI732483, AA536040, AW069227, AI223626, AL119247, AA524229, AA487226, AA618316, AA593537, AW084445, AI923052, AW069412, AI282253, AA535216, AI278972, AA483606, AA704393, AI687343, AA502991, AA719564, AA533025, H07953, AI799607, AI859946, AA570740, AI473671, AI817658, AW023111, R99034, AI040051, AA828834, AI081147, AA809546, AW089016, AI754767, AI733856, AW026305, AA524616, AA492495, AI309059, AA534064, AI254770, AW243793, AI254779, AA584360, AA603413, AI962030, AI253987, AL041375, AA315361, AI300054, AA659832, AA568204, AW020150, AA595661, AA019973, AA013168, AI499954, R94326, AA747757, AW089625, AW408767, AA581903, AA687730, AA410788, AA630854, AW271904, AA530958, T05118, AI369580, AW238484, AW275432, AI267356, AI745151, AI251576, AA632993, AA814503, AI583142, AI362442, AI003626, AA319233, AI291439, AI537995, AC006239, AC006211, AL031602, AL109627, AF134726, Z84486, AP000503, AP000117, AL096791, AC007565, AL049643, AC004771, AL117694, AL031228, AC007421,
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			AC002302, AP000193, AF196779, AC004975, AC005663, AC004796, AC007052, AC005874, AF134471, Y14768, AC005828, AC007664, AC005261, AP000501, U91323, AL109801, AC004181, AP000961, Z93023, AC006480, Z98884, AC006511, AL136295, AP000505, AL096701, AC004991, AC007216, AC005318, AL049539, AC005099, AC000086, AL079303, AC005037, AC006111, AL133163, AF038458, AC006468, AC004653, AP000086, AC004647, AC005231, AC009247, AL022147, AL109628, AC005225, AC005599, AC002316, AL022326, AL133448, AC006388, AC008372, AC008040, AC005046, AC002301, AL031311, AL049856, AC005971, AC007546, AC005668, AL132712, AL049872, AL035086, AC004196, AL009181, AP000547, AL078477, AC004686, AF045555, AB000876, AL034402, AC002553, AL022069, AC010582, AL109798, AL031587, AL035413, AC004531, AP000497, AC003041, AL031282, AC004156, AC003982, AC005358, AC004019, AC007277, AL021154, AC004832, AL031589, Z94056, AC006450, AF067844, AC005808, AC004882, AC006285, Z69917, AC007371, AL049776, AF165926, Z84572, AC004253, AC005295, AC004859, AB000882, AL034417, AP001053, U91318, AC003037, U91322, Z97184, AC004750, AC005670, Z82215, AC004797, Z98946, AC005821, AC005233, AC002472, AC007731, AC007227, AL031283, AC004673, AC000134, AC005500, AC006312, AL022334, AC002996, AP001052, Z82208, AC012627, AC004596, AC004644, AC005730, AC004804, AC004534, AC007842, AC005535, AC006120, AP000510, AF129756, AP000359, AC005280, AC002351, AC007934, AL122023, AC005538, AF111167, AL035407, AC005924, AC005777, AL049795, U80017, Z98200, AC006538, AC006530, U96629, AL117329,

111	HPXAA41	712638	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 862 of SEQ ID NO:111, b is an integer of 15 to 876, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:111, and where b is greater than or equal to a + 14.</p>	<p>Z97352, AP000694, AC005081, AB023048, AP000104, AL035072, AC004921, AC002352, AF053356, AC005071, AC007036, AC004812, AL034549, AC004805, AC005694, AL021155, AC007388, Z82244, AL031005, Z77249, AC005881, U95742, Z93241, AL049569, AC006057, AC004106, AL109984, AC009509, AP000114, AL031659, AL121603, AC005291, AC007993, AC005666, AL023353, AL034548, AC008044, L78833, AC005183, AC004002, AC005529, AC005013, AC005300, AC006441, AC004560, AL049636, AL049779, AP000211, AP000133, Z83844, AL035400, AL031289, AC005039, AL035659, Z97876, AL021939, Z84466, AC004905, U62293, AC004125, AC004821, AC006430, AL135960, AJ131016, AP000046, AL132992, AC006241, AC005030, AC007406, AC005015, Z99716, Z98751, AC004466, AC004874, AC004966, AC005095, AC005102, AC005245, AC002378, N50319, AA236194, AA236183</p>
112	HHSFO42	713301	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 862 of SEQ ID NO:111, b is an integer of 15 to 876, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:111, and where b is greater than or equal to a + 14.</p>	<p>AA910497, AI701451, AA429326, AI743089, AI887812, AI005464, AA041483, AI300993, AA315932, H51256, AA425105, AA921331, AA885637, AL043321, AA903224, AI680678, H51826, AI299003, AW014324, W01644, AI809584, AI762128, AI693885, AW167510, AI630969, AI457315, AW341205, AI630807, AI694045, AA928976, AA931651, N71630, AW295247, AA094470, AF147430, D10920</p> <p>F36273, AA654968, AL119691, AI281881, AA515224, AI298710, AW236342, AI358343, AI351698, AI679045, AW079241, AA084070, AI289447, AI654247, AW304805, AI920876, AI688846, AI358813, AW168342, AA661948, AW020992,</p>

		<p>is any integer between 1 to 368 of SEQ ID NO:112, b is an integer of 15 to 382, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:112, and where b is greater than or equal to a + 14.</p>	AI284640, AI192631, AA502103, AA347927, AW276435, AI857789, AI291124, AW193265, AW270382, AA347930, AI567674, AW089322, T08638, AI500454, AA515051, AW265385, T07451, AW089789, AI929531, AI049634, AA665330, AI431303, AA593247, AI625244, AA284179, AI061313, AL043721, AI858451, AA829106, AW029038, AI962050, AI291268, AI339850, AW238278, AI350211, AA555229, AA324849, AA720025, AA594145, AW193432, AW440836, AI434311, AI469003, F26152, H77643, AI251002, AA483034, AI133636, T06828, AA528516, H86305, AA513999, AI567712, AA229785, AW301350, AW303196, AW274349, AA491767, AI151261, AW071196, AW022379, AA482681, AA225155, AW029526, AA349638, AA747472, AA557686, AI087133, N43757, AA723017, AI830390, AI281697, AA828680, AA310158, AI355224, N95820, AI286264, AI475569, AI889781, AL134330, T09071, AA847499, AA642060, AI890923, AI061296, AI358571, T05101, AA584752, AA441788, N63352, AI674873, AI866908, AA629992, AA831527, AA503947, AA917683, AA745582, AA569471, AI281465, AA669416, AI471481, AA085124, AA719805, AA349366, AW339568, AI189932, AW440662, AW166815, AW302013, AA429481, AA747105, H63607, AI619997, AI471543, AW151896, AA213741, AW238542, AA947547, AA483731, AW302450, AA782318, AA826303, N75391, AA493621, AI049722, AW152057, AI672135, R83585, F25867, AA649642, N66945, AA715004, AI287651, AA338642, AI798266, AW021583, F37169, AW162049, N41759, AA594725, AI571562, AW072587, AI435544, T17016, AL043756, AA837740, AA507547, AI312149, AI871722, AI017024, AA782272, AA074130, AA053128, N53150, AA857486, AI801591, AA503283, U51696, AI148245, R95171, AA338522, AA634227,
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	AW392414, AI859742, H54443, AI608626, AI679782, AA426277, AA346454, AA584201, AA789115, AA846981, AL046409, AI824562, AA502155, AL045298, AW008952, AW438643, AA679672, AA371533, AA385100, AI721122, AL049829, Y10196, M37551, AL109984, U14719, AP000553, U14718, M87919, U14711, U14712, AC004941, U14706, AC009516, AP000032, U14714, AC002073, U95740, AL008629, S77605, U14716, AL050332, D83989, AC002526, X55926, X75335, S75337, AL109837, AP000692, AC016026, U14705, U14715, AC005578, U18392, AC005516, U47924, Z73358, A39972, AC004020, AC004821, U57009, AP000555, AC005619, AL020993, AC006057, AC005081, AC007848, AC008040, AC004167, AC005944, AC005911, AF117829, AL122020, AL049758, AC004771, U18391, AC004895, AC004886, AF190465, U18390, AF111168, U18399, X55925, AC005747, AL109939, AC005251, AC006312, U57006, U18394, U18393, U57005, X54176, I51997, X55928, U14707, AC007845, AC004907, AC004034, U02057, AC004592, U14700, U14695, AC005939, U14710, AL049779, AC006001, AL031846, AC004955, Z30993, S70707, Z68881, U18387, AL034549, AC008101, Z15025, AC004651, AF045555, AC007227, AC006111, AF205588, U14708, AL033381, X55923, U18398, U18395, AP000563, AL133448, U57008, AC006538, X55932, AC007536, AL022318, U02063, AC016830, AF020503, AP000103, AL035684, AC006040, AC007387, U14703, U14701, AL132987, AL050318, U73024, AC004239, U14702, U14684, U14685, U14687, U14699, D00591, AF077058, AC006039, AC005288, AL023574, Z22650, Z84469, AC004876, AC005215, AC005866, AC000353, Z30961, AC005856, AP000497, AC004087, AL031588, AL031677, AP000133, AP000211, Z84814, AL022476, U49740, M19045, J03801, E01888, E02193,

113	HCEIE94	714156	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1056 of SEQ ID NO:113, b is an integer of 15 to 1070, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:113, and where b is greater than or equal to a + 14.</p>	<p>AP000246, AL096701, AP000207, AP000129, Z99496, AL035214, AC016027, AC006195, AC004531, X55930, AC006251, AC005846, U85195, AP000230, AP000144, AC005041, AP000228, AC010072, AP000255, X54178, AE000658, AC004019, U12582, AL035464, AC005225, AF165147, U14686, U14688, U14689, AP000047, AC007687, Z82976, AL109628, AC008064, AC004453, AL031733, AP000556, AP000557, AC005775, AC004235, AL080316, AP000140, AC007444, AC005703, AL034429, AC007270, AP000135, Z93929, X55922, U67829, AC002072, AC005327, AC005229, AC007488, AL024498, AC005166, AP000031, AL079340, AC005480, AL008721, AL033376, AC005696, AL117258, U18400, AL031427, AC007157, AC007971, AD000092, AC006160, AF064863, AC005035, AC009498, AC005104, AL031985, U62317, AC003688, AP000115, AF121781, AC005105, AL133485, Z84721, X54181, AF070718, AL035071, AL0233575</p>
114	HWLQA43	714877	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a</p>	<p>H16630, Z46007, R18668, AA779244, AI742776, AA648586, AL049824</p>

115	HFXHM92	715343	<p>is any integer between 1 to 357 of SEQ ID NO:114, b is an integer of 15 to 371, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:114, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 567 of SEQ ID NO:115, b is an integer of 15 to 581, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:115, and where b is greater than or equal to a + 14.</p>	AA628088, AI640353, AI767467, AI921798, AI810416, AI810681, AI125878, AW073826, AA182773, AI954699, AW293730, AI828389, AI580952, AI313461, AI651050, R49049, AA772043, N33101, AA496896, AA928502, AI031772, AA864471, AI401678, W45009, N93870, T63242, AW194759, AI971721, AI038841, AI979313, AI253064, W32434, AI292264, AI983163, H99107, AI038482, AA604895, AW418876, AW337639, AA461303, AI270459, N50558, AI290061, AI452404, AA099425, AI200622, AA974079, R73465, AI432100, AA081421, AI698923, AI571941, AA480265, AI017448, N64632, AI199075, AA758942, AI982600, T33000, H65188, AI817275, AI684978, N55816, AI827372, AI701353, H28606, AA947626, AA722706, H00447, AI826589, N24348, R55743, H03410, Z41694, F02896, R62185, H45540, N92338, N78793, F26109, N48260, N44922, W38368, AW003189, H00490, AI310166, AI370047, AI313291, AI340484, T90688, R64574, N93394, H45548, F35733, AI308272, AA320558, AA365588, W24522, AA651757, N45701, AA096344, AA099538, N50614, AA083629, AL096842, AB033114, AB020864 W61017, W61009, AA128255, AA806126, AA136365, AA936371, AW150765, AI279977, AA125840, AW448960, AA128312, AA125856, AI186377, AI269647, AI265821, AA873528, AA136280, R07851, R62482, AB031039, AB031040
116	HHSGE44	716212	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 691 of SEQ ID NO:116, b is an integer of</p>	

117	HWLQI33	717222	<p>15 to 705, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:116, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1182 of SEQ ID NO:117, b is an integer of 15 to 1196, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:117, and where b is greater than or equal to a + 14.</p>	<p>AI127903, AI935263, AI741826, AI819372, AI809826, AI524082, AW102619, AI804122, AI540191, AW405122, AI589161, AI860317, AI742839, AA631117, AI809767, AI363498, AA427510, AA480840, AI298899, AI086078, AA847830, AI354791, AI051661, AI675663, AI122706, AI377777, AA503878, AI202112, AI720306, AI394378, AI375978, AA764814, AW406420, AA333282, AI286081, AI298712, AA292572, AI492636, AI867099, AI417659, AI468559, AA971791, AI222922, AA913022, H96909, AA972549, AA992120, AI928774, AW207223, AA814866, AA757376, N35604, AA907092, AW072106, AW166047, AA757394, AI345182, AA457729, AA235704, AW183289, AA430669, Z57528</p>
118	HFIW90	718259	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 961 of SEQ ID NO:118, b is an integer of 15 to 975, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:118, and where b is greater than or equal to a + 14.</p>	<p>H19365, AA286719, N44262, AA447218, AA974582, AC004817</p>
119	HOSEP43	719829	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by</p>	

		the general formula of a-b, where a is any integer between 1 to 317 of SEQ ID NO:119, b is an integer of 15 to 331, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:119, and where b is greater than or equal to a + 14.	
120	HUSGY48	721985	<p>AA731436, AA505796, AA528524, AA886535, AI802907, AA973692, F26324, AA176725, AA658895, AI914394, AI392630, AI338999, AI123694, AA977864, N64163, AA359165, AA975366, AI126532, AA916014, AI832970, AI351443, AA888167, AI093884, AA973611, AI833308, F33502, AW264528, AI709250, AA594324, AI039168, F33691, AA404535, AA340839, AI814033, AI682171, AI719390, F32392, AA680411, AI268514, F10345, AA704675, R38445, R00088, T90966, R02355, AI742966, H79632, R38577, Z20180, D19917, AW419258, AI963625, AI345416, AI345612, AI345415, AL036705, N99088, AL041150, AA715307, AA809974, AL037582, AL037602, AI590043, AI699011, AI364788, AI623535, AI064830, AW161156, AL079728, AA761557, AL042544, AL036403, AI432644, AI581033, AI358701, AL110306, AW161202, AI929108, AW163554, AW020710, AL121270, AA748353, AW082113, AI866465, F30529, AI500061, AW440167, AL045500, AL119399, AI269862, AL046466, AI923989, AI249877, AW403717, AI582912, AI538885, AA641818, AL036631, AL038605, AL036638, AI567582, AW162194, AL043168, AW071417, AI698391, AW151136, AI538850, AI285439, AI582926, AI801793, AW087445, AI433157, AW020373, AI554821, AL121328, AI923509, AI539771, AI859991, AI537677, AL047763, AW021717, AI500659,</p>

	AI815232, AI801325, AI500523, AI582932, AI284517, AL043089, AI500706, AI491776, AI445237, AW151138, AI521560, AI889189, AI500662, AI284509, AI889168, AL120695, AI866573, AI633493, AI434256, AL110402, AI888661, AI284513, AI888118, AL037454, AI909696, AI340519, AI355779, AI440252, AI624543, AW117882, AI473536, AI433037, AW088899, AL038529, AI307557, AW059828, AW009337, AI344817, AI859464, AI335208, AI340603, AW051088, AI689420, AI620284, AI539800, AI251830, AI273179, AI805769, AL119457, AI919593, AA572872, AW129264, AI866581, AL119791, AI866469, AI345467, AW020419, AW160916, AI889147, AI537617, AI349598, AI621341, AI824576, AI241923, AW269097, AW163464, AI539153, AI371251, AW020406, AL043981, AI698401, AW083804, AI648567, AI690946, AL039276, AI344910, AI335363, AI969655, F35299, AI916419, AI623736, AI699865, AI624293, AA768046, AI494201, AL133741, AI683492, AL045163, AL036274, AL037030, AL042745, W38553, AI891125, AI828583, AL042628, AI887775, AI872423, AW172745, AI440239, AI611743, AW020876, AI568114, AW172723, AL042382, AI440263, AI584140, AL046618, AL041772, AI434242, AI500714, AI436429, AL039086, AW162189, AI254727, AI590943, AI371228, AI312210, AI473451, AI491710, AL043152, AW160905, AI344785, AI559872, AL047422, AI863197, AF044957, AR043114, X64898, A74894, I33392, AL137529, AL137480, I48978, AL117648, A65341, AL117460, I09499, AL137533, AF026816, AL133067, AF017437, A65340, A58545, AL049430, AL122100, AF106657, U96683, A08916, A08910, A08909, AB016226,

	AF126247, I89947, A08908, AF158248, A86558, U87620, AL137521, AR038969, AR034821, AL137479, AF090943, AL133072, A08913, AL122049, AJ012755, X92070, AL080148, AL133606, AL049382, AL049314, AL117457, AL137557, A08912, X06146, AJ006417, U49908, AL137463, I48979, AJ000937, M27260, S76508, AF078844, AR013797, I89931, AF111849, S68736, AF002985, AL133049, I49625, AF047716, AL117463, AL049938, AF031147, U58996, AL117435, AL080074, AL122050, I42402, U49434, AF146568, AL096751, U88966, I79595, AL122110, Y10823, AF118094, AL133080, A83556, AL137459, I17544, A03736, U72620, AR020905, AF113694, AF113019, AF090934, AF028823, Y11254, AL080234, AL122098, AF185576, X83508, AR038854, Y11587, X82434, E03348, Y16645, AF067728, X79812, AL049283, U95114, AF118070, AF065135, A77033, A77035, AF087943, A93350, AL137711, AL050116, AF113676, AF177401, X65873, U35846, AF102578, AL122121, AL035458, AL080124, AF111112, U67958, X84990, AF125948, AL110218, A18777, AR068753, AL137640, AF132676, AF061836, AL117583, E06743, AJ238278, AF017152, Z37987, AL080127, E07108, AL096744, AL133568, AL122118, AL133031, AF091084, AL049466, AF111851, AF090886, AL133010, AF104032, AF113013, I00734, E07361, AF100781, AL133637, X56039, X80340, AR029490, U90884, AL137271, AL133081, AL050172, AF210052, AF176651, AL137550, E00617, E00717, E00778, AL137547, AL137294, AB008792, E02221, S78214, I68732, AB008791, I89934, U77594, S61953, AF119337, X66862, Y10936, X62580, AL117416, AF079763, U55017, AF026124, S69510, AF125949, S77771, AL133077, AL050155, AL133619, L04504, AF008439, AL122123, X72889, A58524, A58523, AL133560, AL133093, I26207, AL110196, AR000496,

121	HSLEC18	722249	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2029 of SEQ ID NO:121, b is an integer of 15 to 2043, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:121, and where b is greater than or equal to a + 14.</p>	<p>U39656, A76335, E02349, AF183393, Y14314, AL023657, AF090901, X93495, AL133565, AF113691, A08907, AL050277, I09360, AF118090, AB007812, AL133075, AL110158, AF090900, AL133014, AL117394, AL050138, AL050393, E15569, X53587, AL034417, AL133640, AL117585, AL110221, AF061795, AF151685, AF058921, AL137658, AL133665, AL133113, A23630, AF079765, AC002467, AC004485, AF067790, Y10655, AF113689, S36676, AL050024, AF113699, AL137560</p> <p>N37065, AA826487, AA339231, AI733856, AA904211, AL138182, AA502991, AW328000, AI815210, AW026305, AI421950, AI419337, AA120920, AI696878, AI361090, AI573198, AA425924, AA503298, AL038842, AI859438, AA812684, AW238253, AA714110, AI962030, AL042373, AI612142, AA578621, C06004, AI799569, AW341978, AA832175, AA765925, AA483256, AA857812, AI049955, AA515728, AW327624, AI752365, AL047349, AI689198, AI025930, AA182731, AI904840, AI362442, AA846923, AA613624, AA598892, AI653776, AW274191, AA652834, AI762528, AI887235, AW410784, AA349193, AA833896, N73724, AA833875, AI583252, AI247101, AW082104, AI340832, AA302812, AA993636, AA664604, AW088631, AI306232, AI925065, AI823705, AW089016, AI824476, N68449, AW440368, N23504, AA228349, AW190484, AA595499, AL048275, AI207424, AA832444, AA548610, AL079734, AI583466, AA493226, AL118991, AI431513, AL037632, AA828047, AW081303, N41775, AI360558, AI275982, AL041375, AI821987, AI251576, AI610737, AI732869, AL031602, AC005231, AC007292, AL031311, AC005081, Z84466, AC004922, AC006211, AC002316, AF196779, AL133371, AL022723, AC007542, AL035414, U80017, AF030453,</p>
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	AC005015, AC004914, AC004213, Z95115, AC002551, AL121655, U62293, AL049776, AC006323, AL031681, AC005088, AL035684, AC002429, AC002996, AP000245, AL034379, AL049540, AC003667, AF207550, AC004821, Z82198, AC005037, AC005099, AL020997, AL031774, AD000813, AC002073, AP000501, AL079301, AL035587, AC005512, AF139813, AC006547, AC004813, AF184110, AC003025, AL031289, Z93023, AP000555, X54486, AC004477, AC005484, AL008637, AL031005, AC005786, AP000065, AC003029, AP000553, AL117354, AL031984, AC004659, AC005940, AC002378, AL135783, Z98036, AC002310, AC004990, AC006530, AC012627, AL035455, D88270, AC009516, AC005666, AC002477, AC002550, Z82214, AC009501, AC005921, AL034549, AP000275, Z93241, D86992, AL031659, AC003663, AC005670, AF111169, AL034376, AC005003, AC007371, AL049757, U63721, Z85986, AC007066, AC005722, AL050404, AC004253, AC005399, AL133246, AC007298, AC005548, AP000066, AC005280, AP000967, D86995, AC004883, AL034423, AL031575, AC002116, AC005412, AC006441, AC007358, AC004967, AF200465, AL049643, AC005881, AC003950, AC006581, AC007242, AC006071, AC004590, AL136295, AC006511, AC007488, AC007546, AC010077, M30688, AL121603, AC005519, AC004687, AL078634, AC004896, AC003071, AL096791, Z98752, Z85987, AC005363, AC008040, AC004815, AF064861, AC005803, AC007878, AC004148, AC004019, AC005751, AC005664, AL049761, AC007993, Y07848, AC002301, AF038458, AP000128, AP000206, AC004814, AC006261, AP000692, AC005011, AC005209, AC006468, AC006312, AL022165, AP000212, AP000134, AF001549, Z99716, AL121658, U82668, Z98051, AC002115, Z98884, AC002347,

				<p>AC004865, Z83844, AC005207, AB003151, AL035659, AP000688, AL139054, AC004983, Z69707, AL022320, AL049764, AC006057, AP000105, AP000037, AC006512, AC005480, AC000097, AC008115, AC002072, AC005899, AC006942, Z73417, AF102137, AC005318, AC003982, AP000310, Z97054, AL096766, AC002400, AC000026, AC005358, AP000289, AC002369, AC007216, AL021878, AC005777, AL079342, AL031729, AC006120, AP000354, AP000210, AP000132, AC004797, Z94721, AL023284, AB020873, AP000042, AP000110, AP000514, AC007277, AL035460, AC005300, AL049712, AC005932, AC005972, AP000350, AC007227, AC005900, AC005953, AP000213, AL022319, AC003037, AR036572, U91328, AC006013, Z85996, AC007649, AC006344, AL121934, AL021154, AL110502, AC005378, AC005544, AP000356</p>
122	HUFAC36	722258	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2863 of SEQ ID NO:122, b is an integer of 15 to 2877, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:122, and where b is greater than or equal to a + 14.</p>	<p>AW361997, AW362047, AW364154, AW362053, AW364497, AW363892, AI828567, AI560739, AW362017, AI559571, AI961395, AI922922, AI858291, AI601204, AI623850, AI679451, AI478715, AI922711, AI858408, AI457140, AI978816, AW150719, AI862126, AI923293, AI935885, AI870181, AI858824, AA588739, AA916673, AA555066, AW008365, AI860756, AI812031, AI923408, AI636160, AI827323, AW338713, AW150078, AI635039, AI420765, AI554505, AA582775, AI564401, AW177640, AW151832, AI433333, AI274367, AA418161, AI955997, AI640719, AI625261, AW191047, AI857830, AI588841, AI721066, AI858311, AI683781, AW361718, AI581904, AI373075, AI628535, AW364741, AI564624, AI587610, AA652197, AA553882, AI859018, AW193154, AI858269, W52120, AI445544, AW062541, AI659775, AI859238, AI417458, AW338495, AW298327,</p>

	AW364615, AW364573, AW351747, AI799729, AI565909, AI963778, AW192191, AI564392, W53028, AW363898, AW375899, AI799381, AI275979, AI559141, AW351538, AW364165, AI811969, AI867651, AI648422, AI422584, AA376957, C02400, AA366895, AA377282, AI669320, AI811793, AI933548, AA295047, AA417910, AI537846, AA372630, AI833145, AI824496, T34936, AI699868, T35412, AW002752, AI832493, AI982524, AI805205, AI985980, AI648451, AW376236, AA531507, AW376235, AI933787, AW366558, AW365133, AI601121, AW364616, AI659355, AW364639, AI561337, AI866055, T24880, AW351876, AI833173, AW364580, T24837, T35699, AI418084, AW364778, AW378106, AI588899, AW375551, AI564245, AW362832, AI540524, AI568068, C06052, T24521, AW361270, T24449, AI553666, AW364574, AW374350, T24582, AI721090, AI973152, T25155, AI635639, AW360840, AW364785, AI860027, AI669171, AI453248, AI690813, AI540674, AI538829, AI572717, AI918677, AI796743, AW105431, AW087191, AW194014, AL045496, AW089844, AI927233, AA937566, AI873550, AI049669, AI491775, AI537191, AI559752, AI683270, AI918809, AI699865, AI445829, AI342710, AI081740, R40363, AW083573, AI500658, AI630932, AI590043, AI440238, AW084396, AW103628, N25033, AI471909, AI621341, AW029216, AI815232, AI863002, AW105460, AW084896, AI539260, AF097021, I68732, AF026816, AF090903, D83032, U89295, X89602, AF199027, AF069506, AR022283, AR029490, AL023657, AF115410, AF061795, AF151685, AF017437, I89947, AL137537, AL049938, AF185614, AR038854, AL050277, X06146, AF124396, A60092, AL133665, A60094, AF031572, A77033, A77035, U87620, E12747, A21103, E03671,

123	HFFHB49	723136	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 667 of SEQ ID NO:123, b is an integer of 15 to 681, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:123, and where b is greater than or equal to a + 14.</p>	<p>AR068466, AL117438, AF040723, U38419, AF060555, AL133558, AF080068, AF200464, AL122121, AL133623, AL080139, U86379, I22020, AL080234, AL137281, AF161413, AL137550, AF167995, A08912, AF106657, X93328, AF008439, A08911, A65341, E12580, A93914, AL133047, I32738, X68497, X97332, AL137533, X83544, AF060866, AL133557, S76508, AJ001388, A15345, A26498, E12888, S63521, AF067728, AL117416, AF080622, S73498, AF102578, A58545, AR050959, AL133067, A07588, AF038847, X80340, AF026008, A21625, AL137665, AL080163, Z35309, AL049276, AL122103, AF090943, AF109683, I33392, AL117460, Z97214, A18777, A08907, AL080124, Y18680, AF087943, X70685, X72624, AF111849, U31501, AR034821, AF032666, A12522, AF111112, AF098484, AR066485, A76335, X52128, AL137554, AL110221, AF177401, AF054599, X52220, AL137548, AL136884, AF161699, Y16645, AB031064, AL080146, U57715, Z82022, AL133075, AF124728, AL137284, AF029750, AL133031, AF061943, X82397, AL109672, AL117626, AL049423, AF141289, M85165</p>
124	HFIBH05	725110	<p>Preferably excluded from the present invention are one or more</p>	<p>AA054421, T24430, AW206410, AI660910, AC004202, AP000518, AB023054, Y07828</p> <p>AA625451, AI089287, AA282874, AA398984, H72493, AA137263, AI434776, N33821, AA482849, H79114,</p>

125	HKIAA57	725201	<p>polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 592 of SEQ ID NO:124, b is an integer of 15 to 606, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:124, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1197 of SEQ ID NO:125, b is an integer of 15 to 1211, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:125, and where b is greater than or equal to a + 14.</p>	<p>R23405, R25093, AI983837</p> <p>AA166776, AI741792, AI675413, AI620910, AW027395, AI799988, AA659728, AA883923, AI361118, AI694798, R39993, AI421599, AI421231, AW299501, D53031, AI193736, AA166749, R73993, AA306989, D59334, W21931, AA918493, R73900, AA059363, AI368574, T10593, AA476990, R43798, AA410954, T10567, AB020676</p>
126	HRKAB52	726122	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 867 of SEQ ID NO:126, b is an integer of 15 to 881, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:126, and where b is greater than or equal to a + 14.</p>	<p>AL047265, AI733029, AI810538, AI291282, AI346511, AI288746, AI340353, AI318112, AI301846, AI304527, AI274206, AA878571, AI147583, AW204451, AW129463, AW075794, AI830488, AA812848, T68446, AA732362, T93796, AI720888, AA906537, AI681040, Z79996, AC002394, AC006059, Z95126, AC007198, AL022336, AC007065, AC004220, AC002980, AL024493, AC005549, AF181449, U91325, AL021182, AC007380, AC005228, Z82205, Z83826, AC004551, AC003119, AF039905, AP000292, AP000043, AP000111, AL008626, AC002992, U80460, AC004088</p> <p>AA007664, AI803958, AI167454, AI968968, AI247561, AA148881, AA007627, AI375078, W23292</p>
127	HPCAN95	727365	<p>Preferably excluded from the present invention are one or more</p>	

128	HCQCV54	729143	<p>polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 903 of SEQ ID NO:127, b is an integer of 15 to 917, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:127, and where b is greater than or equal to a + 14.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1273 of SEQ ID NO:128, b is an integer of 15 to 1287, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:128, and where b is greater than or equal to a + 14.</p>	N45700, H63509, H54749, AA789241, AI073405, AL137699
129	HLJEA54	729231	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 589 of SEQ ID NO:129, b is an integer of 15 to 603, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:129, and where b is greater than or equal to a + 14.</p>	AI079148, AA532656, AP0000548, AL031120, AP000365
130	HTWCR70	731881	<p>Preferably excluded from the present invention are one or more</p>	AI246796, AA847499, AL047080, N22516, AA504694, T40848, R91796, AA492015, AA503468, N70293,

		<p>polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 518 of SEQ ID NO:130, b is an integer of 15 to 532, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:130, and where b is greater than or equal to a + 14.</p>	<p>AW024018, AW028943, AI886629, F04766, AL038901, AI249688, AI491828, AL038533, N23846, AI963045, AA515138, AW274182, AI916406, AW302711, AA535937, AW439480, AA488746, AA515727, AJ246003, AC006241, AC007421, AL121658, U91323, AL109623, AC002558, AL096701, AL009181, AC002551, AC006449, AC005480, AC007055, AC004382, AL035086, AC007283, AC004263, AC007546, AC002091, AC000379, AC003101, U95742, AC005527, AL139054, AC005399, AL049829, AC004983, AC005529, AL050307, AP000553, AF196969, AC005488, AC005225, AL133245, AL049576, AC005015, AC007225, AL022165, AC004638, AC004703, AL031432, U91321, AC007216, AC000353, AC000025, AC007050, U62293, AC007637, AC002565, AL080243, AL121603, AC005231, AL049830, AF109907, AC006537, AP000692, AC005288, AC004131, AC005180, Z95113, AL022476, AF196779, AC002312, AL109758, AC005920, AC016025, AC005914, AL031588, AC004408, AC006120, AC004686, AL096791, AC004491, AL009183, AC004858, AF134726, AC004383, AC005520, AC004859, AC004813, AL049843, Z98941, AP000212, AP000134, AC005089, Z83840, AC006211, AC006960, U96629, AC005091, AF001549, AC002300, AC006157, AC002288, AC004883, Z98884, AC007151, AC004953, AL031680, AC005933, AC005081, AC007666, AL079342, AC002470, AC004967, AL035413, AC005257, AP000030, AC003043, AC007227, AL031985, AC004257, AP000248, AC006088, AL031577, Z82244, AL022318, AC004999, AC002996, AC005823, AC005972, AC005280, U80017, AC002070, AC004820, AL023807, AC006530, AC007226, AC002310, AL049692, AC004675, AL133382, AL133163, AL031283, AC007114, AL049776, AC006111, AL109613, AC004019,</p>
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				AL031984, AC006312, AF053356, AC007371, Z98051, AL034548, Z97055, AC006141, AP000141, AC005702, AC002352, AL078638, AC005632, Z95152, D87675, AL109628, AC005839, Z82201, AC005740, AC005932, AF001552, AL049872, U82668, AC005207, AC005412, AP000065, AC002045, AC004812, AC004134, AC006121, AC005264, AF165926, AC002477, AC004106, AC004531, AL050341, AL022238, AC004583, AC006538, AF111168, AC004217, AC005037, AC005829, AC007124, Z84469, AF067844, AL020997, Z84480, AL035420, AL049709, AL024507, AC004955, AC005082, AC006501, AC000159, AC004596, AC005484, AC005210, AC006441, AC002059, AL031311, AC004098, AL135744, AC006254, AC010205, AL035461, AC000004, AC004991, AF139813, AC012384, AC007370, AC005531, AL049780, AC005874, AF134471, AC016830, AL031685, AL021546, AL035400, AC005776, AC003002, AC002400, AL132642, AL021938, AP000689, AC007685, AC004685, U47924, Z84466, AL034555, AF207550, AL031602, AB003151, AC005031, AC008372, AL049869, AC009731, AC000052, AL022323, AC003071, AP000211, AC002126, AC004067, AL122023, AL133448, AC009721, AP000555
131	HSXDD55	732280	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 762 of SEQ ID NO:131, b is an integer of 15 to 776, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:131, and where b is greater than</p>	H19388, AA121710, H12126, AA429913, AA446069, AW104301, AB002349

132	HSTAB63	732932	<p>or equal to $a + 14$.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 675 of SEQ ID NO:132, b is an integer of 15 to 689, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:132, and where b is greater than or equal to $a + 14$.</p>	<p>AI633551, AA825156, AA459252, AA379178, AA193434, H84915, AI478844, AI572369</p>
133	H6BSI11	733034	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 541 of SEQ ID NO:133, b is an integer of 15 to 555, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:133, and where b is greater than or equal to $a + 14$.</p>	<p>AI654484, AI675680, AA779583, AA922674, AA776643, AI927651, T65302, AI802381, AI004237, N29771, T16284, AW117573, AI688100, AW299953, AA468748, AI095730, AW137454, Z38671, T30227, AA627776, AI474940, F09810, F04332, AA373631, AI916074, AI810865, AI682308, AI522209, AA190709, AI766752, AW139240, AA095317, AL122036, X99270, U82695</p>
134	HDQPP57	734012	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 776 of SEQ ID NO:134, b is an integer of 15 to 790, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:134, and where b is greater than</p>	<p>H80171, AA971126, T80926</p>

135	HAGEX59	735603	<p>or equal to $a + 14$.</p> <p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1394 of SEQ ID NO:135, b is an integer of 15 to 1408, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:135, and where b is greater than or equal to $a + 14$.</p>	<p>W39020, T74318, H23063, Z43413, F12669, AA436729, AI138441, AI400746, AL035409</p>
136	HAVMG19	739061	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 888 of SEQ ID NO:136, b is an integer of 15 to 902, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:136, and where b is greater than or equal to $a + 14$.</p>	<p>AA043107, AA460757, AA808519, AA482341, AW088728, AL041651, AI305256, AA885398, AI808361, D53182, AI689825, AI123220, N99552, AW130266, AA861771, AA040860, AI278439, AA134816, W87524, W89049, AI301074, AA927150, W87525, AI086181, AI683247, AI633628, AI301808, AW236826, AA339816, AA649134, AA806264, AI078052, AA460158, AA909561, R46365, R54321, AI472152, T23855, AI769853, AW074642, W57681, AA039402, AW072224, T80969, AA991845, AI472163, AI831540, AI686045, AA716427, AA029761, T97173, AI738802, T81108, R67010, AA482244, W89104, R49077, T40888, AI583709, N71544, AB028951, AL122055</p>
137	HLEAL50	741134	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 716 of SEQ ID NO:137, b is an integer of 15 to 730, where both a and b correspond to the positions of</p>	<p>AA745961, AI110640, AA581433, AW419403, AL119355, AA843874, AA309370, AI439860, AI887321, AW130042, AA174085, AI110720, AL133942, AW177226, AA601264, AW177120, AI818151, AW150375, AA152091, AW089864, AI925647, AW157413, AI983921, AI927861, AI367384, AI858607, AA493735, AW089655, W03759, H97952, AI811494, AW190486, AI761656, AI685116, AW167319, AI610776, AA679519, AI688902,</p>

nucleotide residues shown in SEQ ID NO:137, and where b is greater than or equal to a + 14.	<p>AI732743, AA493998, AL137994, AI872415, AI264673, AI334099, AA136637, AA659014, AL044349, AA189081, AA130536, AA773359, H64113, AI924175, AA767353, AA631430, AI874256, AW177231, AW235478, N24958, AI088796, W49501, AW090739, AW090210, AI801377, AW151307, AI749571, AI376984, AI817158, AA778304, AI082077, AI433018, AI735074, AI675848, AI819528, AI568919, AI862874, AL041411, AI147839, N64574, AW074001, C06012, N76274, T16214, AA598786, AA932087, AI963795, AW167452, AI627862, AI479035, AA427754, AI860964, AI499811, AW440317, H90881, AW073349, AI110786, AI189033, AA121916, AA130476, AA152017, AI590151, AI733728, AA663566, W87732, AI811854, W58442, AW084901, N26540, N79242, AL036881, T69719, AL041417, R80440, AI250812, AI418614, AW168798, AI346802, AW242735, AI591192, AW139132, AI628043, AA868708, AA055654, AA953572, AI499286, AW004844, AA287329, AI091583, AI114529, AA346162, AA176355, AL133889, AA501873, AA807609, R91915, AI133073, AI570877, AA709024, AI557354, AA878800, AI375534, AA911409, AA135303, AW242205, AA470572, AI246569, HI2832, AA946637, AI832184, R48563, AI453790, H91008, AI110627, AA654837, AL043039, AA081993, AI025602, AI272961, T41165, M62281, H73189, AA854527, AI560839, AI696653, AI921101, AI632138, AA889273, AI538654, AW083198, AW102963, AI095849, AA363058, AI973178, T69889, T06932, AA862481, AA524883, AI862212, AA771730, R94240, AA825161, AI291353, AC008394, AL079352, AL031663, AL136018, AL109799, U20230, AL049794, AF064866, AC008064, K00628, AC003082, AC004467, AL049561, AC005194, L29074, AC009320, AP000687, AJ229041, AC005138,</p>

	AL117339, AC005034, AL031903, AC004070, AL049734, Z80107, AL022401, AC007370, AL122126, AC005951, AC003081, AC007671, AC003686, AC005939, AC005016, AL022576, AL132718, AL035411, AC005823, AC006362, AL022397, AC008082, AC006070, Z75741, AC004081, AF198095, AC007372, AC005509, AC008170, Z81001, AC010168, Z81007, AC006561, Z76735, AC004750, AL035088, Z83827, AC010382, AC004647, AF020802, AL009173, AL031676, AC004957, AC006484, AC002556, AC004063, AC003969, AC006578, AC007319, Z83820, AC004454, AL121578, AC006371, AF064864, AC006197, AL033403, AC006037, AF064860, AL034399, AC006032, AE000659, AC004057, AL034369, AC000377, AL133512, AL049837, AC005045, AC006971, AC000114, AL009172, Z99495, AC005213, AC009479, Z82899, AC006206, AC006226, AC005392, AL133381, AC004538, AF128525, AC005610, AC007243, AL050306, AC002288, AL050308, AC004470, Z96810, AL009174, AC005386, AL021326, AC003016, Z93928, AC004959, AJ006345, AL030996, Z83819, AL033521, AL096829, AC004048, AL121767, AL033397, AL049546, AF165142, AC005859, AC006946, AP000473, AL031655, AL034403, AL021068, AC006144, Z98255, AC006548, AL022161, AC002524, AL049564, AB033055, AL109759, AL049775, AC010849, AC007110, Z70225, Z82242, AC007543, AL049565, AL049828, AC004783, AC005352, AC004911, AL078474, Y10196, AL121782, AC006316, AL109662, AL133249, AL009176, AL049691, AF188025, AC004535, AC006455, AC007090, AC002367, AJ006343, AC004820, AC004907, AL008710, AL034408, AL031673, AL031985, AP000536, AC007364, AL023283, AL022151, AC005221, AC007450, AC005017, AC005066, AP000474, AC004869, AC004415,

138	HCPAC07	741257	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 510 of SEQ ID NO:138, b is an integer of 15 to 524, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:138, and where b is greater than or equal to a + 14.</p>	<p>AC004158, AL133239, AL121838, AC006112, AC006324, AL022577, AC007402, AC004674, AJ272265, AC002526, AL022146, AC002452, AC006504, AC004082, AC005184, AC008009, AL033379, Z72001, AF002991, AC002478, AF165175, AC005201, AL031114, Z70232, AC002070, AC004949, AC004831, AL049642, Z94055, Z70049, AP000014, AC004128, AC004006, AC007971, AL117326, U80460, AC000111, AL049710, AC003693, AL096773, AP000454, AC000056, AC005873, AP000127, AP000205, Z75747, AL121757, AP000948, Z84720, AL034561, AC004917, U58675, AC006002, AC007535, AL035427, Z92545, AL049176, AL031782, AL031586, AC005271, AC005050, AL117325, AL079303, AP000244, AC002422, AC007628, AC004130, AL109753, Z69649, AP000496, AB023054, AC004677</p>
139	HOSEQ61	741804	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 855 of SEQ ID NO:139, b is an integer of 15 to 869, where both a and b</p>	<p>AA729528, AI659354, H92153, AI609659, AC007842</p> <p>AI191412, AI917623, AW188995, AI817093, AI682959, AI352688, AI684692, AI921724, AI742357, AA932743, AI920893, AI056062, AW080580, AW264806, AI684110, AI399967, AI288672, N47530, AI025387, R37474, AI399768, AI082088, AI051895, AI670819, AA992114, AW172410, AA804760, AI277609, AI419244, AI581273, AW264450, AI690471, AI201792,</p>